OM of: US-09-019-441-1 to: PIR_71:*    out_format : pfs

Date: Sep 23, 2002 10:02 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US0901941/runat_23092002_095258.6306/app_query.fasta_1.1860
-DB=PIR_71 -QFMT=fastan -SUFFIX=rpr -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -USER=US09019441_@CGN1_1_227
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-019-441-1
Query length: 390
Database: PIR_71:*
Database sequences: 283138
Database length: 96089334
Search time (sec): 132.110000

score_list:

| Sequence | Strd | Orig | ZScore | EScore | Len | Documentation |
|---|---|---|---|---|---|---|
| pir2:S16848 | + | 579.00 | 880.71 | 4.2e-41 | 136 | ! Ig lambda chain V-II region pre |
| pir2:S25758 | + | 559.00 | 846.73 | 1.9e-39 | 235 | ! Ig lambda chain - human |
| pir2:S14675 | + | 557.00 | 843.71 | 2.8e-39 | 235 | ! Ig lambda chain - human |
| pir2:S25759 | + | 544.00 | 824.04 | 3.5e-38 | 235 | ! Ig lambda chain - human |
| pir2:S04519 | + | 528.00 | 804.52 | 8.6e-37 | 136 | ! Ig lambda chain precursor V-II |
| pir2:S44105 | + | 490.50 | 748.15 | 1.2e-33 | 112 | ! Ig lambda chain V-J region - hu |
| pir2:S19671 | + | 478.00 | 729.30 | 1.4e-32 | 111 | ! Ig lambda chain V region (clone |
| pir2:S51149 | + | 473.50 | 722.55 | 3.4e-32 | 110 | ! antibody light chain v region |
| pir2:S46396 | + | 470.00 | 717.19 | 6.7e-32 | 111 | ! Ig lambda chain V region - huma |
| pir2:S31515 | + | 469.50 | 716.38 | 7.3e-32 | 112 | ! Ig lambda chain V region - huma |
| pir2:S36281 | + | 468.00 | 714.17 | 9.3e-32 | 111 | ! Ig lambda chain V region (clone |
| pir2:S44123 | + | 466.50 | 711.84 | 1.3e-31 | 112 | ! Ig lambda chain V-J region - hu |
| pirl:L2HUMC | + | 461.00 | 703.58 | 3.8e-31 | 111 | ! Ig lambda chain V-II region (Mc |
| pirl:L2HUNG | + | 460.50 | 702.76 | 4.2e-31 | 112 | ! Ig lambda chain V-II region (Ni |
| pir2:S46395 | + | 460.50 | 702.76 | 4.2e-31 | 111 | ! Ig lambda chain V region - huma |
| pir2:S57412 | + | 460.00 | 702.13 | 4.6e-31 | 110 | ! Ig lambda chain V-J region - hu |
| pirl:L2HUTR | + | 460.00 | 702.07 | 4.6e-31 | 111 | ! Ig lambda chain V-II region (Tr |
| pir2:S36057 | + | 458.00 | 699.82 | 6.9e-31 | 99 | ! Ig lambda chain - human (fragme |
| pir2:S38497 | + | 458.00 | 699.04 | 6.8e-31 | 111 | ! Ig lambda chain - human (fragme |
| pir2:S36056 | + | 457.00 | 698.31 | 8.4e-31 | 99 | ! Ig lambda chain - human (fragme |
| pir2:S46397 | + | 457.00 | 697.53 | 8.3e-31 | 111 | ! Ig lambda chain V region (VL-16 |
| pirl:L2HUNI | + | 456.00 | 696.01 | 1.0e-30 | 111 | ! Ig lambda chain V-II region (Ne |
| pir2:S36256 | + | 454.00 | 692.99 | 1.5e-30 | 111 | ! Ig lambda chain V region (clone |
| pirl:L2HUVL | + | 453.00 | 691.48 | 1.8e-30 | 111 | ! Ig lambda chain V-II region (Vi |
| pir2:S57442 | + | 448.00 | 683.97 | 4.8e-30 | 110 | ! Ig lambda chain V-J region - hu |
| pirl:L2HUBH | + | 443.00 | 676.35 | 1.3e-29 | 111 | ! Ig lambda chain V-II region (Bc |
| pir2:S36055 | + | 439.00 | 671.07 | 2.8e-29 | 99 | ! Ig lambda chain - human (fragme |
| pirl:L2HUBR | + | 439.00 | 670.42 | 2.7e-29 | 109 | ! Ig lambda chain V-II region (Bu |
| pirl:L2HUBO | + | 437.00 | 667.27 | 4.9e-29 | 111 | ! Ig lambda chain V-II region (Bc |
| pirl:L2HUTG | + | 436.00 | 665.76 | 4.9e-29 | 111 | ! Ig lambda chain V-II region (Tc |
| pirl:L2HUWN | + | 435.00 | 664.25 | 5.9e-29 | 111 | ! Ig lambda chain V-II region (Wi |
| pir2:S19673 | + | 429.00 | 655.17 | 1.9e-28 | 111 | ! Ig lambda chain V region (clone |
| pir2:S38499 | + | 426.00 | 650.63 | 3.4e-28 | 111 | ! VL lambda protein (RH-E1) - hum |
| pir2:S36058 | + | 425.00 | 649.90 | 4.2e-28 | 99 | ! Ig lambda chain - human (fragme |
| pir2:S25746 | + | 423.50 | 641.72 | 5.0e-28 | 236 | ! Ig lambda chain - human |
| pir2:S09712 | + | 414.00 | 631.40 | 3.4e-27 | 130 | ! Ig lambda chain v region - huma |
| pir2:S05270 | + | 412.00 | 624.35 | 4.7e-27 | 235 | ! Ig lambda chain precursor - hum |
| pir2:S78057 | + | 411.00 | 626.86 | 6.1e-27 | 130 | ! Ig lambda chain precursor V-J r |
| pir2:S78058 | + | 409.00 | 623.89 | 9.0e-27 | 129 | ! Ig lambda chain precursor V-J r |
| pir2:S25752 | + | 407.00 | 616.85 | 1.2e-26 | 233 | ! Ig lambda chain - human |
| pir2:S23626 | + | 406.50 | 619.13 | 1.4e-26 | 149 | ! Ig lambda chain V region' - h |
| pir2:S25744 | + | 406.00 | 615.33 | 1.5e-26 | 233 | ! Ig lambda chain - human |
| pir2:S12627 | + | 405.00 | 618.45 | 2.0e-26 | 118 | ! Ig lambda chain precursor v |
| pir2:S25742 | + | 404.00 | 612.34 | 2.2e-26 | 232 | ! Ig lambda chain - human |
| pir2:S25754 | + | 402.50 | 609.98 | 3.0e-26 | 235 | ! Ig lambda chain - human (fra |

seq_name: pir2:S16848

seq_documentation_block:
Ig lambda chain V-II region precursor - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S60297; S16848
R;Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.
Immunol. Lett. 34, 57-62, 1992
A;Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive
A;Reference number: S60295; MUID:93122853
A;Accession: S60297
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <KU2>
A;Cross-references: EMBL:X62125; NID:g38334; PIDN:CAA44056.1; PID:g38335
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-111/Domain: immunoglobulin homology <IMM>

alignment_scores:
                 Quality:    579.00          Length:      130
                 Ratio:        4.669          Gaps:          0
    Percent Similarity:       95.385    Percent Identity:   82.308

alignment_block:
US-09-019-441-1 x S16848

Align seg 1/1 to: S16848   from: 1  to: 136

    1 ATGGCCTGGACTCTGCTCCTCCTCACCCTCCTCACTCAGGGCACAGGATC  50
      ||||||||||:::||||||||||||:::||||||||||||||||||||||
    1 MetAlaTrpAlaLeuLeuLeuLeuThrLeuLeuThrGlnGlyThrGlySe  17

   51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCCGTGTCTGGGTCTCCTG  100
      ||||||||||||||||| ||||||||||:::||||||||:::||||||||
   17 rTrpAlaGlnSerAlaLeuThrGlnProProSerAlaSerGlySerProG  34

  101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGGATGACGTTGGTGGT  150
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   34 lyGlnSerValThrIleSerCysThrGlyThrSerSerAspValGlyAla  50

  151 TATAACTATGTCTCCTGGTACCAACACCAGCAAGCCCCAAACT  200
      ||||||||||:::||:::||||| ||||||||| |||||||||
   51 TyrAsnTyrValSerTrpTyrGlnHisProGlyLysAlaProLysLe  67

  201 CATGATTATGATGTCCTAAGCGGGCCTCAGGGTCTCAGGGTCTCGATGCGTTCT  250
      ||||:::|||:::|||:::||||| |||||||| ||||||||
   67 uMetMetTyrGluValSerGluArgProSerGlyValProAspArgPhes  84

  251 CTGGCTCCAAGTCTGGCCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG  300
      |||||||||||||||||:::||||||||||||||||:::||||||||||||
   84 erGlySerLysSerGlyAsnThrAlaSerLeuThrValSerGlyLeuGln  100

  301 GCTGAGGACGAGGCTGATTATTACTGTTGTTGTCATATACAACCAGTAGCAC  350
      ||||||||||||||||||||||||||||||||||||:::||||||||
  101 AlaGluAspGluAlaAspTyrTyrCysThrSerTyrAlaGlySerAsnSe  117

  351 TTTGTTATTCGGAAGAGGGACCCGGTTGACCCTCCTAGGT  390
      :::::|||||| ||||:::|||||:::||||||||||||
  117 rPheValPheGlyThrGlyThrLysValThrValLeuGly  130

seq_name: pir2:S25758

seq_documentation_block:
Ig lambda chain - human

C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25758
R;Combriato, G.; Klobeck, H.G.
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162
A;Accession: S25758
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-235 <COM>
A;Cross-references: EMBL:X57823; NID:g33745; PIDN:CAA40960.1; PID:g33746
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;150-218/Domain: immunoglobulin homology <IMM>

alignment_scores:
        Quality:    559.00             Length:    130
        Ratio:      4.620              Gaps:      0
Percent Similarity:  93.077   Percent Identity:  81.538

alignment_block:
US-09-019-441-1 x S25758

Align seg 1/1  to: S25758   from: 1  to: 235

  1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCCTCACTCAGGGCACAGGATC  50
    ||||||:|||||||||:||||||||||||||||||||||||||||||||||
  1 MetAlaTrpAlaLeuPheLeuThrLeuLeuThrGlnGlyThrGlySe  17

 51 CTGGGCTCAGTCGCCCGACTCAGCCTCCTCTGTGTCTGGGTCTCCTG  100
    ||||||||||| |||||||  |||||||||  |||||||||||||||||
 17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG  34

101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT  150
    |||||||||||:||||||||:::|||||:|||||::||||||:|||||:||
 34 lyGlnSerValThrIleSerCysThrGlySerSerSerAspValGlyGly  50

151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACT  200
    |||||||||||||||||||||||||:|||||::||||||||||||||||
 51 TyrAsnTyrValSerTrpTyrGlnHisProGlyLysAlaProLysLe  67

201 CATGATTTATGATGTCCTAAGCGGCCTCTGATCCGCTTCT  250
    |||||||  ::|||||||||||  ||||| :::|||||||||
 67 uMetIleTyrAspValThrAsnArgProSerGlyValSerAsnArgPheS  84

251 CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG  300
    ||||||||||||||||||||||||||||||||||||||||||||||||
 84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln  100

301 GCTGAGGACGAGGCTGATTATTACTGTTCATATAACAACCAGTAGCAC  350
    |||||||||||| |||| |||:::||||
101 ProGluAspGluAlaAspTyrTyrCysSerTyrLysThrSerSerSerPh  117

351 TTTGTTATTCGGAAGAGGACCCGGTTGACCGTCCTAGGT  390
    :||:||||||||||||||||||||||||||||||||||
117 eTyrValPheGlyThrGlyThrLysValSerValLeuGly  130

seq_name: pir2:S14675

seq_documentation_block:
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000
C;Accession: S14675; S12445
R;Vasicek, T.J.
submitted to the EMBL Data Library, February 1990
A;Reference number: S16439; MUID:91257162
A;Accession: S14675
A;Molecule type: DNA
A;Residues: 1-235 <VAS1>
A;Cross-references: EMBL:X51754

R;Vasicek, T.J.; Leder, P.
J. Exp. Med. 172, 609-620, 1990
A;Title: Structure and expression of the human immunoglobulin lambda genes.
A;Reference number: S12440; MUID:90324881
A;Accession: S12445
A;Molecule type: DNA
A;Residues: 1-129 <VAS2>
A;Cross-references: EMBL:X51754
C;Genetics:
A;Introns: 16/1; 130/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;150-218/Domain: immunoglobulin homology <IMM>

alignment_scores:
        Quality:    557.00             Length:    130
        Ratio:      4.528              Gaps:      0
Percent Similarity:  94.615   Percent Identity:  80.000

alignment_block:
US-09-019-441-1 x S14675

Align seg 1/1  to: S14675   from: 1  to: 235

  1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCCTCACTCAGGGCACAGGATC  50
    ||||||:|||||||||:||||||||||||||||||||||||||||||||||
  1 MetAlaTrpAlaLeuPheLeuThrLeuLeuThrGlnGlyThrGlySe  17

 51 CTGGGCTCAGTCGCCCGACTCAGCCTCCTCTGTGTCTGGGTCTCCTG  100
    ||||||||||| |||||||  |||||||||  |||||||||||||||||
 17 rTrpAlaGlnSerAlaLeuThrGlnProSerAlaSerGlySerLeuG  34

101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT  150
    |||||||||||:||||||||:::|||||:|||||::||||||:|||||:||
 34 lyGlnSerValThrPheSerCysSerSerSerAspIleGlyAsn  50

151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACT  200
    |||||||||||||||||||||||||:|||||::||||||||||||||||
 51 TyrAsnTyrValSerTrpTyrArgGlnHisProGlyLysAlaProLysLe  67

201 CATGATTTATGATGTCCTAAGCGGCCTCAGGGGTCTCGATCGCTTCT  250
    |||||||  ::|||||||||||  |||||||  :::|||||||||
 67 uMetIleTyrGluValThrLysArgProSerGlyValProAsnArgPheS  84

251 CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG  300
    ||||||||||||||||||||||||||||||||||||||||||||||
 84 erGlySerLysSerGlyAsnThrAlaSerLeuThrValSerGlyLeuGln  100

301 GCTGAGGACGAGGCTGATTATTACTGTTCATATAACAACCAGTAGCAC  350
    |||||||||||| |||| |||:::||||
101 AlaGluAspGluAlaAspTyrTyrCysSerSerTyrAlaGlySerAsnSe  117

351 TTTGTTATTCGGAAGAGGACCCGGTTGACCGTCCTAGGT  390
    :||:::||||||||||||||||||||||||||||||||
117 rLeuIlePheGlyGlyGlyThrArgLeuThrValLeuGly  130

seq_name: pir2:S25759

seq_documentation_block:
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25759
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A;Reference number: S16439; MUID:91257162
A;Accession: S25759
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-235 <COM>
A;Cross-references: EMBL:X57824; NID:g33747; PIDN:CAA40961.1; PID:g33748

## Left block

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C;Superfamily: immunoglobulin; immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetraner; immunoglobulin
F;150-218/Domain: immunoglobulin homology <IMM>

alignment_scores:
       Quality:   544.00            Length:    130
         Ratio:     4.496            Gaps:        0
Percent Similarity:  93.077    Percent Identity:  78.462

alignment_block:
US-09-019-441-1 x S04519

Align seg 1/1  to: S25759  from: 1  to: 235

  1 ATGGCCTGGACTCTGCTCCTCCTCACCCTCCTCACTCAGGCCACAGGATC  50
    ||||||||||||||||||||||||||:::::||||||||||||||||||
  1 MetAlaTrpThrLeuLeuPheLeuLeuThrLeuLeuThrGlnGlyThrGlySe  17

 51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTG 100
    ||||||||||||  ||||||||  ||||||||||||||||||||||||
 17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG  34

101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGT 150
    ||||:::|||::||||||||||||  ||||||||||::::||||||:::
 34 lyGlnSerIleThrIleSerCysIleGlyThrSerSerAspIleGlyAla  50

151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCCAAACT 200
    |||  :::||||||||||||||  ||||||||||||||||||||||||
 51 TyrTyrPheValSerTrpTyrGlnGlnTyrProGlyLysAlaProLysLe  67

201 CATGATTTATGATGTCCTCAGGGGTCTCTCGATGATCGCTTCT 250
    |::::||:::||||||  |||||:::||::||||||
 67 uLeuIlePheAspValSerGlyArgProSerGlyIleSerSerArgPheS  84

251 CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
    ||||||||||||||||||||||||||||||||||||||:||||||||
 84 erGlySerLysSerGlySerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100

301 GCTGAGGACGAGGCTGATTATTACTGTTCTCATATACAACCAGTAGCAC 350
    ||||||||||||||||||||:::::||||||||:::|||||||
101 AlaGluAspGluAlaAspTyrTyrCysSerTyrAlaArgSerSerTh 117

351 TTTGTTATTCGGAAGAGGGACCCCGTTGACCGTCCTAGGT 390
    |::::||||  ||||  ||::||||||||||
117 rValValPheGlyGlyGlyThrServalThrValLeuGly 130
```

```
seq_name: pir2:S04519

seq_documentation_block:
Ig lambda chain precursor V-II region (2.1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S04519
R;Brockly, F.; Alexandre, D.; Chuchana, P.; Huck, S.; Lefranc, G.; Lefranc, M.P.
Nucleic Acids Res. 17, 3976, 1989
A;Title: First nucleotide sequence of a human immunoglobulin variable lambda gene belong
A;Reference number: S04519; MUID:8928402
A;Accession: S04519
A;Molecule type: DNA
A;Residues: 1-118 <BRO>
A;Cross-references: EMBL:X14616; NID:g33749; PIDN:CAA32770.1; PID:g736248
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetraner; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-118/Product: Ig lambda chain V-II region #status predicted <MAT>
F;34-111/Domain: immunoglobulin homology <IMM>

alignment_scores:
       Quality:   528.00            Length:    118
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## Right block

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                   Ratio:     4.757            Gaps:        0
Percent Similarity:  94.068    Percent Identity:  85.593

alignment_block:
US-09-019-441-1 x S04519

Align seg 1/1  to: S04519  from: 1  to: 118

  1 ATGGGCTGGACTCTGCTCCTCCTCACCCTCCTCACTCAGGCACAGGATC  50
    |||||||||||||||||||:::||||||||||||  ||||||||||||
  1 MetAlaTrpAlaLeuLeuLeuLeuThrLeuLeuThrGlnAspThrGlyLySe  17

 51 CTGGGCTCAGTCAGCTGCCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTG 100
    ||||||||||||  ||||||||  ||||||||||||||||||||
 17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG  34

101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGT 150
    ||||:::|||:||||||||||||||||||||||||::::||||||:::
 34 lyGlnSerIleThrIleSerCysThrGlyThrSerSerAspValGlySer  50

151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCCAAACT 200
    |||| ||||||||||||||||:::||||||||||||||||||||||
 51 TyrAsnLeuValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLe  67

201 CATGATTTATGATGTCCTAAGCGGGCCTCAGGGGTCTCTGATCGCTTCT 250
    |::::||::     ||||||||||:::||::||||||||||||||
 67 uMetIleTyrGluGlySerLysArgProSerGlyValSerAsnArgPheS  84

251 CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
    |||||||||||||||||||||||||||||||||||||||||||||
 84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100

301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC 350
    |||||||||||||||||||||:::::||||||||:::|||||||
101 AlaGluAspGluAlaAspTyrTyrCysSerTyrAlaGlySerSerTh 117

351 TTTG 354
    ||||
117 rLeu 118
```

```
seq_name: pir2:S44105

seq_documentation_block:
Ig lambda chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44105
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variabl
A;Reference number: S44105
A;Accession: S44105
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-112 <HAW>
A;Cross-references: EMBL:Z31388; NID:g472959; PIDN:CAA83263.1; PID:g940517
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

alignment_scores:
       Quality:   490.50            Length:    112
         Ratio:     4.671            Gaps:        1
Percent Similarity:  93.750    Percent Identity:  84.821

alignment_block:
US-09-019-441-1 x S44105

Align seg 1/1  to: S44105  from: 1  to: 112

 58 CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTC 107
    ||||||||||  ||||||||||||||||||||||||||||||||||||
```

```
  1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17

108 GGTCACCATCTCCTGTCACTGGAACCAGCCATGACGTTGGTGTTATAACT 157
    |:::|||||||||||||||||||||:::||||||||||||||||||||||
 17 rIleThrIleSerCysThrGlyThrSerSerAspValGlyValTyrAsnT 34

158 ATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACTCATGATT 207
    |||||||:::||:|||||||||||||||||||||||||||||||||||||
 34 yrValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuMetIle 50

208 TATGATGTCGCTAGGCAGGGGCCTCAGGGGTCTCCTGATCGTTCTCTGGCTC 257
    |||||||||||:::||| |||||||||||||||||||||||||||||||||
 51 TyrAspValSerArgProSerGlyValSerAsnArgPheSerGlySe 67

258 CAAGTCTGCAACACGGCCTCCCTGACCATCTCGGCTCCAGGCTGAGG 307
    |||||||||||||||||||:|||||||||||||||||||||||||||
 67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84

308 ACGAGGCTGATTATTACTGTGTTCATATACAACCAGTAGCACT...TTG 354
    |||||||||||||||||||| ||||||||||:::|||||||||
 84 spGluAlaAspTyrTyrCysValHisIleGlnProValAlaLeu...Leu 100

355 TTATTCGGAGAGGAGGGACCCGGTTGACCGTCCTAGGT 390
    :::|||||| ||||||::||||||||||||||||||||
101 ValPheGlyThrGlyThrLysValThrValLeuGly 112

seq_name: pir2:S19671

seq_documentation_block:
Ig lambda chain V region (clone alpha-TEL13) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19671; S25460
A;Reference number: S24442
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
   J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on pha
A;Reference number: S19663; MUID:92085276
A;Accession: S19671
A;Molecule type: mRNA
A;Residues: 1-111 <MAR>
A;Cross-references: EMBL:X61643
R;Jones, P.T.
   submitted to the EMBL Data Library, October 1991
A;Reference number: S24442
A;Accession: S25460
A;Molecule type: mRNA
A;Cross-references: EMBL:X61643; NID:g7855; PIDN:CAA43824.1; PID:g1335383
A;Residues: 1-39,'Q',41-65,'A',67-111 <JON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

alignment_scores:
      Quality:     478.00      Length:      107
      Ratio:       4.686       Gaps:        0
Percent Similarity:  95.327   Percent Identity:  83.178

alignment_block:
US-09-019-441-1 x S19671    ..

Align seg 1/1  to: S19671  from: 1  to: 111

 70 ACTCAGCCTCCCTCGTCGTCTGGGTCTCCTGGACAGTCGGTCACCATCTC 119
    |||||||| ||||||||:::||||||||||||||||||::::||||||||
  5 ThrGlnProAlaSerValSerGlySerProGlyGlnSerIleThrIleSe 21

120 CTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGT 169
    ||||||||||||:::||| |||||||||:::||||||||||||||||||
 21 rCysThrGlySerArgAspValGlyGlyTyrAsnTyrValSerTrpT 38

170 ACCAACACCACCCAGGCAAAGCCCCAAACTCATGATTTATGATGTCGCT 219
    |||||||||||||||||||||||||||||||||::::|| :::||:::
```

```
 38 yrGlnHisHisProGlyLysAlaProLysLeuLeuIleSerGluValThr 54

220 AAGCGGGCCTCAGGGGTCTCGATCGGTCCTTCTCTGGCTCCAAGTCTGGCAA 269
    :::||| |||||||||||||||||||||||||||||||||||||||||||
 55 AsnArgProSerGlyValSerAsnArgPheSerGlySerLysSerGlyAs 71

270 CACGGGCCTCCCTGACCATCTCGGGCTCCAGGCTGAGGACGAGGCTGATT 319
    |||||||||||||||||||||:::||||||||||||||||||||||||||
 71 nThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluAlaAspT 88

320 ATTACTGTGTTCATATACAACCAGTAGCACTTTGTTATTCGGAAGAGGG 369
    |||||||||||||||||||||:::|||| |||:||||||||||||||
 88 yrPheCysAlaSerTyrThrSerSerLysThrTyrValPheGlyArgGly 104

370 ACCCGGTTGACCGTCCTAGGT 390
    |||::|||||||||||||||||
105 ThrLysLeuThrValLeuGly 111

seq_name: pir2:S51149

seq_documentation_block:
antibody light chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S51149
R;de Kruif, J.; Boel, E.; Logtenberg, T.
   submitted to the EMBL Data Library, January 1995
A;Reference number: S51147
A;Accession: S51149
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-110 <DEK>
A;Cross-references: EMBL:X83712
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;13-90/Domain: immunoglobulin homology <IMM>

alignment_scores:
      Quality:     473.50      Length:      107
      Ratio:       4.688       Gaps:        1
Percent Similarity:  94.393   Percent Identity:  85.047

alignment_block:
US-09-019-441-1 x S51149    ..

Align seg 1/1  to: S51149  from: 1  to: 110

 70 ACTCAGCCTCCCTCGTCGTCTGGGTCTCCTGGACAGTCGGTCACCATCTC 119
    ||||||||||||||||||||:::||||||||||||||:::||||||||||
  3 ThrGlnProProSerValSerGlySerProGlyGlnSerIleThrIleSe 19

120 CTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGT 169
    ||||||||||||:::||||:|||||||||||:::|||||||||||||||
 19 rCysThrGlyThrSerSerAspValGlySerTyrAsnLeuValSerTrpT 36

170 ACCAACACCACCCAGGCAAAGCCCCAAACTCATGATTTATGATGTCGCT 219
    ||||:::|||||||||||||||||||||||||||||||||||||:::||
 36 yrGlnHisHisProGlyLysAlaProLysLeuMetIleTyrGluValSer 52

220 AAGCGGGCCTCAGGGGTCTCGATCGGTCCTTCTCTGGCTCCAAGTCTGGCAA 269
    ||||| |||||||||||||||||||||||||||||||||||||||||||
 53 LysArgProSerGlyValSerAsnArgPheSerGlySerLysSerGlyAs 69

270 CACGGGCCTCCCTGACCATCTCGGGCTCCAGGCTGAGGACGAGGCTGATT 319
    ||||||||||||||||||||||:::||||||||||||||||||||||||
 69 nThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluAlaAspT 86

320 ATTACTGTGTTCATATACAACCAGTAGCACTTTGTTATTCGGAAGAGGG 369
    ||||||||||:::|||:|| |||:::||||||||||||||
 86 yrTyrCysCysSerTyrAlaGlySerSer...TrpValPheGlyGlyGly 101

370 ACCCGGTTGACCGTCCTAGGT 390
```

```
          |||::::|||||||||||||
      102 ThrLysLeuThrValLeuGly 108

seq_name: pir2:S46396

seq_documentation_block:
Ig lambda chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46396
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A:Reference number: S46390; MUID:94254092
A:Accession: S46396
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-111 <FIG>
A:Cross-references: EMBL:Z31684; NID:g509793; PIDN:CAA83489.1; PID:g1335168
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

alignment_scores:
         Quality:    470.00           Length:    111
         Ratio:    4.563              Gaps:     0
Percent Similarity:  92.793    Percent Identity: 81.081

alignment_block:
US-09-019-441-1 x S46396       ..

Align seg 1/1  to: S46396  from: 1  to: 111

     58 CAGTCTGCCCGACTCAGCCTCCCTGTCTGGGTCTCCTGGACAGTC 107
        ||||||||  ||||||||  |||||||||||||||||||||||||
      1 GlnSerAlaLeuThrGlnProAlaSerValSerProGlyGlnSe  17

    108 GGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACT 157
        |::|||||||||||||||||||  ::||||||::|||::|:::|
     17 rIleThrIleSerCysThrGlyThrSerAspValGlyAlaTyrLysT  34

    158 ATGTCTCCTGGTACCAACACCACCCCAGGCAAAGCCCCAAACTCATGATT 207
        |||||||||||||:::|||||||||||||||||||||||||||||||
     34 yrValSerTrpTyrGlnHisProGlyLysAlaProLysLeuMetIle  50

    208 TATGATGTCGCTAAGCGGCGCTCAGGGGTCTCTGATCGGTTCTCTGGCTC 257
        ||||||||||||||::||||||||||||||||:::||||||||||||||
     51 SerGluValSerAspArgProSerGlyValSerAsnArgPheSerGlySe  67

    258 CAAGTCTGCCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGG 307
        |||||||||||||||||||||||||||||||||||||::||||||||
     67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA  84

    308 ACGAGGCTGATTATTACTGTGTTCATATACAACCAGTAGCACTTGTTA 357
        ||||||||||||  |||:::|||||||||||||||||||  :::
     84 spGluAlaAspTyrTyrCysSerSerTrpThrSerSerThrTyrVal 100

    358 TCCGGAGAGGGACCCGGTTGACCGTCCTAGGT 390
        |||||  |||||:::::||||||||||||
    101 PheGlyThrGlyThrLysValThrValLeuGly 111

seq_name: pir2:S31515

seq_documentation_block:
Ig lambda chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S31515
R:van der Heijden, R.W.J.; Uytdehaag, F.G.C.M.; Osterhaus, A.D.M.E.
submitted to the EMBL Data Library, January 1993
A:Description: V-lambda-2 gene sequence of a high affinity anti-idiotypic IgM antibody f
A:Reference number: S31515
```

```
A:Accession: S31515
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-112 <VAN>
A:Cross-references: EMBL:Z19546; NID:g33754; PIDN:CAA79606.1; PID:g33755
C:Superfamily: immunoglobulin V region; immunoglobulin
C:Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

alignment_scores:
         Quality:    469.50           Length:    111
         Ratio:    4.514              Gaps:     1
Percent Similarity:  93.694    Percent Identity: 81.081

alignment_block:
US-09-019-441-1 x S31515       ..

Align seg 1/1  to: S31515  from: 1  to: 112

     58 CAGTCTGCCCGACTCAGCCTCCCTGTCTGGGTCTCCTGGACAGTC 107
        ||||||||  ||||||||  |||||||||||||||||||||||||
      1 GlnSerAlaLeuThrGlnProAlaSerValSerProGlyGlnSe  17

    108 GGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACT 157
        |::|||||||||||||||||||  ::||||||::|::|:::|
     17 rIleThrIleSerCysThrGlyThrSerAspSerGlyAspTyrAspT  34

    158 ATGTCTCCTGGTACCAACACCACCCCAGGCAAAGCCCCAAACTCATGATT 207
        |||||||||||||:::|||||||||||||||||||||||||||||||
     34 yrValSerTrpTyrGlnHisProGlyLysAlaProLysLeuMetIle  50

    208 TATGATGTCGCTAAGCGGCGCTCAGGGGTCTCTGATCGGTTCTCTGGCTC 257
        ||||||||||||||::::|||  ||||||||||:::|||||||||||||
     51 TyrAspValSerAsnArgProSerGlyValSerAsnArgPheSerGlySe  67

    258 CAAGTCTGCCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGG 307
        |||||||||||||||||||||||||||||||||||||::||||||||
     67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA  84

    308 ACGAGGCTGATTATTACTGTGTTCATATACAACCAGTAGCACTTTG... 354
        ||||||||  |||||||||::::|||||||::|||
     84 spGluAlaAspTyrTyrCysSerSerTyrThrSerThrAsnThrLeuTrp 100

    355 TTATTCGGAAGAGGGACCCGGTTGACCGTCCTA 387
        ::|||||| ||||||:::::||||||||
    101 ValPheGlyGlyThrLysValThrValLeu 111

seq_name: pir2:S36281

seq_documentation_block:
Ig lambda chain V region (clone alpha-FOG1-A3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36281
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty,
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display librarie
A:Reference number: S36256; MUID:93178448
A:Accession: S36281
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-111 <GRI>
A:Cross-references: EMBL:Z18823; NID:g33414; PIDN:CAA79275.1; PID:g939907
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

alignment_scores:
         Quality:    468.00           Length:    111
         Ratio:    4.500              Gaps:     0
Percent Similarity:  93.694    Percent Identity: 78.378
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alignment_block:
US-09-019-441-1 x S36281

Align seg 1/1  to: S36281  from: 1 to: 111

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 58 CAGTCTGCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTGGACAGTC 107
    ||||||||  ||||||||  ||||||||||||||||:|||||||
  1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17

108 GGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACT 157
    |||||||||  ||||||||||||||||||:::|||||||
 17 rIleThrIleSerCysThrGlyThrSerSerAspValGlyGlyTyrAsnI 34

158 ATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACTCATGATT 207
    |||||||||||||||:::||||||||||||||||||||:::|||
 34 yrValSerTrpTyrGlnGlnTyrProGlyLysAlaProLysLeuLeuIle 50

208 TATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGACGGTCTTCTGGCTC 257
    |||.::||:||||  |||||| |||||||||||||||||||||||
 51 TyrGluValSerLysArgProSerGlyValSerAsnArgPheSerGlySe 67

258 CAAGTCTGGCAACACGGCCTCCTGACCATCTCTGGGCTCCAGGCTGAGG 307
    ||||||||||||||||||||||||||||||||||||:||||||||
 67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnThrGluA 84

308 ACGAGGCTGATTATTACTGTGTTCATATACAACCAGTAGTAGCACTTGTTA 357
    ||||||||||||||::::|||:::     :|||:|
 84 spGluAlaAspTyrTyrPheCysSerAlaTyrAlaProThrGlyIleMetMet 100

358 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
    ||||||||:::||||||||||||||||||
101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
```

seq_name: pir2:S44123

alignment_scores:
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Quality:             466.50      Length:     112
Ratio:               4.574       Gaps:         1
Percent Similarity:  91.071      Percent Identity: 82.143
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alignment_block:
US-09-019-441-1 x S44123

Align seg 1/1  to: S44123  from: 1 to: 112

```
 58 CAGTCTGCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTGGACAGTC 107
    ||||||||  ||||||||  ||||||||||||||||:|||||||
  1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17

108 GGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACT 157
    |||:::|||||||||||||||||||||||:::||||||
 17 rIleThrIleSerCysThrGlyThrSerSerAspValGlySerTyrAsnL 34
```

---

```
158 ATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACTCATGATT 207
    |||||||||||||||::||||||||||||||||||||||||
 34 euGlySerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuMetIle 50

208 TATGATGTCGCTAAGCGGCCTCAGGGGTCTCTGACGGTCTTCTGGCTC 257
    ||||::.  :::||||| ||||||||||||||||||||||||
 51 TyrGluGlySerLysArgProSerGlyValSerAsnArgPheSerGlySe 67

258 CAAGTCTGGCAACACGGCCTCCTGACCATCTCTGGGCTCCAGGCTGAGG 307
    ||||||||||||||||||||||||||||||||||||||||||
 67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84

308 ACGAGGCTGATTATTACTGTGTTCATATACAACCAGTAGCACT...TTG 354
    |||||||||||||||:||||| :|||||   ||||||
 84 spGluAlaAspTyrTyrCysCysSerTyrAlaGlySerSerThrSerTrp 100

355 TTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
    :::|||||||||||||||||||||||||||
101 ValPheGlyGlyGlyThrLysLeuThrValLeuGly 112
```

seq_name: pir1:L2HUMC

alignment_scores:
```
Quality:             461.00      Length:     111
Ratio:               4.564       Gaps:         0
Percent Similarity:  90.991      Percent Identity: 79.279
```

alignment_block:
US-09-019-441-1 x L2HUMC

Align seg 1/1  to: L2HUMC  from: 1 to: 111

```
 58 CAGTCTGCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTGGACAGTC 107
    ||||||||| |||||||||||||||||:||||||||||:|||||||
  1 GlnSerAlaLeuThrGlnProProSerAlaSerGlySerLeuGlyGlnSe 17
```

```
108 GGTCACCATCTCCTGCACTGGAACCAGCAGGATGACGTTGGTTGGTTATAACT 157
    |||||||||||||||||||||::||||||::::||||||||||
 17 rValThrIleSerCysThrGlyThrSerSerAspValGlyTyrAsnT 34

158 ATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACTCATGATT 207
    |||||||||||::||| ||||||||||||::::||
 34 yrValSerTrpTyrGlnGlnHisAlaGlyLysAlaProLysValIleIle 50

208 TATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGATCGCTTCTCTGGCTC 257
    ||||:|| |||||||  |||||||  ||||:::  ||||||||||
 51 TyrGluValAsnLysArgProSerGlyValProAspArgPheSerGlySe 67

258 CAAGTCTGCCAACACGGCCTCCCTGACCATCTCGGCTCCAGGCTGAGG 307
    |||||||||||||||||||||||||||||:::|||||||||||||
 67 rLysSerGlyAsnThrAlaSerLeuThrValSerGlyLeuGlnAlaGluA 84

308 ACGAGGCTGATTATTACTGTTGTCATATACAACCAGTAGCACTTTGTTA 357
    |||||||||||||| |||||| ||||:|::::::::
 84 spGluAlaAspTyrTyrCysSerSerTyrGluGlySerAspAsnPheVal 100

358 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
    |||||||  |||||||||||||||||||
101 PheGlyThrGlyThrLysValThrValLeuGly 111
```

seq_name: pir1:L2HUNG

seq_documentation_block:
Ig lambda chain V-II region (Nig-84) - human
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 02-Sep-1997
C;Accession: A01971
R;Tonoike, H.; Kametani, F.; Hoshi, A.; Shinoda, T.; Isobe, T.
FEBS Lett. 185, 139-141, 1985
A;Title: Amino acid sequence of an amyloidogenic Bence Jones protein in myeloma-associat
A;Reference number: A01971; MUID:85204383
A;Accession: A01971
A;Molecule type: protein
A;Residues: 1-112 <TON>
C;Comment: This is a Bence Jones protein isolated from an individual with myeloma-associ
C;Genetics:
A;Gene: GDB:IGLVø
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: amyloid; heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>
F;22-90/Disulfide bonds: #status predicted

alignment_scores:
        Quality:    460.50                      Length:       112
        Ratio:        4.471                      Gaps:           1
Percent Similarity:  91.964      Percent Identity: 78.571

alignment_block:
US-09-019-441-1 x L2HUNG   ..

Align seg 1/1  to: L2HUNG    from: 1  to: 112

```
 58 CAGTCTGCCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTGGACAGTC 107
    |::::|||||| ||||||| |||||||||||||||||||||||
  1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17

108 GGTCACCATCTCCTGCACTGGAACCAGCAGGATGACGTTGGTTGGTTATAACT 157
    |||||||||||||||||||||::||||||::::||||||||||
 17 rIleThrIleSerCysThrGlyThrSerSerAspValGlyTyrAspP 34

158 ATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCCAAACTCATGATT 207
    |||||||||||::||| ||||||||||||:::||
 34 heValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuLeuIle 50
```

```
208 TATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGATCGCTTCTCTGGCTC 257
    |||||||| |||||||  |||||||  ||||:::  ||||||||||
 51 TyrAspValAsnSerArgProSerGlyIleSerAsnArgPheSerGlySe 67

258 CAAGTCTGGCAACACGGCCTCCCTGACCATCTCGGCTCCAGGCTGAGG 307
    |||||||||||||||||||||||||||||||::::|||||||||||||
 67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84

308 ACGAGGCTGATTATTACTGTTGTCATAT...ACAACCAGTAGCACTTTG 354
    |||||||| ||||||| ||||:::
 84 spGluAlaAspTyrTyrCysSerSerPheThrThrAsnSerArgAla 100

355 TTAATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
    ::::|||||     ||||::::|||:::|||||||
101 ValPheGlyGlyGlyThrLysLeuSerValLeuGly 112
```

seq_name: pir2:S46395

seq_documentation_block:
Ig lambda chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46395
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage
A;Reference number: S46390; MUID:9254092
A;Accession: S46395
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-112 <FIG>
A;Cross-references: EMBL:Z31683; NID:g509791; PIDN:CAA83488.1; PID:g1135167
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

alignment_scores:
        Quality:    460.50                      Length:       112
        Ratio:        4.471                      Gaps:           1
Percent Similarity:  91.964      Percent Identity: 81.250

alignment_block:
US-09-019-441-1 x S46395   ..

Align seg 1/1  to: S46395    from: 1  to: 112

```
 58 CAGTCTGCCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTGGACAGTC 107
    |::::|||||| ||||||| |||||||||||||||||||||||
  1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17

108 GGTCACCATCTCCTGCACTGGAACCAGCAGGATGACGTTGGTTGGTTATAACT 157
    |::::|||||||||||||||||::::|||||||::||||||||||
 17 rIleThrIleSerCysThrGlyThrSerSerAspValGlySerTyrLysL 34

158 ATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACTCATGATT 207
    |||||||||||::|||||||||||||||||||||
 34 euValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLysMetIle 50

208 TATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGATCGCTTCTCTGGCTC 257
    |||:::|| |||||||  |||||||  ||||:::  ||||||||||
 51 TyrGluValAsnSerArgProSerGlyValSerAsnArgPheSerGlySe 67

258 CAAGTCTGGCAACACGGCCTCCCTGACCATCTCGGCTCCAGGCTGAGG 307
    |||||||||||||||||||||||||||||||||||||||||||
 67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84

308 ACGAGGCTGATTATTACTGTTGTCATATACAACCAGTAGCACTTTG... 354
    |||||||| |||||||||||| ||||||||||||:::
 84 spGluAlaGlyTyrTyrCysSerSerTyrThrSerSerThrValArg 100

355 TTAATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
```

Mon Sep 23 16:30:39 2002

us-09-019-441-1.rpr

```
      ||||||   ||||||:::||||||||||||||||
  101 SerPheGlyGlyGlyThrLysLeuThrValLeuGly 112
```

OM of: US-09-019-441-1 to: SwissProt_40:*      out_format : pfs

Date: Sep 23, 2002 10:24 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_n2p_model -DEV-xlp
-Q=/cgn2_1/USPTO_spool/US0901944l/runat_23092002_095259_6394/app_query.fasta_1.1860
-DB=SwissProt_40 -QFMT=fastan -SUFFIX=rsp -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPEXT=4.500 -QGAPOP=4.050 -XGAPOP=10.000 -XGAPEXT=-0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0901944l_@CGN_1_91 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-019-441-1
Query length: 390
Database: SwissProt_40:*
Database sequences: 105224
Database length: 38719550
Search time (sec): 62.410000

score_list:

| sequence | Strd | Orig | ZScore | EScore | Len | ! Documentation |
|---|---|---|---|---|---|---|
| SwissProt_40:LV2F_HUMAN | + | 461.00 | 792.31 | 1.8e-36 | 111 | ! P01709 homo sapiens (human) |
| SwissProt_40:LV2K_HUMAN | + | 460.50 | 791.38 | 2.0e-36 | 112 | ! P04209 homo sapiens (human) |
| SwissProt_40:LV2D_HUMAN | + | 460.00 | 790.60 | 2.2e-36 | 111 | ! P01707 homo sapiens (human) |
| SwissProt_40:LV2B_HUMAN | + | 456.00 | 783.73 | 5.3e-36 | 111 | ! P01705 homo sapiens (human) |
| SwissProt_40:LV2H_HUMAN | + | 453.00 | 778.58 | 9.3e-35 | 111 | ! P01711 homo sapiens (human) |
| SwissProt_40:LV2C_HUMAN | + | 443.00 | 761.41 | 2.2e-34 | 111 | ! P01706 homo sapiens (human) |
| SwissProt_40:LV2E_HUMAN | + | 439.00 | 754.69 | 3.5e-34 | 109 | ! P01708 homo sapiens (human) |
| SwissProt_40:LV2G_HUMAN | + | 437.00 | 751.10 | 4.3e-34 | 111 | ! P01710 homo sapiens (human) |
| SwissProt_40:LV2A_HUMAN | + | 436.00 | 749.39 | 5.4e-34 | 111 | ! P01704 homo sapiens (human) |
| SwissProt_40:LV2I_HUMAN | + | 435.00 | 747.67 | 9.7e-31 | 111 | ! P01712 homo sapiens (human) |
| SwissProt_40:LV1G_HUMAN | + | 401.00 | 687.97 | 1.9e-29 | 130 | ! P06316 homo sapiens (human) |
| SwissProt_40:LV2J_HUMAN | + | 387.50 | 666.19 | 1.6e-26 | 110 | ! P01713 homo sapiens (human) |
| SwissProt_40:LV1D_HUMAN | + | 359.00 | 617.18 | 1.6e-26 | 111 | ! P01702 homo sapiens (human) |
| SwissProt_40:LV2L_HUMAN | + | 357.00 | 613.74 | 2.2e-26 | 111 | ! P80422 homo sapiens (human) |
| SwissProt_40:LV6E_HUMAN | + | 355.50 | 609.78 | 2.0e-25 | 131 | ! P06319 homo sapiens (human) |
| SwissProt_40:LV1B_HUMAN | + | 345.50 | 593.92 | 2.2e-25 | 112 | ! P01700 homo sapiens (human) |
| SwissProt_40:LV1A_HUMAN | + | 345.00 | 593.14 | 2.7e-25 | 111 | ! P01699 homo sapiens (human) |
| SwissProt_40:LV1C_HUMAN | + | 344.00 | 591.42 | 4.2e-25 | 111 | ! P01701 homo sapiens (human) |
| SwissProt_40:LV1F_HUMAN | + | 342.00 | 588.14 | 3.8e-24 | 109 | ! P04208 homo sapiens (human) |
| SwissProt_40:LV1H_HUMAN | + | 331.50 | 569.88 | 1.2e-23 | 112 | ! P06317 homo sapiens (human) |
| SwissProt_40:LV6D_HUMAN | + | 327.00 | 562.23 | 2.8e-23 | 111 | ! P06318 homo sapiens (human) |
| SwissProt_40:LV4E_HUMAN | + | 323.00 | 555.75 | 3.4e-23 | 106 | ! P06889 homo sapiens (human) |
| SwissProt_40:LV1E_HUMAN | + | 322.00 | 554.27 | 6.0e-23 | 112 | ! P01703 homo sapiens (human) |
| SwissProt_40:LV6A_HUMAN | + | 319.50 | 549.28 | 1.0e-22 | 112 | ! P01721 homo sapiens (human) |
| SwissProt_40:LV1I_HUMAN | + | 317.00 | 545.21 | 1.3e-22 | 109 | ! P06888 homo sapiens (human) |
| SwissProt_40:LV6C_HUMAN | + | 316.00 | 543.35 | 3.1e-22 | 111 | ! P06687 homo sapiens (human) |
| SwissProt_40:LV4A_HUMAN | + | 312.00 | 536.86 | 3.1e-22 | 106 | ! P01715 homo sapiens (human) |
| SwissProt_40:LV4B_HUMAN | + | 306.00 | 526.56 | 1.2e-21 | 106 | ! P01716 homo sapiens (human) |
| SwissProt_40:LV6B_HUMAN | + | 302.50 | 520.09 | 2.5e-21 | 112 | ! P01722 homo sapiens (human) |
| SwissProt_40:LV3A_HUMAN | + | 299.00 | 512.67 | 6.8e-21 | 108 | ! P01714 homo sapiens (human) |
| SwissProt_40:LV1_CHICK | + | 294.50 | 506.28 | 1.5e-20 | 113 | ! P04210 gallus gallus (chicken) |
| SwissProt_40:LV4C_HUMAN | + | 289.00 | 497.29 | 4.9e-20 | 107 | ! P01717 homo sapiens (human) |
| SwissProt_40:LV4D_HUMAN | + | 286.00 | 492.22 | 9.6e-20 | 106 | ! P01718 homo sapiens (human) |
| SwissProt_40:LV3B_HUMAN | + | 283.00 | 486.68 | 1.9e-19 | 111 | ! P80748 homo sapiens (human) |
| SwissProt_40:LV5A_HUMAN | + | 279.00 | 480.05 | 4.5e-19 | 108 | ! P01719 homo sapiens (human) |
| SwissProt_40:LV7A_HUMAN | + | 264.00 | 454.06 | 1.2e-17 | 111 | ! P01720 homo sapiens (human) |
| SwissProt_40:LV1B_MOUSE | + | 257.50 | 441.64 | 5.2e-17 | 129 | ! P01724 mus musculus (mouse) |
| SwissProt_40:LV1D_MOUSE | + | 255.50 | 438.20 | 8.0e-17 | 129 | ! P01726 mus musculus (mouse) |
| SwissProt_40:LV0A_HUMAN | + | 253.50 | 435.50 | 1.2e-16 | 117 | ! P04211 homo sapiens (human) |
| SwissProt_40:KV1W_HUMAN | + | 252.50 | 433.05 | 1.6e-16 | 129 | ! P04431 homo sapiens (human) |
| SwissProt_40:LV1E_MOUSE | + | 252.50 | 433.05 | 1.6e-16 | 129 | ! P01727 mus musculus (mous |
| SwissProt_40:KV4B_HUMAN | + | 252.00 | 431.94 | 1.7e-16 | 133 | ! P06313 homo sapiens (huma |
| SwissProt_40:KV07_RABIT | + | 248.00 | 426.82 | 4.1e-16 | 108 | ! P01688 oryctolagus cunicu |
| SwissProt_40:KV6K_MOUSE | + | 246.00 | 423.38 | 6.4e-16 | 108 | ! P04945 mus musculus (mous |
| SwissProt_40:KV6G_MOUSE | + | 245.00 | 421.74 | 8.0e-16 | 107 | ! P04941 mus musculus (mous |

seq_name: SwissProt_40:LV2F_HUMAN

seq_documentation_block:
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ID   LV2F_HUMAN     STANDARD;      PRT;    111 AA.
AC   P01709;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-II region MGC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75013804; PubMed=4415202;
RA   Fett J.W., Deutsch H.F.;
RT   "Primary structure of the Mcg lambda chain.";
RL   Biochemistry 13:4102-4114(1974).
RN   [2]
RP   LAMBDA CHAIN GENES.
RX   MEDLINE=76093781; PubMed=812801;
RA   Fett J.W., Deutsch H.F.;
RT   "A new lambda-chain gene.";
RL   Immunochemistry 12:643-652(1975).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA   Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
RA   Panagiotopoulos N.;
RT   "Rotational allomerism and divergent evolution of domains in
RT   immunoglobulin light chains.";
RL   Biochemistry 14:3953-3961(1975).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=90133913; PubMed=2515285;
RA   Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
RT   "Three-dimensional structure of a light chain dimer crystallized in
RT   water. Conformational flexibility of a molecule in two crystal
RT   forms.";
RL   J. Mol. Biol. 210:601-615(1989).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC   -!- MISCELLANEOUS: THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH
CC       A VERY UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY,
CC       SUGGESTING THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
CC       MARKERS.
DR   PIR; A01975; L2HUMC.
DR   PDB; 2MCG; 15-JUL-92.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure;
KW   PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       1      1       BY SIMILARITY.
FT   DISULFID     22     90
FT   STRAND        5      5
FT   STRAND       10     12
FT   STRAND       18     23
FT   TURN         26     32
FT   STRAND       36     40
FT   TURN         42     43
FT   STRAND       50     51
FT   TURN         52     54
FT   STRAND       55     55
FT   TURN         62     63
FT   TURN         66     68
FT   STRAND       72     77
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FT   HELIX            82     84
FT   STRAND           86     93
FT   STRAND           99    101
FT   STRAND          105    109
FT   NON_TER         111    111
SQ   SEQUENCE        111 AA;  11558 MW;  7CC1D6E2FA3377BA CRC64;

alignment_scores:
          Quality:   461.00                    Length:    111
          Ratio:       4.564                    Gaps:        0
Percent Similarity:   90.991    Percent Identity:  79.279

alignment_block:
US-09-019-441-1 x LV2F_HUMAN

Align seg 1/1 to: LV2F_HUMAN    from: 1 to: 111

    58 CAGTCTGCCCGACTCAGCCTCCCTGTGTCTGGGGTCTCCTGGACAGTC 107
       |||||||| ||||||||||||||::||||||| |||||| |||||||
     1 GlnSerAlaLeuThrGlnProProSerAlaSerGlySerLeuGlyGlnSe 17

   108 GGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACT 157
       |||||||||||||||||||||||::::||||||||||||||||||:::
    17 rValThrIleSerCysThrGlyThrSerSerAspValGlyGlyTyrAsnT 34

   158 ATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACTCATGATT 207·
       |||||||||||||||||||:::||| ||||||||||||||::::::||
    34 yrValSerTrpTyrGlnGlnHisAlaGlyLyLysAlaProLysVallelle 50

   208 TATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGATCGCTTCTCTGGCTC 257
       ||:::|||  ||||||  |||||||||||||||||
    51 TyrGluValAsnLysArgProSerGlyValProAspArgPheSerGlySe 67

   258 CAAGTCTGGCAACACGGCCTCCTCCGACCATCTCTGGGCTCCAGGCTGAGG 307
       |||||||||||||||||||||||||||||:::||||||||||||||||
    67 rLysSerGlyAsnThrAlaSerLeuThrValSerGlyLeuGlnAlaGluA 84

   308 ACGAGGCTGATTATTACTGTTGTCATATACAACCAGTACACTTTGTTA 357
       ||||||||||||||||| |||||    ||:::::::::::
    84 spGluAlaAspTyrTyrCysSerSerTyrGluGlySerAspAsnPheVai 100

   358 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
       |||||||||||||:::::||||||||||||
   101 PheGlyThrGlyThrArgLeuThrValLeuGly 111

seq_name: SwissProt_40:LV2K_HUMAN

seq_documentation_block:
ID   LV2K_HUMAN   STANDARD;       PRT;   112 AA.
AC   P04209;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-II region NIG-84.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=85204383; PubMed=3922791;
RA   Tonoike H., Kametani F., Hoshi A., Shinoda T., Isobe T.;
RT   "Amino acid sequence of an amyloidogenic Bence Jones protein in
RT   myeloma-associated systemic amyloidosis.";
RL   FEBS Lett. 185:139-141(1985).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN
CC       INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.
DR   PIR; A01971; L2HUNG.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
```

```
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region; Amyloid; Bence-Jones protein.
FT   DISULFID         22     90       BY SIMILARITY.
FT   NON_TER         112    112
SQ   SEQUENCE        112 AA;  11581 MW;  988FFF363A1E4F3 CRC64;

alignment_scores:
          Quality:   460.50                    Length:    112
          Ratio:       4.471                    Gaps:        1
Percent Similarity:   91.964    Percent Identity:  78.571

alignment_block:
US-09-019-441-1 x LV2K_HUMAN

Align seg 1/1 to: LV2K_HUMAN    from: 1 to: 112

    58 CAGTCTGCCCGACTCAGCCTCCCTGTGTCTGGGGTCTCCTGGACAGTC 107
       ||||||||  ||||||||||||||::|||||||||||| |||||||
     1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17

   108 GGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACT 157
       :::||||||||||||||||||||||:::::||||||||||||||:::::
    17 rIleThrIleSerCysThrGlyThrSerSerAspValGlyGlyTyrAspP 34

   158 ATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACTCATGATT 207
       :::||||||||||||||:::::||| ||||||||||||||::::::||
    34 heValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuLeuIle 50

   208 TATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGATCGCTTCTCTGGCTC 257
       ||||||||  :::||||  |||||||||||||||
    51 TyrAspValAsnSerArgProSerGlyIleSerAsnArgPheSerGlySe 67

   258 CAAGTCTGGCAACACGGCCTCCTCCGACCATCTCTGGGCTCCAGGCTGAGG 307
       ||||||||||||||||||||||||||||:::||||||||||||||||
    67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84

   308 ACGAGGCTGATTATTACTGTTGTTCATAT...ACAACCAGTAGCACTTTG 354
       |||||||||||||||||  |||::    |||:::|||
    84 spGluAlaAspTyrTyrCysSerSerPheThrThrAsnSerArgAla 100

   355 TTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
       :::||||||  -|||||::::||:::||||||||
   101 ValPheGlyGlyGlyThrLysLeuLeuValLeuGly 112

seq_name: SwissProt_40:LV2D_HUMAN

seq_documentation_block:
ID   LV2D_HUMAN   STANDARD;       PRT;   111 AA.
AC   P01707;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-II region TRO.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80114123; PubMed=118915;
RA   Scholz R., Yang C., Hilschmann N.;
RT   "Rule of antibody structure. Primary structure of a human monoclonal
RT   IgAl-immunoglobulin (myeloma protein Tro). VI. Amino acid sequence of
RT   the L-chain, lambda-type, subgroup II.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 360:1903-1918(1979).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01973; L2HUTR.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
```

## Left column

```
KW   Immunoglobulin V region.
FT   MOD_RES        1      1    PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID      22     90    BY SIMILARITY.
FT   NON_TER      111    111
SQ   SEQUENCE     111 AA;   11561 MW;  99DC457A12E8F6E1 CRC64;

alignment_scores:
          Quality:   460.00             Length:    111
            Ratio:   4.510                Gaps:      0
Percent Similarity:  91.892    Percent Identity:  79.279

alignment_block:
US-09-019-441-1 x LV2D_HUMAN

Align seg 1/1  to: LV2D_HUMAN  from: 1  to: 111

  58 CAGTCTGCCCGACTCAGCCTCCCTGTGTCTGGGTCTTCCTGGACAGTC 107
     |||||||  |||||||| |||||||||||||||||||||||||||
   1 GlnSerAlaLeuThrGlnProArgSerValSerGlySerProGlyGlnSe 17

 108 GGTCACCATCTCCTGCACTGGAACCAGCCAGCGATGACGTTGGTTATAACT 157
     ||||||||||||||||||||||||||||||||||||:::||||||
  17 rValThrIleSerCysThrGlyThrSerSerAspValGlyAlaTyrAsnS 34

 158 ATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACTCATGATT 207
     |||||||||||||::|||||||||||||||||||||||||||||
  34 erValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuMetIle 50

 208 TATGATGTCGCTAAGCGGCGCCTCAGGGGTCTCTGATCGCTTCTCTGGCTC 257
     ::::|||||||||  ||||||  ||||||:::||||||||
  51 PheAspValThrLysArgProSerGlyValProAspArgLeuSerGlySe 67

 258 CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGG 307
     |||||||||||||||||||||||||||||||||:::|||||
  67 rLysSerGlyAspThrAlaSerLeuThrIleSerGlyLeuArgAlaAspA 84

 308 ACGAGGCTGATTATTACTGTGTTCATATACAACCAGTAGCACTTTGTTA 357
     ||||||||||||||||||||||||        :::::::::
  84 spGluAlaAspTyrTyrCysValSerSerTyrAlaGlyArgTyrSerValIle 100

 358 TTCGGAAGAGGGACCCCGGTTGACCGTCCTAGGT 390
     |||||  ||||||:::||||||||||||
 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
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seq_name: SwissProt_40:LV2B_HUMAN

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seq_documentation_block:
ID   LV2B_HUMAN    STANDARD;     PRT;    111 AA.
AC   P01705;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-II region NEI.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72233223; PubMed=5043326;
RA   Garver F.A., Hilschmann N.;
RT   "The primary structure of a monoclonal human lambda-type
RT   immunoglobulin L-chain of subgroup II (Bence-Jones protein NEI).";
RL   Eur. J. Biochem. 26:10-32(1972).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01970; L2HUNI.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein; Glycoprotein.
```

## Right column

```
FT   MOD_RES        1      1    PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID      22     90    BY SIMILARITY.
FT   CARBOHYD      96     96    N-LINKED (GLCNAC. . .).
FT   NON_TER      111    111
SQ   SEQUENCE     111 AA;   11591 MW;  AD6D156584D087EB CRC64;

alignment_scores:
          Quality:   456.00             Length:    110
            Ratio:   4.471                Gaps:      0
Percent Similarity:  92.727    Percent Identity:  79.091

alignment_block:
US-09-019-441-1 x LV2B_HUMAN

Align seg 1/1  to: LV2B_HUMAN  from: 1  to: 111

  58 CAGTCTGCCCGACTCAGCCTCCCTGTGTCTGGGTCTTCCTGGACAGTC 107
     |||||||  |||||||| |||||||||||||||||||||||||||
   1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17

 108 GGTCACCATCTCCTGCACTGGAACCAGCCAGCGATGACGTTGGTTATAACT 157
     |:::||||||||||||||||||||||||||||:::||:||||||
  17 rIleThrIleSerCysThrGlyThrSerSerAspValGlySerTyrAsnP 34

 158 ATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACTCATGATT 207
     ::|||||||||||||||:::||||||||||||||||||||||||
  34 heValSerTrpTyrGlnGlnAsnProGlyLysAlaProLysLeuMetIle 50

 208 TATGATGTCGCTAAGCGGCGCCTCAGGGGTCTCAGGGGTCTCTCTGGCTC 257
     |||::   |||||  ||||||  ||||||:::||||||||
  51 TyrGluGlyAsnLysArgProSerGlyValSerAsnArgPheSerGlySe 67

 258 CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGG 307
     |||||||||||||||||||||||||||||||||:::|||||
  67 rLysSerGlyLysThrAlaSerLeuThrIleSerGlyLeuGlnValAlaGluA 84

 308 ACGAGGCTGATTATTACTGTGTTCATATACAACCAGTAGCACTTTGTTA 357
     ||||||||||||||||||||||||        :::|||||
  84 spGluAlaAspTyrTyrCysCysSerTyrAlaGlyAsnSerThrArgVal 100

 358 TTCGGAAGAGGGACCCCGGTTGACCGTCCTA 387
     |||||  ||||||:::||||||||||
 101 PheGlyGlyGlyThrArgValThrValLeu 110
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seq_name: SwissProt_40:LV2H_HUMAN

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seq_documentation_block:
ID   LV2H_HUMAN    STANDARD;     PRT;    111 AA.
AC   P01711;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-II region VIL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71215142; PubMed=5087637;
RA   Ponstingl H., Hilschmann N.;
RT   "Structural rule of antibodies. Complete primary structure of a
RT   monoclonal immunoglobin L chain of the lambda type, subgroup II
RT   (Bence Jones protein VIL).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 352:859-877(1971).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01977; L2HUVL.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
```

KW   Immunoglobulin V region; Bence-Jones protein.
FT   DISULFID      22      90              BY SIMILARITY.
FT   NON_TER      111     111
SQ   SEQUENCE     111 AA;   11445 MW;  3913736B3EF367E0 CRC64;

alignment_scores:
              Quality:  453.00          Length:  110
                Ratio:    4.485            Gaps:    0
Percent Similarity: 91.818      Percent Identity: 79.091

alignment_block:
US-09-019-441-1 x LV2H_HUMAN      ..

Align seg 1/1  to: LV2H_HUMAN    from: 1  to: 111

 61 TCTGCCCGACTCAGCCTCCCTCTGTCTGGGTCTCCTGGACAGTCGGT 110
    ||||| ||||||| |||||||| ||||||||||||||| ||||||||
  2 SerAlaLeuThrGlnProAlaSerValSerGlySerLeuGlyGlnSerIle 18

111 CACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGTTATAACTATG 160
    ||||||||||||||||||::||||||||||||||:|||||||||||||
 18 eThrIleSerCysThrGlyThrSerSerAspValGlyGlyTyrAsnTyrV 35

161 TCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACTCATGATTTAT 210
    |||:||:::|||::|||||||||||||||||||||::|||
 35 alSerTrpPheGlnGlnHisProGlyThrAlaProLysLeuIleIleSer 51

211 GATGTCGCTAAGCGGCCTTCTGATCGCTTCTCTGGCTCCAA 260
    :::||| :::||| ||||||::|||||||||||||||||
 52 GluValArgAsnArgProSerGlyValSerAsnArgPheSerGlySerLy 68

261 GTCTGCAACACGGCCTCCCTGACCATCTCTGGGCTCGAGGACG 310
    ||||::|||||||||||||||||||||||||||||||||||
 68 sSerAlaAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluAspG 85

311 AGGCTGATTATTACTGTTGTCATATACAACCAGTAGCACTTTGTTATTC 360
    |||||| |||||||||:::::::::|::::::|||:|||
 85 luAlaAspTyrTyrCysSerSerTyrThrSerSerAsnSerValValPhe 101

361 GGAAGAGGGACCCCGGTTGACCGTCCTAGGT 390
    ||| ||||||||||||||||||||||||||
102 GlyGlyGlyThrLysLeuThrValLeuGly 111

seq_name: SwissProt_40:LV2C_HUMAN

seq_documentation_block:
ID   LV2C_HUMAN    STANDARD;     PRT;   111 AA.
AC   P01706;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-II region BOH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. /
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75115478; PubMed=804002;
RA   Kohler H., Rudofsky S., Kluskens L.;
RT   "The primary structure of a human lambda II chain.";
RL   J. Immunol. 114:415-421(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE OZ+ MARKER.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01972; L2HUBH.
HSSP; P01709; 2MCG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   MOD_RES       1       1        PYRROLIDONE CARBOXYLIC ACID.

---

FT   DISULFID      22      90              BY SIMILARITY.
FT   NON_TER      111     111
SQ   SEQUENCE     111 AA;   11650 MW;  9A520309932623E8 CRC64;

alignment_scores:
              Quality:  443.00          Length:  111
                Ratio:    4.567            Gaps:    0
Percent Similarity: 87.387      Percent Identity: 79.279

alignment_block:
US-09-019-441-1 x LV2C_HUMAN      ..

Align seg 1/1  to: LV2C_HUMAN    from: 1  to: 111

 58 CAGTCTGCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTGGACAGTC 107
    ||||||| ||||||| |||||| |||||||||||||||||||||||
  1 GlnSerAlaLeuThrGlnProArgSerValSerGlySerProGlyGlnSe 17

108 GGTCACCATCTCCTGCACTGGAACCAGCAGGATGACGTTGGTGGTTATAACT 157
    |||||||||||||||||::||||||||||||||||:|||||||||||
 17 rValThrIleSerCysAlaGlyThrSerSerAspValGlyGlyAsnHisP 34

158 ATGTCCTGTACCAACACCACCACCAGGCAAAGCCCCAAACTCATGATT 207
    ::|||||||||||||||::||||||||||||||||||:::|||||
 34 heValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuIleIle 50

208 TATGATGTCGCTAAGCGGCCTCAGGGGTCTCGATCGCTTCTCTGGCTC 257
    |||| ||||| |||||| ||||||||||||||||||||||||||||
 51 TyrGlyValAsnLysArgProSerGlyValProTyrArgPheSerGlySe 67

258 CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGG 307
    ||||||||||||||||||||||||||||||||||||||||||||||
 67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84

308 ACGAGGCTGATTATTACTGTTGTCATATACAACCAGTAGCACTTTGTTA 357
    |||||||  |||||||||::::::::::|:::::::|||   :::||
 84 spGluAlaHisTyrTyrCysCysSerTyrAlaGlyArgThrPhePheVal 100

358 TTCGGAAGAGGGACCCCGGTTGACCGTCCTAGGT 390
    :||| ||||||||||||||||||||||||||||
101 PheGlyGlyGlyThrArgAsnLeuThrValLeuGly 111

seq_name: SwissProt_40:LV2E_HUMAN

seq_documentation_block:
ID   LV2E_HUMAN    STANDARD;     PRT;   109 AA.
AC   P01708;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-II region BUR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80006606; PubMed=113407;
RA   Infante A.J., Putnam F.W.;
RT   "Primary structure of a human IgA1 immunoglobulin. V. Amino acid
RT   sequence of a human IgA lambda light chain (Bur).";
RL   J. Biol. Chem. 254:9006-9016(1979).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
CC       MARKERS.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01974; L2HUBR.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.

```
FT   MOD_RES          1      1      PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID        22     90      BY SIMILARITY.
FT   SITE            91     91      APPEARS TO BE A FREE BUT UNREACTIVE
FT                                  SULFHYDRYL GROUP.
FT   NON_TER        109    109
SQ   SEQUENCE       109 AA;  11506 MW;  BFD8AE1C5D267FAB CRC64;

alignment_scores:
            Quality:   439.00              Length:    111
              Ratio:     4.480               Gaps:      1
Percent Similarity:    88.288      Percent Identity:  77.477

alignment_block:
US-09-019-441-1 x LV2E_HUMAN       ..

Align seg 1/1  to: LV2E_HUMAN  from: 1  to: 109

   58  CAGTCTGCCCGACTCAGCCTCCTCTGTGTCTGGGTCTCCTGGACAGTC 107
       ||||||||| |||||||||| |||||||||||||||||:||||||||
    1  GlnSerAlaLeuThrGlnProArgSerValSerGlySerProGlyHisSe 17

  108  GGTCACCATCTCCTGCACTGGAACCAGCCGATGACGTTGGTGGTTATAACT 157
       ||||||||||||||||| ||||||||||:::||||  ||||:::|
   17  rValThrIleSerCysIleGlyThrSerSerAsnValGlyAspTyrLysT 34

  158  ATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACTCATGATT 207
       ||||||||||||||||||||:::||||||||||||||||||:::||
   34  yrValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuValIle 50

  208  TATGATGTCGCTAAGCGGCCGCCTCAGGGGTCTCTGATCGCTTCTGGCTC 257
       ||||:::||||:|||||||| ||||||| |||||:::|||||||||
   51  TyrGluValSerSerArgProSerGlyValProAspArgPheSerGlySe 67

  258  CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGG 307
       |||||||||||||||||||||||||||||||||||||||||||||
   67  rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84

  308  ACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 357
       |||||||||||||||||||||| |||                ::|
   84  spGluAlaAspTyrTyrCysCysSerTyrIleGlySer......TyrVal 98

  358  TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
       |||||| ||||:::|||||||||||
   99  PheGlyThrGlyThrLysValIleValLeuGly 109

seq_name: SwissProt_40:LV2G_HUMAN

seq_documentation_block:
ID   LV2G_HUMAN      STANDARD;      PRT;     111 AA.
AC   P01710;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-II region BO.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71103825; PubMed=5532228;
RA   Wikler M., Putnam F.W.;
RT   "Amino acid sequence of human lambda chains. 3. Tryptic peptides,
RT   chymotryptic peptides, and sequence of protein BO.";
RL   J. Biol. Chem. 245:4488-4507(1970).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01976; L2HUBO.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
```

```
KW   Immunoglobulin v region; Bence-Jones protein.
FT   MOD_RES          1      1      PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID        22     90      BY SIMILARITY.
FT   NON_TER        111    111
SQ   SEQUENCE       111 AA;  11785 MW;  92F5A1BF72421BAC CRC64;

alignment_scores:
            Quality:   437.00              Length:    110
              Ratio:     4.327               Gaps:      0
Percent Similarity:    91.818      Percent Identity:  74.545

alignment_block:
US-09-019-441-1 x LV2G_HUMAN       ..

Align seg 1/1  to: LV2G_HUMAN  from: 1  to: 111

   58  CAGTCTGCCCGACTCAGCCTCCTCTGTGTCTGGGTCTCCTGGACAGTC 107
       ||||||| ||||||||||||||:::|||||||||||||||||||||
    1  GlnSerAlaLeuThrGlnProSerAlaSerGlySerProGlyGlnSe 17

  108  GGTCACCATCTCCTGCACTGGAACCAGCAGCGATGACGTTGGTGGTTATAACT 157
       ||||||||||||||||| ||||||||:::|||||  ||||:::||||
   17  rValThrIleSerCysThrGlyThrSerSerAspValGlyAspAsnLysT 34

  158  ATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACTCATGATT 207
       ||||||||||||||||||||:::||||||||||||||||||:::||
   34  yrValSerTrpTyrGlnGlnHisProGlyArgAlaProLysLeuValIle 50

  208  TATGATGTCGCTAAGCGGCCGCCTCAGGGGTCTCTGATCGCTTCTGGCTC 257
       ::::||||:::||| ||||||| |||||||||| |||||||||||||
   51  PheGluValSerGlnArgProSerGlyValProAspArgPheSerGlySe 67

  258  CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGG 307
       |||||||||||||||||||||||||||||||:::|||::|||||||
   67  rLysSerAspAsnThrAlaSerLeuThrValSerGlyLeuArgAlaGluA 84

  308  ACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 357
       |||||||||||||| |||||::  ::::::::::||||:::||:||
   84  spGluAlaAspTyrTyrCysSerSerTyrValAspAsnAsnPheVal 100

  358  TTCGGAAGAGGGACCCGGTTGACCGTCCTA 387
       |||||| ||||:::|||||||||||||
  101  PheGlyGlyThrLysLeuThrValLeu 110

seq_name: SwissProt_40:LV2A_HUMAN

seq_documentation_block:
ID   LV2A_HUMAN      STANDARD;      PRT;     111 AA.
AC   P01704;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-II region TOG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80048495; PubMed=500108;
RA   Nabeshima Y., Ikenaka T.;
RT   "Primary structure of cryo Bence-Jones protein (Tog) from the urine
RT   of a patient with IgD myeloma.";
RL   Mol. Immunol. 16:439-444(1979).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01969; L2HUTG.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region; Bence-Jones protein.
```

## Left column

```
FT   MOD_RES      1      1     PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID    22     90     BY SIMILARITY.
FT   NON_TER    111    111
SQ   SEQUENCE   111 AA;  11713 MW;  FD20AEF4CE5364E2 CRC64;

alignment_scores:
            Quality:   436.00          Length:  110
            Ratio:      4.360           Gaps:      0
Percent Similarity:  90.909    Percent Identity:  74.545

alignment_block:
US-09-019-441-1 x LV2A_HUMAN   ..

Align seg 1/1  to: LV2A_HUMAN   from: 1  to: 111

  58 CAGTCTGCCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTGGACAGTC 107
     ||||||||| |||||||  ||||||||||:||||||||||||||||
   1 GlnSerAlaLeuThrGlnProAlaSerValSerAlaSerProGlyGlnSe 17

 108 GGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACT 157
     |:|:||||||||||||||||||:||:::||||:|||||:||||:||:|
  17 rIleThrIleSerCysThrGlyThrThrAsnAspIleGlySerTyrSerT 34

 158 ATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACTCATGATT 207
     |:|||||||||||:::||||||||:|||||||||||||||||:||:|||
  34 yrValSerTrpTyrGlnGlnTyrProGlyLysAlaProLysValLeuIle 50

 208 TATGATGTCGGTAAGCGGCCTCAGGGTCTCTGATCGCTTCTCTGGCTC 257
     ::|||||  |||||  |||||||||||||  ||||||||||||||
  51 PheAspValAsnSerArgProSerGlyValSerHisArgPheSerGlySe 67

 258 CAAGTCTGGCAACACGGCCTCCCTGACCATCTCGGGCTCCAGGCTGAGG 307
     ||||||||||||||||||||||||||||||||||||||||||
  67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84

 308 ACGAGGCTGATTATTACTGTTGTCATATACAACCAGTAGCACTTTGTTA 357
     ::|||||||||||||::|||||   |||||||||||||||
  84 spGluAlaHisTyrPheCysSerSerTyrArgThrSerGlyThrIleIle 100

 358 TTCGGAAGAGGGACCCGGTTGACCGTCCTA 387
     ||||||  ||||::|||||||||||||
 101 PheGlyGlyThrTyrTyrValThrValLeu 110
```

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seq_name: SwissProt_40:LV2I_HUMAN

seq_documentation_block:
ID   LV2I_HUMAN     STANDARD;      PRT;    111 AA.
AC   P01712;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-II region WIN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79062503; PubMed=103365;
RA   Chen B.L., Chiu Y.-Y.H., Humphrey R.L., Poljak R.J.;
RT   "Amino acid sequence of the human myeloma lambda chain Win.";
RL   Biochim. Biophys. Acta 537:9-21(1978).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01978; L2HUWN.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   MOD_RES      1      1     PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID    22     90     BY SIMILARITY.
```

## Right column

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FT   NON_TER    111    111
SQ   SEQUENCE   111 AA;  11694 MW;  8C3CE95FE721B87C CRC64;

alignment_scores:
            Quality:   435.00          Length:  111
            Ratio:      4.439           Gaps:      0
Percent Similarity:  88.288    Percent Identity:  76.577

alignment_block:
US-09-019-441-1 x LV2I_HUMAN   ..

Align seg 1/1  to: LV2I_HUMAN   from: 1  to: 111

  58 CAGTCTGCCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTGGACAGTC 107
     ||||||||| |||||||  ||||||||||||||||||||||||||||
   1 GlnSerAlaLeuThrGlnProProArgValSerGlySerProGlyGlnSe 17

 108 GGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACT 157
     |:||||||||||||||:|||||::::|||   |||||||||||||:
  17 rValThrIleSerCysThrGlySerTyrSerAsnValThrGlyTyrTyrAsnH 34

 158 ATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACTCATGATT 207
     ::|||||||||||||:|||||||||||||||||||||||||||||||
  34 isValSerTrpTyrGlnGlnAspProGlyLysValProLysLeuMetIle 50

 208 TATGATGTCGGTAAGCGGCCTCAGGGTCTCGATCGGTTCTCTCGGCTC 257
     ||||||  ||||||  ||||||||||||  ||||||||||||||
  51 TyrAspValAspLysArgProSerGlyValProAspArgPheSerGlySe 67

 258 CAAGTCTGGCAACACGGCCTCCCTGACCATCTCGGGCTCCAGGCTGAGG 307
     ||||||||||||||||||||||||||||||||||||||:::
  67 rLysSerAlaAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaAsnA 84

 308 ACGAGGCTGATTATTACTGTTGTCATATACAACCAGTAGCACTTTGTTA 357
     ::||||||||||||||||||:|||||   |||:||||||||
  84 snGluAlaAspTyrTyrCysSerSerTyrGlyThrTyrSerLeuIle 100

 358 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
     |||||||||||::|||||||||||||||
 101 PheGlyGlyThrLysLeuThrValLeuGly 111
```

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seq_name: SwissProt_40:LV1G_HUMAN

seq_documentation_block:
ID   LV1G_HUMAN     STANDARD;      PRT;    130 AA.
AC   P06316;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-I region BL2 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85062823; PubMed=6095199;
RA   Tsujimoto Y., Croce C.M.;
RT   "Molecular cloning of a human immunoglobulin lambda chain variable
RT   sequence.";
RL   Nucleic Acids Res. 12:8407-8414(1984).
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; X01147; CAA25598.1; -.
DR   PIR; A01966; L1HUBL.
```

```
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003556; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    130       IG LAMBDA CHAIN V-I REGION BL2.
FT   DOMAIN      20    115       V SEGMENT.
FT   DOMAIN     116    130       J SEGMENT.
FT   DISULFID    41    108       BY SIMILARITY.
FT   NON_TER    130    130
SQ   SEQUENCE   130 AA;  13564 MW;  FA44BB17D3A55EBF CRC64;

alignment_scores:
           Quality:    407.00          Length:     131
           Ratio:       3.634          Gaps:          2
Percent Similarity:  85.496   Percent Identity:  63.359

alignment_block:
US-09-019-441-1 x LV1G_HUMAN   ..

Align seg 1/1  to: LV1G_HUMAN  from: 1  to: 130

  1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCCTCACTCAGGGCACAGGATC  50
    | ||::  ::: ||||||::||||||   :::   |||||||
  1 MetThrCysSerProLeuLeuThrLeuLeuHisCysThrGlySe  17

 51 CTGGGCTCAGTCGCCCCAGACTCCTCCTCCTCGTGTCGTGGGTCTCCTG 100
    ||||||||||||::: ||||||||||||||:::::::||||
 17 rTrpAlaGlnSerValLeuThrGlnProProSerAlaAlaProG  34

101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT 150
    ||||:||||||||||||::||||:::    ||||| :||:
 34 lyGlnLysValThrIleSerCysSerGlySerSerAsnIleGlyAsn  50

151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACT 200
    ::|||||||||||||::: |||||||||||||||||
 51 ...AspTyrValSerTrpTyrGlnGlnHisProGlyThrAlaProLysLe  66

201 CATGATTTATGATGTCGCTAAGCGGCCCTCAGGGGTCTCGATCGCTTCT 250
    |:::|||||||| |||||| ||||||:::  |||||||||
 66 uLeuIleTyrAspAsnAsnLysArgProSerGlyIleProAspArgPheS  83

251 CTGGCTCCAAGTCTGGCAACACGGCCCTCCCTGACCATCTCGGGCTCCAG 300
    |||||||||||::::||||| ||::|||  ||||||||:
 83 erGlySerLysSerGlyThrSerAlaThrLeuGlyIleThrGlyLeuGln  99

301 GCTGAGGACGAGGCTGATTATTACTGTGTTCATATAACACCAGT...AG 347
    ::: |||||||||||||||||    ::::::::|| |
100 ThrGlyAspGluAlaAspTyrTyrCysGlyThrTrpAsnAsnSerLeuSe 116

348 CACTTTGTTATTCCGGAAGAGGGACCCGGTTGACCGTCCTAGT 390
    ::|||||| |||||||:::||||||||||
116 rGlyTrpValPheGlyGlyGlyThrLysLeuThrValLeuGly 130
```

seq_name: SwissProt_40:LV2J_HUMAN

seq_documentation_block:
ID   LV2J_HUMAN    STANDARD;    PRT;    110 AA.
AC   P01713;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-II region NIG-58.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=81215386; PubMed=6787031;
RA   Takayasu T., Takahashi N., Shinoda T., Okuyama T., Tomioka H.;
RT   "Comparative studies on the structure of the light chains of human
RT   immunoglobulins. III. Amino acid sequence of a lambda type Bence
RT   Jones euglobulin.";
RL   J. Biochem. 89:421-436(1981).
DR   PIR; A01979; L2HU58.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region.

```
FT   MOD_RES      1      1       PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
FT   DISULFID    22     90       BY SIMILARITY.
FT   NON_TER    110    110
SQ   SEQUENCE   110 AA;  11455 MW;  76C9F4C6B20312B6 CRC64;

alignment_scores:
           Quality:    387.50          Length:     110
           Ratio:       4.122          Gaps:          1
Percent Similarity:  85.455   Percent Identity:  71.818

alignment_block:
US-09-019-441-1 x LV2J_HUMAN   ..

Align seg 1/1  to: LV2J_HUMAN  from: 1  to: 110

 58 CAGTCTGCCCCAGCCTCAGCCTCCCTGTCTGTCTGGGTCTCCTGGACAGTC 107
    ||||||||  |||||||| ||||||||||||||||||||||||||||||||
  1 GlnSerAlaLeuThrGlnProArgSerValSerGlySerProGlyGlnSe  17

108 GGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACT 157
    :::||||||||||||||||:::::||   |||||  :::
 17 rLeuThrIleSerCysSerGlyAlaProCysAspValAspGlyCysGlyGlus 34

158 ATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACTCATGATT 207
    |||||||||||||||||||||||||||||||||||||||||||||||
 34 erValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuIleIle 50

208 TATGATGTCGCTAAGCGGCCCTCAGGGGTCTCGATCGCTTCTCTGGCTC 257
    |||  ::|||||||||||||||||||||||||||||||||||||||||
 51 TyrGlyPheSerAsnArgProSerGlyIleValProLeuArgPheSerGlySe 67

258 CAAGTCTGGCAACACGGCCCTCCCTGACCATCTCGGGCTCCAGGCTGAGG 307
    ||||||||||::::||||||||||||||||||||||::::|||
 67 rLysSerGlyAspAlaAlaSerLeuThrIleSerGlyLeuGlnValGluA 84

308 ACGAGGCTGATTATTACTGTGTTCATATAACAACCAGTAGCACTTTGTTA 357
    ||||||||||:::  ||||||:::  :||
 84 spGluAlaAspTyrTyrCysSerSerTyrAlaAspSerSer...ValIle 99

358 TTCGGAAGAGGGACCCGGTTGACCGTCCTA 387
    ||||||  |||:::||||||||||||||||
100 PheGlyAlaGlyThrLysLeuThrValLeu 109
```

seq_name: SwissProt_40:LV1D_HUMAN

seq_documentation_block:
ID   LV1D_HUMAN    STANDARD;    PRT;    111 AA.
AC   P01702;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-I region NIG-64.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83186114; PubMed=6404900;
RA   Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,

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RA   Shimizu A.;
RT   "Comparative studies on the structure of the light chains of human
RT   immunoglobulins. IV. Assignment of a subsubgroup.";
RL   J. Biochem. 93:421-429(1983).
DR   PIR; A01965; L1HUNG.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     89       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11454 MW;  A21C6121C18A61E0 CRC64;

alignment_scores:
        Quality:     359.00                    Length:     112
        Ratio:         3.740                    Gaps:         2
Percent Similarity:   85.714    Percent Identity:   64.286

alignment_block:
US-09-019-441-1 x LV1D_HUMAN

Align seg 1/1  to: LV1D_HUMAN  from: 1  to: 111

   58 CAGTCTGCCCGACTCAGCTCCCTGTCTGTCTGGGTCTTCCTGGACAGTC 107
      ||||||::: ||||||||||||||||:::::||||||||::
    1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnGl 17

  108 GGTCACCATCTCCTGCACTGGAACCAGCAGGATGACGTTGGTGGTTATAACT 157
      ||||||||||||||||:: ||:::||:||:||: |||:
   17 uValThrIleSerCysSerGlySerSerAsnIleGlyAsp...AsnP 33

  158 ATGTCTCCTGTACCAACAACCACCAGGCAAAGCCCCAAACTCATGATT 207
      ::||||||||||||:: |||| ||||||||||||::::|||
   33 heValSerTrpTyrGlnGlnLeuProGlyThrAlaProLysLeuLeuIle 49

  208 TATGATGTGCTCAAGCGGCCTCAGGGGTCTCTGATCGGTTCTCTGGCTC 257
      |||||| ||||| |::|||||||||||||||||||||
   50 TyrAspAsnAsnLysArgProSerGlyIleProAspArgPheSerGlySe 66

  258 CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGTGAGG 307
      |||||||||:::::||:||| ||::||||||||||| :|||
   66 rLysSerGlyThrSerAlaThrLeuGlyIleThrGlyLeuGlnThrGlyA 83

  308 ACGAGGCTGATTATTACTGTGTTCATATAACAACCAGT...AGCACTTTG 354
      ||||||||||||||||| :::::: ::||| |||:::
   83 spGluAlaAspTyrTyrCysGlyThrTrpAspSerSerLeuSerValGly 99

  355 TTATTCGGAGAGAGGGACCCGGTTGACCGTCCTAGGT 390
      ||:|||||||||| |||||||||||||||||||||
  100 MetPheGlyGlyGlyThrLysLeuThrValLeuGly 111

seq_name: SwissProt_40:LV2L_HUMAN

seq_documentation_block:
ID   LV2L_HUMAN     STANDARD;      PRT;   111 AA.
AC   P80422;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma lambda chain V-II region DOT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95255298; PubMed=7737190;
RA   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT   "Characterization of the two unique human anti-flavin monoclonal
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RT   immunoglobulins.";
RL   Eur. J. Biochem. 228:886-893(1995).
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region.
FT   DISULFID     22     90       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11787 MW;  F358B1EA2CD7109A CRC64;

alignment_scores:
        Quality:     357.00                    Length:     110
        Ratio:         4.011                    Gaps:         0
Percent Similarity:   80.909    Percent Identity:   63.636

alignment_block:
US-09-019-441-1 x LV2L_HUMAN

Align seg 1/1  to: LV2L_HUMAN  from: 1  to: 111

   61 TCTGCCCGACTCAGCTCCCTGTCTGTCTGGGTCTTCCTGGACAGTCGGT 110
      |||||| |||||| |||:::||||||||||||||||||||:::||
    2 SerAlaLeuThrGlnProArgSerLeuSerGlySerProGlyGlnAlaVa 18

  111 CACCATCTCCTGCACTGGAACCAGCAGGATGACGTTGGTGGTTATAACTATG 160
      ||||||||||||||||| ::: ||| |||::::
   18 lThrIleSerCysThrGlyLeuProSerValAlaAspAspAsnPheV 35

  161 TCTCCTGGTACCAACAACCACCAGGCAAAGCCCCAAACTCATGATTTAT 210
      |||||||||||||||||||||||||||||:::||||::::||
   35 alSerTrpTyrGlnGlnThrProGlyArgAlaProArgLeuLeuIleTyr 51

  211 GATGTGCTAAGCGGCCTCAGGGGGTCTCTGATCGGCTTCTCTGGCTCCAA 260
      ||| ||| ||||||||| :::|||||||||||||||||
   52 AspAspSerLeuArgProSerGlyValProAsnArgPheSerGlySerLy 68

  261 GTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACG 310
      |||| ::: |||||||||||||||||| :::|||
   68 sSerAspThrLysAlaAlaLeuThrIleSerGlyLeuGlnProAspAspG 85

  311 AGGCTGATTATTACTGTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
      ||||| |||||||||| : ||| |:||| |||
   85 luAlaThrTyrPheCysSerSerTyrValGlyAsnTyrIlePheValPhe 101

  361 GGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
      ||:::||||| |||||||||||||
  102 GlyGlnGlyThrAspLeuThrValLeuGly 111

seq_name: SwissProt_40:LV6E_HUMAN

seq_documentation_block:
ID   LV6E_HUMAN     STANDARD;      PRT;   131 AA.
AC   P06319;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-VI region EB4 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85215660; PubMed=392440;
RA   Anderson M.L.M., Brown L., McKenzie E., Kellow J.E., Young B.D.;
RT   "Cloning and sequence analysis of an Ig lambda light chain mRNA
RT   expressed in the Burkitt's lymphoma cell line EB4.";
RL   Nucleic Acids Res. 13:2931-2941(1985).
DR   PIR; A01990; L6HUEB.
DR   HSSP; P01709; 2MCG.
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```
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    131       IG LAMBDA CHAIN V-VI REGION EB4.
FT   DOMAIN       20    131       FRAMEWORK-1.
FT   DOMAIN       42     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     69       FRAMEWORK-2.
FT   DOMAIN       70     76       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       77    110       FRAMEWORK-3.
FT   DOMAIN      111    118       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      119    131       FRAMEWORK-4.
FT   DISULFID     41    110       BY SIMILARITY.
FT   NON_TER     131    131
SQ   SEQUENCE    131 AA;  14147 MW;  02A9179C8C05C2CD CRC64;
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alignment_scores:
           Quality:   355.50            Length:    132
           Ratio:       3.354           Gaps:        2
Percent Similarity:   80.303   Percent Identity:  56.818

alignment_block:
US-09-019-441-1 x LV6E_HUMAN

Align seg 1/1  to: LV6E_HUMAN  from: 1  to: 131

   1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCCTCACTCAGGGCACAGGATC  50
     |!||!||||:::  |||||!|| |||!|||||:::::: ||
   1 MetAlaTrpAlaProLeuLeuLeuThrLeuLeuAlaHisCysThrAspCy  17

  51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCGTGTCTGGGTCTCCTG  100
     |!||||:::       ||||!||| ||||!|||| |||||||
  17 sTrpAlaAsnPheMetLeuThrGlnProHisSerValSerGluSerProG  34

 101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTCGTGGT  150
     ||:::::||||||||||||||||||||||:::|||   :::::::::||
  34 lyLysThrValThrIleSerCysThrGlyAsnSerGlySerIleAlaSer  50

 151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCCAAAACT  200
     |||!|||||:::|||||||:::::: |:::::::   ::!||||
  51 ...AsnTyrValGlnTrpTyrGlnHisArgArgValSerAlaProThrIl  66

 201 CATGATTATGATGTCGCTAAGCGGCGCTCAGGGGTCTCTGATCGCTTCT  250
     :::!|||||:::    :::|||   !||||| |||||||!|||||
  66 eValIleTyrGluAspAsnGlnArgProLeuGlyValProAspArgPheS  83

 251 CTGGCTCC......AAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGG  294
     ||||||||       ::!||:::|||:::|||||||||||||||||||
  83 erGlySerIleAspSerSerSerAsnSerAlaSerLeuThrIleSerGly  99

 295 CTCCAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAAACCAG  344
     |||:::::||||||||||||||||||||  ||!::: :::!|
 100 LeuLysThrGluAspGluAlaAspTyrTyrCysGlnSerPheAspAsnTh  116

 345 TAGCACTTTGTTATTCGGAGAGAGGGACCCGGTTGACCGTCCTAGGT  390
     :::  :::!|||||  :::!||||!||:::||||||||||||
 116 rAsnGlnGlyValPheGlyGlyGlyThrLysLeuThrValLeuGly  131
```

```
OM of: US-09-019-441-1 to: SPTREMBL_19:*     out_format : pfs
Date: Sep 23, 2002 10:23 AM
About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09019441/runat.23092002_095259_6361/app_query.fasta_1.1860
-DB-SPTREMBL_19 -QFMT=fastan -SUFFIX=rspt -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.000
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09019441_@CGN1_1_409 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-019-441-1
Query length: 390
Database: SPTREMBL_19:*
Database sequences: 562222
Database length: 172994929
Search time (sec): 228.280000
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score_list:

| Sequence | Strd | Orig | ZScore | EScore | Len | ! Documentation |
|---|---|---|---|---|---|---|
| sp_human:Q96E61 | + | 427.50 | 785.50 | 8.9e-36 | 236 | ! Q96e61 homo sapiens (human). un |
| sp_human:Q96JD1 | + | 329.50 | 609.91 | 1.1e-25 | 112 | ! Q96jd1 homo sapiens (human). am |
| sp_human:Q96JD0 | + | 328.00 | 606.82 | 1.6e-25 | 116 | ! Q96jd0 homo sapiens (human). am |
| sp_human:Q96SB0 | + | 323.00 | 598.15 | 3.5e-25 | 108 | ! Q96sb0 homo sapiens (human). ar |
| sp_human:Q96JD2 | + | 317.00 | 586.69 | 2.3e-24 | 112 | ! Q96jd2 homo sapiens (human). am |
| sp_human:Q9NSD6 | + | 300.00 | 555.50 | 1.3e-22 | 107 | ! Q9nsd6 homo sapiens (human). hy |
| sp_rodent:Q99M11 | + | 299.00 | 546.78 | 1.8e-22 | 235 | ! Q99m11 mus musculus (mouse). hy |
| sp_human:Q96I69 | + | 292.00 | 533.85 | 9.3e-22 | 233 | ! Q96i69 homo sapiens (human). un |
| sp_human:Q9UL82 | + | 286.50 | 530.42 | 3.2e-21 | 107 | ! Q9ul82 homo sapiens (human). my |
| sp_human:Q91V32 | + | 254.00 | 463.24 | 8.0e-18 | 233 | ! Q91v32 m adult male small intes |
| sp_invertebrate:Q9U410 | + | 246.00 | 455.25 | 4.9e-17 | 106 | ! Q9u410 schistosoma japonicum |
| sp_human:Q9UL81 | + | 241.50 | 446.81 | 1.4e-16 | 107 | ! Q9ul81 homo sapiens (human). my |
| sp_human:Q9UL78 | + | 241.00 | 445.72 | 1.6e-16 | 109 | ! Q9ul78 homo sapiens (human). my |
| sp_human:Q96SA9 | + | 235.50 | 435.66 | 6.0e-16 | 107 | ! Q96sa9 homo sapiens (human). ar |
| sp_human:Q9UL70 | + | 234.00 | 432.79 | 8.6e-16 | 108 | ! Q9ul70 homo sapiens (human). my |
| sp_human:Q9UL77 | + | 233.00 | 430.93 | 1.1e-15 | 108 | ! Q9ul77 homo sapiens (human). my |
| sp_rodent:Q9JL78 | + | 231.00 | 427.80 | 1.7e-15 | 101 | ! Q9jl78 mus musculus (mouse). my |
| sp_human:Q91W12 | + | 231.00 | 420.43 | 1.9e-15 | 235 | ! Q91w12 mus musculus (mouse). ur |
| sp_rodent:Q9JL76 | + | 229.00 | 424.44 | 2.8e-15 | 97 | ! Q9jl76 mus musculus (mouse). ant |
| sp_human:Q9JL79 | + | 227.50 | 420.71 | 4.0e-15 | 108 | ! Q9jl79 homo sapiens (human). my |
| sp_rodent:Q9ERZ9 | + | 227.00 | 419.87 | 4.5e-15 | 107 | ! Q9erz9 mus musculus (mouse). an |
| sp_human:Q9UL85 | + | 226.50 | 418.78 | 5.1e-15 | 109 | ! Q9ul85 homo sapiens (human). my |
| sp_human:Q9UL86 | + | 224.00 | 414.13 | 9.3e-15 | 109 | ! Q9ul86 homo sapiens (human). my |
| sp_rodent:Q9QYF0 | + | 220.50 | 398.85 | 2.4e-14 | 298 | ! Q9qyf0 mus musculus (mouse). cr |
| sp_mammal:Q9N0W5 | + | 218.00 | 402.98 | 3.9e-14 | 109 | ! Q9n0w5 oryctolagus cuniculus (r |
| sp_rodent:Q920E6 | + | 218.00 | 402.98 | 3.9e-14 | 109 | ! Q920e6 mus musculus (mouse). ad |
| sp_human:Q91XK2 | + | 217.00 | 398.11 | 5.1e-14 | 154 | ! Q91xk2 mus musculus (mouse). my |
| sp_human:Q9UL83 | + | 214.00 | 395.63 | 1.0e-13 | 108 | ! Q9ul83 homo sapiens (human). my |
| sp_human:Q9R1A5 | + | 214.00 | 389.66 | 1.1e-13 | 214 | ! Q9r1a5 mus musculus (mouse). ka |
| sp_rodent:Q920E9 | + | 212.00 | 391.68 | 1.6e-13 | 111 | ! Q920e9 mus musculus (mouse). pt |
| sp_rodent:Q9ET13 | + | 211.00 | 389.98 | 2.1e-13 | 109 | ! Q9et13 mus musculus (mouse). in |
| sp_rodent:Q91WS9 | + | 209.50 | 380.56 | 3.2e-13 | 233 | ! Q91ws9 mus musculus (mouse). hy |
| sp_human:Q99M37 | + | 208.00 | 377.59 | 4.6e-13 | 238 | ! Q99m37 mus musculus (mouse). hy |
| sp_rodent:Q9JL82 | + | 207.50 | 383.88 | 4.7e-13 | 104 | ! Q9jl82 mus musculus (mouse). ar |
| sp_human:Q91WF8 | + | 206.50 | 374.95 | 6.6e-13 | 234 | ! Q91wf8 mus musculus (mouse). hy |
| sp_human:Q9UL80 | + | 204.50 | 377.51 | 9.7e-13 | 114 | ! Q9ul80 homo sapiens (human). my |
| sp_human:Q9UL76 | + | 200.50 | 371.85 | 2.5e-12 | 93 | ! Q9ul76 homo sapiens (human). myC |
| sp_rodent:Q92SS9 | + | 200.50 | 369.13 | 2.6e-12 | 127 | ! Q92ss9 mus musculus (mouse). in |
| sp_human:Q96PF6 | + | 200.00 | 369.00 | 2.9e-12 | 116 | ! Q96pf6 homo sapiens (human). ka |
| sp_rodent:Q91XL0 | + | 200.00 | 363.78 | 3.1e-12 | 211 | ! Q91xl0 mus musculus (mouse). ad |
| sp_rodent:Q921A6 | + | 199.00 | 360.76 | 4.0e-12 | 241 | ! Q921a6 mus musculus (mouse). |
| sp_rodent:Q9JL74 | + | 197.00 | 364.80 | 5.7e-12 | 99 | ! Q9jl74 mus musculus (mouse). |
| sp_rodent:Q9JL84 | + | 180.50 | 333.47 | 2.9e-10 | 107 | ! Q9jl84 mus musculus (mouse). |
| sp_rodent:Q9JL80 | + | 177.00 | 327.30 | 6.8e-10 | 103 | ! Q9jl80 mus musculus (mouse). |
| sp_rodent:Q61243 | + | 173.00 | 318.32 | 1.8e-09 | 123 | ! Q61243 mus musculus (mouse). |

seq_name: sp_human:Q96E61

```
seq_documentation_block:
ID   Q96E61      PRELIMINARY;      PRT;        236 AA.
AC   Q96E61;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   UNKNOWN (PROTEIN FOR MGC:17259).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC012876; AAH12876.1; -.
SQ   SEQUENCE 236 AA;  24712 MW;  7EC9FB3622FED957 CRC64;
```

alignment_scores:
```
Quality:              427.50                  Length:        131
Ratio:                  3.922                  Gaps:            1
Percent Similarity:    83.206   Percent Identity:   65.649
```

alignment_block:
US-09-019-441-1 x Q96E61

Align seg 1/1 to: Q96E61   from: 1  to: 236

```
  1 ATGGCCTGGACTCGTCCTCGTCACCCTCCTCACTCAGGGCACAGGATC  50
    ||||||||||::::  ||||||:|||||||||||:::::::  |||||||
  1 MetAlaTrpSerProLeuLeuLeuThrLeuLeuAlaHisCysThrGlySe 17

 51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCGTGTCTGGGTCTCCTG 100
                 |||||| ||||||||| ::::   ||||||
 17 rTrpAlaGlnSerValLeuAlaGlnProProSerValSerGlyAlaProG 34

101 GACAGTCGGTCACCATCTCCTCGACTGGAACCAGCCGATGACGTTGGTGGT 150
    ||||::|||||||||||||||||||||::::  || ||::::||
 34 lyGlnThrValThrIleSerCysThrGlySerThrAsnIleGlyValAla  50

151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACT 200
    |||    ||||||||:::   |||||| :::||::
 51 GlyTyrAlaValHisTrpTyrGlnGlnPheProGlyAlaAlaProLysVa 67

201 CATGATTTATGATGTCGCTAAGCGGCGCCTCAGGGGTCTCTGATCGCTTCT 250
    :::|||||                  |||||| ||||::||
 67 lLeuIleTyrGlyAsnTyrAsnArgProSerGlyValProAspArgPhes  84

251 CTGGCTCCAAGTGTCGGCAACACGCGTCCCTGACCATCTCTGGGCTCCAG 300
    ||||||||||::::::||| ||||||:||:::|||||||||:||||||||
 84 erGlySerLysSerGlyThrSerAlaSerLeuAlaIleThrGlyLeuGln 100

301 GCTGAGGACGAGGCTGATTATTACTGTGTTCATATACAACCAGT...AG 347
    ||||||||||||||||||||||||||||||||||||:::||  ||
101 AlaGluAspGluAlaAspTyrTyrCysGlnSerTyrAspGlySerLeuSe 117

348 CACTTTGTTATTCGGAAGAGAGGGACCCGGTTGACCGTCCTAGGT 390
    :::||||  ||||||||::::::::||||||::|||||||||
117 rGlySerValPheGlyAlaGlyThrLysValThrValLeuGly 131
```

seq_name: sp_human:Q96JD1

seq_documentation_block:

ID      Q96JD1          PRELIMINARY;      PRT;      112 AA.
AC      Q96JD1;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE      AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION PIP (FRAGMENT).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=BONE MARROW;
RA      Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT      "Amyloid lambda 6 light chain variable region PIP.";
RL      Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AF267874; AAK58586.1; -.
FT      NON_TER         1         1
FT      NON_TER       112       112
SQ      SEQUENCE      112 AA;   12047 MW;   0D3B85AC23567B9F CRC64;

alignment_scores:
        Quality:    329.50          Length:    109
        Ratio:      3.621           Gaps:      2
Percent Similarity:  83.486    Percent Identity:  61.468

alignment_block:
US-09-019-441-1 x Q96JD1

Align seg 1/1  to: Q96JD1  from: 1  to: 112

  70 ACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTC 119
     |||||||||  ||||||   ||||||::::||||:::||||||||||||||
   5 ThrGlnProHisSerValSerGluSerProGlyLysThrIleThrIleSe  21

 120 CTGCACTGGAACCAGCAGCGATGACGTTGGTGGTTATAACTATGTCCTGGT 169
     ||||||   :::||||   ||:::||       ||||||||||  :::|||
  21 rCysThrArgSerSerGlyAlaSer...AsnTyrValGlnTrpT  37

 170 ACCAACACCACCCAGGCAAAGCCCCAAACTCATGATTATGATGTCCGCT 219
     ||||||::||||||||||||   :::||||||        ::||||:::|
  37 yrGlnLeuArgProGlySerAlaProThrThrValIleTyrGluAspAsn  53

 220 AAGCGGGCCTCAGGGGTCTGATCGCTTCTCTGGCTCC......AAGTC 263
     ::::||  ||||||||||   |||||||||||||||||      :::||
  54 GlnArgProSerGlyValProAspArgPheSerGlySerIleAspSerSe  70

 264 TGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGG 313
     |::::||:::||||||||||||||||||:::||||||||||||||||||||
  70 rSerAsnSerAlaSerLeuThrIleSerGlyLeuGlnThrGluAspGluA  87

 314 CTGATTATTACTGTTGTTCATATAACACCAGTAGCACTTTGTTATTCGGA 363
     ||||||||||||   |||||   :::|||   |||   :::|||  |||||
  87 laAspTyrTyrCysGlnSerTyrAspSerAsnAsnTyrAlaLeuPheGly 103

 364 AGAGGACCCGGTTGACCGTCCTAGGT 390
     |||||||||||:::||||||||||||
 104 GlyGlyThrGlnLeuThrValLeuGly 112

seq_name: sp_human:Q96JD0

seq_documentation_block:
ID      Q96JD0          PRELIMINARY;      PRT;      116 AA.
AC      Q96JD0;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE      AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION SAR (FRAGMENT).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;

---

RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=BONE MARROW;
RA      Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT      "Amyloid lambda 6 light chain variable region SAR.";
RL      Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AF267875; AAK58587.1; -.
FT      NON_TER         1         1
FT      NON_TER       116       116
SQ      SEQUENCE      116 AA;   12294 MW;   F7B0E9F49FAE369E CRC64;

alignment_scores:
        Quality:    328.00          Length:    110
        Ratio:      3.565           Gaps:      3
Percent Similarity:  83.636    Percent Identity:  62.727

alignment_block:
US-09-019-441-1 x Q96JD0

Align seg 1/1  to: Q96JD0  from: 1  to: 116

  70 ACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTC 119
     |||||||||  ||||||   ||||||::::|||::::||||||||||||||
   5 ThrGlnProHisSerValSerGluSerProGlyLysThrValThrIleSe  21

 120 CTGCACTGGAACCAGCAGCGATGACGTTGGTGGTTATAACTATGTCCTGGT 169
     ||||||   :::||||   ||:::|       :::|||||||||  ::|||
  21 rCysThrArgSerSerGlySerIle...AlaThrAsnTyrValGlnTrpT  37

 170 ACCAACACCACCCAGGCAAAGCCCCAAACTCATGATTATGATGTCCGCT 219
     ||||   :::|||||||||   :::||||:|        :::|||||:::
  37 yrGlnLeuArgProGlySerAlaProThrThrValIleTyrGluAspAsn  53

 220 AAGCGGGCCTCAGGGGTCTCGATCGCTTCTCGGCTCC......AAGTC 263
     ::::||  ||||||||||   |||||||||||||||||      ::||
  54 GlnArgProSerGlyValProAspArgPheSerGlySerIleAspSerSe  70

 264 TGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGG 313
     |::::||:::||||||||||||||||||:::||||||||||||||||||||
  70 rSerAsnSerAlaSerLeuThrIleSerGlyLeuLysThrGluAspGluA  87

 314 CTGATTATTACTGTTGTTCATATACAACAGT...AGCACTTTGTTATTC 360
     |||||||||||   |||||   :::|||         :::|||  |||||
  87 laAspTyrTyrCysGlnSerTyrAspSerArgIleGlyAsnValIlePhe 103

 361 GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
     |||  |||||||||||:::||||||||||
 104 GlyGlyGlyThrGlnLeuThrValLeuGly 113

seq_name: sp_human:Q96SB0

seq_documentation_block:
ID      Q96SB0          PRELIMINARY;      PRT;      108 AA.
AC      Q96SB0;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE      ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN
DE      VARIABLE REGION (FRAGMENT).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=9837593; PubMed-9712075;
RA      Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT      "Molecular analysis of polyreactive monoclonal antibodies from
RT      rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT      antibody V region genes.";
RL      J. Immunol. 161:2020-2031(1998).
DR      EMBL; U96394; AAB68783.1; -.

```
FT   NON_TER      1      1
SQ   SEQUENCE   108 AA;   11594 MW;   F4B5DC478A043F48 CRC64;

alignment_scores:
        Quality:   323.00              Length:    109
        Ratio:     3.589               Gaps:        3
Percent Similarity:  82.569     Percent Identity:  61.468

alignment_block:
US-09-019-441-1 x Q96SB0

Align seg 1/1 to: Q96SB0 from: 1 to: 108

 58 CAGTCGCCCCGACTCAGCCTCCCTGTGTCGGGTCCTCCTGGACAGTC 107
    ||||||:    |||||||||||||||||::||||::||||||||||||
  1 GlnSerValLeuThrGlnProSerAlaSerGlyThrProGlyGlnAr  17

108 GGTCACCATCTCCTGCACTGGAACCAGCGATGAGCGTTGGTTATAACT 157
    |||||||||||::||:||||||||:||:|||::||||:::  |||
 17 gValThrIleSerCysSerGlySerSerAsnIleGlySer...AsnI  33

158 ATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACTCATGATT 207
    |||||  |||  ||||||:::|||||||||||||||||:::|||||||
 33 yrValTyrrTrpTyrGlnGlnLeuProGlyThrAlaProLysLeuLeuIle  49

208 TATGATGTCGCTAAGCGGGCCTCAGGGGTCTCGATCGGTTCTCTGGCTC 257
    |||||||||||  :::|||  ||||||||||||||||||||||||||
 50 TyrArgAsnAsnGlnArgProSerGlyValProAspArgPheSerGlySe  66

258 CAAGTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGG 307
    ||||||||||||||||||||||||||||||||||:||||||||||||
 66 rLysSerGlyThrSerAlaSerLeuAlaIleSerGlyLeuArgSerGluA  83

308 ACGAGGCTGATTATTACTGTGTTCATAT.........ACAACCAGTAGC 348
    ||||||||||||||||||||||::::::           :::::
 83 spGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerArgLeuSerGly.Ph  99

349 ACTTTGTTATTCGGAAGAGGGACCC 373
    :::  |||||| ||||||||
 99 eMetTrpTyrSerAlaGluGlyPro 107
```

seq_name: sp_human:Q96JD2

seq_documentation_block:
```
ID   Q96JD2      PRELIMINARY;      PRT;      112 AA.
AC   Q96JD2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION NEG (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BONE MARROW;
RA   Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT   "Amyloid lambda 6 light chain variable region NEG.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF267873; AAK58585.1; -.
FT   NON_TER      1      1
FT   NON_TER    112    112
SQ   SEQUENCE   112 AA;   11908 MW;   0B0B4B37E2360B06 CRC64;
```

alignment_scores:
```
        Quality:   317.00              Length:    109
        Ratio:     3.446               Gaps:        3
Percent Similarity:  84.404     Percent Identity:  60.550
```

alignment_block:

---

```
US-09-019-441-1 x Q96JD2

Align seg 1/1 to: Q96JD2 from: 1 to: 112

 70 ACTCAGCTCCCTCTGTGTCTGGTCTCGGTCTCCTGGACAGTCGGTCACCATCTC 119
    ||||||||  |||||||||||||||||||||||||:::::::::||||||||||
  5 ThrGlnProHisSerValSerGlySerProGlyLysThrIleThrIleSe  21

120 CTGCACTGGAACCAGCCATGAGACGTTGGTGGTTATAACTATGTCTCCTGGT 169
    ||||||||||:::|||       :::::::  |||  |||:::|||| ||||
 21 rCysThrGlySerSerGlyArgIleAlaSer...AsnSerValGlnTrpT  37

170 ACCAACACCACCAGGCAAAGCCCCAAACTCATGATTTATGATGTCGCT 219
    |||||::::||||||||||||||||||||:::|||::||||||:||||
 37 yrGlnGlnArgProGlySerAlaProAsnIleValMetTyrGluAsnAsn  53

220 AAGCGGGCCTCAGGGGTCTGATCGGTTCTCTGGCTCC.....AAGTC 263
    :::||| |||||||  ||||||||||||||||||||       :::|
 54 GlnArgProSerGlyValProAspArgPheSerGlySerIleAspSerSe  70

264 TGGCAACACGGCCTCCTCCGACCATCTCGGGCTCCAGGCTGAGGACGAGG 313
    |::::||:|||||||||||||||||||||||||||||||:|||||||||
 70 rSerAsnSerAlaSerLeuThrIleSerGlyLeuMetThrGluAspGluA  87

314 CTGATTATTACTGTGTTCATATACAACCAGTAGCACTTTG...TTATTC 360
    |||||||||:|||   |||:::|||||||||||||||||       ::|
 87 laAspTyrTyrCysGlnSerPheAspAspSerThrAsnGlnGlyValPhe 103

361 GGAAGAGGACCCGGTTGACCGTCCTA 387
    |||  |||||||||||||||||||
104 GlyGlyGlyThrArgLeuThrValLeu 112
```

seq_name: sp_human:Q9NSD6

seq_documentation_block:
```
ID   Q9NSD6      PRELIMINARY;      PRT;      107 AA.
AC   Q9NSD6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL PROTEIN (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LYMPHOCYTE;
RA   Hohmann A.;
RT   "Autoimmunity.";
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; L43092; AAA69746.2; -.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    107    107
SQ   SEQUENCE   107 AA;   11306 MW;   A2B04B37187A5F00 CRC64;
```

alignment_scores:
```
        Quality:   300.00              Length:    108
        Ratio:     3.571               Gaps:        3
Percent Similarity:  77.778     Percent Identity:  60.185
```

alignment_block:
US-09-019-441-1 x Q9NSD6

Align seg 1/1 to: Q9NSD6 from: 1 to: 107

 70 ACTCAGCCTCCCTCTGTGTCTGGTCTCCTGGACAGTCGGTCACCATCTC 119
```

```
                                        |||||      |||     ||||||       ||||||::
                                     3 ThrGlnAspProValSerValAlaLeuGlyGlnThrValArgIleTh  19

                                   120 CTGCACTGGAACCAGCGATGACGTTGGTGTTATAAACTATGTCTCCTGGT 169
                                       |||| |||     |||:::||   ||::||:||||||:
                                    19 rCysGlnGly......AspSerLeuArgSerTyr...TyrAlaSerTrpT  33

                                   170 ACCAACACCACCAGGCAAAGCCCCAAACTCATGATTATGATGTCGCT 219
                                       |||::||| ::|||::: |||||::|||||
                                    33 yrGlnGlnLysProGlyGlnAlaProValLeuValIleTyrGlyLysAsn  49

                                   220 AAGCCGGCCTCAGGGGTCTCTGATCGCTTCTGCTCCAAGTCTGGCAA 269
                                       ::::||| |||||:::    ||||||||||||||||::||||||
                                    50 AsnArgProSerGlyIleProAspArgPheSerGlySerSerGlyAs  66

                                   270 CACGGCTCCCTGACCATCTCGGGCTCCAGGCTGAGGACGAGGCTGATT 319
                                       ||||||||||||||:::||  ||||||||||||||||||
                                    66 nThrAlaSerLeuThrIleThrGlyAlaGlnAlaGluAspGluAlaAspT  83

                                   320 ATTACTGTGTTCATATACAACCAGTAGCACT...TTGTTATTCGGAAGA 366
                                       ||||||||     ::||:||||||||||||||
                                    83 yrTyrCysAsnSerArgAspSerGlyAsnHisAlaValPheGlyGly  99

                                   367 GGGACCGGTTGACCGTCCTAGGT 390
                                       |||||::::|||||||||||||
                                   100 GlyThrLeuThrValLeuGly 107

                          seq_name: sp_rodent:Q99Ml1

                          seq_documentation_block:
                          ID   Q99Ml1        PRELIMINARY;       PRT;    235 AA.
                          AC   Q99Ml1;
                          DT   01-JUN-2001 (TrEMBLrel. 17, Created)
                          DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
                          DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                          DE   HYPOTHETICAL 25.4 KDA PROTEIN.
                          OS   Mus musculus (Mouse).
                          OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                          OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                          OX   NCBI_TaxID=10090;
                          RN   [1]
                          RP   SEQUENCE FROM N.A.
                          RA   Strausberg R.;
                          RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                          DR   EMBL; BC002129; AAH02129.1; -.
                          DR   HSSP; P01703; 7FAB.
                          DR   InterPro; IPR003599; Ig.
                          DR   InterPro; IPR003597; Ig_cl.
                          DR   InterPro; IPR003600; Ig_like.
                          DR   InterPro; IPR003006; Ig_MHC.
                          DR   InterPro; IPR003596; Ig_v.
                          DR   Pfam; PF00047; ig; 2.
                          DR   SMART; SM00409; IG; 2.
                          DR   SMART; SM00407; IGc1; 1.
                          DR   SMART; SM00406; IGv; 1.
                          DR   SMART; SM00410; IG_like; 2.
                          DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                          KW   Hypothetical protein.
                          SQ   SEQUENCE  235 AA;  25403 MW;  39807BFE6782A3FB CRC64;

                          alignment_scores:
                                  Quality:     299.00             Length:      131
                                  Ratio:        2.990             Gaps:          3
                          Percent Similarity:  76.336       Percent Identity:  51.145

                          alignment_block:
                          US-09-019-441-1 x Q99Ml1

                          Align seg 1/1   to: Q99Ml1   from: 1   to: 235

                               1 ATGGCCTGGACTCTGCTCCGTCACCCTCCACTCAGGGCACAGGATC 50
                                 ||:::||||:::   ||||||||||::::::|||   |||||||||
```

```
                                        1 MetThrTrpAlaProLeuLeuValPheLeuHisHisLeuThrGlySe  17

                                       51 CTGGGCTCAGTCTGCCCGACTCAGCCTCCCTGTGTCTGGTCTCCTG 100
                                          ||||||       ||||||||    :::  ||||||||||| |||
                                       17 rCysAlaGlnLeuValLeuThrGlnProSerValSerThrSerLeuG  34

                                      101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT 150
                                          |!:::||||        ::|||   |||   |||||:::::|::|||
                                       34 lySerThrAlaLysLeuProCysLysAlaSerThrGlyAsnIleGlyAsp  50

                                      151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACT 200
                                          ::|||||||||        ||||| ::|||||:::::||||||||||
                                       51 ...SerTyrValAsnTrpTyrGlnInTyrMetGlyArgSerProThrAs  66

                                      201 CATGATTTATGATGTCGCTAAGCCGGCCTCAGGGGTCTCTGATCGCTTCT 250
                                          ||||||||        ||    ||||||||||||||||||||||||
                                       66 nMetIleTyrGlyAspSerGlyValSerAspArgPheS  83

                                      251 CTGGCTCC......AAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGG 294
                                          ||||||||       ::::||||:::|||   ||||||||||||||||
                                       83 erGlySerIleAspSerSerAsnSerAlaPheLeuThrIleGlnAsn  99

                                      295 CTCCAGGCTGAGGACGAGGCTGATTATTACTGTGTTCATATACAACCAG 344
                                          ::||||||||||||||||||||||    |||||     :::||  :||:
                                      100 ValGlnAlaAspGluAlaAspTyrTyrCysGlnSerTyr...SerSe  115

                                      345 TAGCACTTTGTTATTCGGAAGAGGGACCGGTTGACCGTCCTA 387
                                          |:::    ::|||||||||||||||||  :||||||||||||
                                      115 rGlyIleArgValPheGlyGlyGlyThrLysLeuThrValLeu 129

                          seq_name: sp_human:Q96I69

                          seq_documentation_block:
                          ID   Q96I69        PRELIMINARY;       PRT;    233 AA.
                          AC   Q96I69;
                          DT   01-DEC-2001 (TrEMBLrel. 19, Created)
                          DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
                          DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                          DE   UNKNOWN (PROTEIN FOR MGC:12849).
                          OS   Homo sapiens (Human).
                          OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                          OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                          OX   NCBI_TaxID=9606;
                          RN   [1]
                          RP   SEQUENCE FROM N.A.
                          RC   TISSUE=PRIMARY B-CELLS FROM TONSILS;
                          RA   Strausberg R.;
                          RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                          DR   EMBL; BC007782; AAH07782.1; -.
                          SQ   SEQUENCE  233 AA;  24802 MW;  C694F8397B27650B CRC64;

                          alignment_scores:
                                  Quality:     292.00             Length:      131
                                  Ratio:        2.949             Gaps:          2
                          Percent Similarity:  75.573       Percent Identity:  48.092

                          alignment_block:
                          US-09-019-441-1 x Q96I69

                          Align seg 1/1   to: Q96I69   from: 1   to: 233

                               1 ATGGCCTGGACTCTGCTCCGTCACCCTCCACTCAGGGCACAGGATC 50
                                 ||||||||||||:::|||||||::::::|||   |||||||||||
                               1 MetAlaTrpThrValLeuLeuLeuGlyLeuLeuSerHisCysThrGlySe  17

                              51 CTGGGCTCAGTCGCCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTG 100
                                 | :|:::   |||||||||    :::  ||||||||||| :::|||
                              17 rGlyThrSerTyrValLeuThrGlnProAlaSerValSerAlaProG  34

                             101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT 150
                                 ||:::|||||    ::|||   ||   |||:::::|::|||||
                              34 lyGlnThrAlaArgIleThrCysGlyGlySerAsn......LeuGly 47
```

```
151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACT 200
        :::   ||:::||||||     :::||||||:||||  ||
 48 SerLysSerValAsnTrpTyrGlnLeuArgProGlyGlnAlaProIleLe 64

201 CATGATTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGATCGCTTCT 250
     |:::||:::     ::|||   ::|||::::   ::||||:::::|
 64 uValValTyrGluAsnLysGluArgProAlaGlyIleProGluArgLeuS 81

251 CTGGCTCCAAGTCTGCAACACGGACCGGCTCCCTGACCATCTCTGGGCTCCAG 300
     ||:::          |||    |||||||||||||||   :::|||||
 81 erAlaLeuThrSerGluGluThrAlaThrLeuThrIleSerSerValVal 97

301 GCTGAGGACGAGGCTGATTATTACTGTGTTCATAT...ACAACCAGTAG 347
     |||  |||||||||||||:::||         :::    |||:||||:
 98 AlaGlyGluAspGluAlaAspTyrTyrCysGlnValTrpAspThrThrSerGl 114

348 CACTTTGTTATTCGGAAGAGGGACCCGGTTGACCCGTCCTAGGT 390
        :::|||||||||:::||||||||||||
114 nGlnTyrValPheGlyThrGlyThrGlnValThrValLeuGly 128
```

seq_name: sp_human:Q9UL82

seq_documentation_block:
ID   Q9UL82          PRELIMINARY;          PRT;        107 AA.
AC   Q9UL82;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035032, AAD56268.1; -.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     107     107
SQ   SEQUENCE    107 AA;   11445 MW;   52F0CC1AB26821DC CRC64;

alignment_scores:
          Quality:  286.50          Length:     106
            Ratio:    3.411          Gaps:         1
Percent Similarity:  79.245     Percent Identity: 53.774

alignment_block:
US-09-019-441-1 x Q9UL82

Align seq 1/1 to: Q9UL82 from: 1 to: 107

```
 70 ACTCAGCCTCCCTCGTGTCTGGGCTCCTCCGGACAGTCGGTCACCATCTC 119
     ||||||||   |||||||||   |||||||||||:::||     :||::|
  5 ThrGlnProSerProValSerGlyLeuLeuProGlyGlnThrAlaArgIleTh 21

120 CTGCACTGGAACCAGCAGCGATGCAGTTGGTGGTTATAACTATGTCTCTGGT 169
     :||::::|||   :::    ::|      ::|||:::|||:||:::|||
 21 rCysSerGly.........AspLeuLeuAlaLysLysTyrAlaArgTrpP 35

170 ACCAACACCACCCAGGCAAAGCCCCAAACTCATGATTATGATGTCGCT 219
```

```
        ::|||::     ||||||     ||:::|||||    ||:::|||::
 35 heGlnGlnLysProGlyGlnAlaProIleLeuValIlePheLysAspThr 51

220 AAGCGGGCCTCAGGGGTCTCTGATCGCTTCTCTGGCTCCAAGTCTGGCAA 269
     ::::|||     ::|||||||||     :::|||||||||||||:::||
 52 GluArgProSerGlyIleProGluArgPheSerGlySerSerGlyTh 68

270 CACGGGACCGGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATT 319
     ::|::::|||||||||||||   |||||||||||||||||||||||||||||
 68 rThrValThrIleSerGlyAlaGlnValGluAspGluAlaAspT 85

320 ATTACTGTGTTCATATACAACCAGTAGCACTTGTTATTCGGAAGAGGG 369
     |||||||     ||    :::::        :::|||||||   |||
 85 yrTyrCysTyrSerAlaSerAspAsnAsnGlyArgValPheGlyGlyGly 101

370 ACCCGGTTGACCGTCCTA 387
     ||:::||||||||||||
102 ThrLysLeuThrValLeu 107
```

seq_name: sp_rodent:Q91V32

seq_documentation_block:
ID   Q91V32          PRELIMINARY;          PRT;        233 AA.
AC   Q91V32;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ADULT MALE SMALL INTESTINE cDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE   CLONE:2010203H01, FULL INSERT SEQUENCE (ADULT MALE SMALL INTESTINE
DE   cDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2010005L06, FULL
DE   INSERT SEQUENCE) (ADULT MALE SMALL INTESTINE cDNA, RIKEN FULL-LENGTH
DE   ENRICHED LIBRARY, CLONE:2010013G21, FULL INSERT SEQUENCE).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA   Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
RA   Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
RA   Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
RA   Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y.,
RA   Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
RA   Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";

RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
DR   EMBL; AK008421; BAB25659.1; -.
DR   EMBL; AK008129; BAB25479.1; -.
DR   EMBL; AK008232; BAB25546.1; -.
SQ   SEQUENCE    233 AA;  24874 MW;  C4E896D46AABD2C1 CRC64;

alignment_scores:
        Quality:      254.00              Length:        130
        Ratio:        2.791               Gaps:          1
Percent Similarity:   70.000       Percent Identity:   42.308

alignment_block:
US-09-019-441-1 x Q91V32      ..

Align seg 1/1 to: Q91V32 from: 1 to: 233

   1 ATGGGCTGGACTCGTCCTCGTCACCCTCCTCACTCAGGGCACAGGATC  50
     ||||||||     |||    |||:::::::||||||::.  :::::|||:
   1 MetAlaTrpIleSerLeuIleLeuSerLeuLeuAlaLeuSerSerGlyAl  17

  51 CTGGGCTCAGTCTGCCCGACTCAGCCTCCCTCTGTCTGGGTCTCCTG  100
     :.:::|||:::::::  |||||   :::::::|||||:      ||||||
  17 aIleSerGlnAlaValValThrGlnGluSerAlaLeuThrSerProG  34

 101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGCGATGACGTTGGTGGT  150
     |||||||||||  |::::::|||     :::::::||
  34 lyGluThrValThrIleThrCysArgSerSerThrGlyAlaValThrThr  50

 151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACT  200
     ||||||||||| |||::::   |||
  51 SerAsnTyrAlaAsnTrpValGlnHisLysProAspHisLeuPheThrGl  67

 201 CATGATTATGATGTCGCTAAGCGGCCTCAGGGTCTCTGATCGCTTCT  250
     :::|||   ::.:||||| ||||||     |||||||     ||||||
  67 yLeuIleGlyGlyThrAsnAsnArgAlaProGlyValProAlaArgPheS  84

 251 CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG  300
     |||||||     :::::|||||::::.:|||||     ||:::|||||
  84 erGlySerLeuIleGlyAspLysAlaAlaLeuThrIleThrGlyAlaGln  100

 301 GCTGAGGACGAGGCTGAATTATTACTTGTTGTTCATATACAACCAGTAGCAC  350
     :::|||||||||    ||:::||   :::     |||::      :::||:
 101 ThrGluAspGluAlaIleTyrPheCysAlaLeuTrp......TyrSerSe  115

 351 TTTGTTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT  390
     :::||||| |||||||||::||||||||||||||||||||
 115 rTrpValPheGlyGlyGlyThrLysLeuThrValLeuGly  128

seq_name: sp_invertebrate:Q91V32

seq_documentation_block:
ID   Q91V32      PRELIMINARY;     PRT;     106 AA.
AC   Q91V32;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE   VARIABLE REGION (FRAGMENT).

OS   Schistosoma japonicum (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC   Schistosomatoidea; Schistosomatidae; Schistosoma.
OX   NCBI_TaxID=6182;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT   "Amplification, cloning and sequence analysis of the light chain
RT   variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT   Schistosoma japonicum.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF207620; AAF19434.1; -.
DR   HSSP; P01679; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     106     106
SQ   SEQUENCE    106 AA;  11478 MW;  F20F544426BAE63E CRC64;

alignment_scores:
        Quality:      246.00              Length:        104
        Ratio:        3.075               Gaps:          3
Percent Similarity:   76.923       Percent Identity:   50.000

alignment_block:
US-09-019-441-1 x Q9U410      ..

Align seg 1/1 to: Q9U410 from: 1 to: 106

  70 ACTCAGCCTCCCTCTG...TCTGGGTCTCCTGGACAGTCGGTCACCAT  116
     ||||| |||::::::::|  |||:::||||||||::::||||||
   5 ThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMe  21

 117 CTCCTGCACTGGAACCAGCAGCGATGACGTTGGTGGTTATAACTATGTCTCCT  166
     :::||:::::::||     ::.:||||
  21 tThrCysSerAlaSerSer...........SerValSerTyrValTyrT  34

 167 GGTACCAACACCACCCAGGCAAAGCCCCAAACTCATGATTATGATGTC  216
     ||||| ||||::|:||||   |||::.:::||||||:::|||||||
  34 rPTyrLeuGlnLysProGlySerSerProArgLeuLeuIleTyrAspThr  50

 217 GCTAAGCGGGCTCAGGGTCTCTGATCGCTTCTGGCTCCAAGTCTGG  266
     ::::.| ||||||||||     |||||||||     ||||
  51 SerAsnLeuAlaSerGlyValProValArgPheSerGlySerGlySerGl  67

 267 CAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTG  316
     ::.:.:|||||     :::|||||     ||||||||:::|||||||
  67 yThrSerTyrSerLeuThrIleSerArgMetGluAlaGluAspAlaAlaT  84

 317 ATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTCGGAAGA  366
     ||||||||     ||:::     ||||||     ||||||||
  84 hrTyrTyrCysGlnGlnTrp...ThrSerTyrProPheThrPheGlySer  99

 367 GGGACCCGGTTG  378
     ||||::|||:||
 100 GlyThrLysLeu  103

seq_name: sp_human:Q9UL81

seq_documentation_block:
ID   Q9UL81      PRELIMINARY;     PRT;     107 AA.
AC   Q9UL81;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035033; AAD56269.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1
FT   NON_TER    107     107
SQ   SEQUENCE   107 AA;   11501 MW;   070549FDE0754748 CRC64;

alignment_scores:
            Quality:  241.50              Length:      103
            Ratio:      3.096             Gaps:          3
Percent Similarity:  75.728      Percent Identity:  51.456

alignment_block:
US-09-019-441-1 x Q9UL81

Align seg 1/1  to: Q9UL81  from: 1  to: 107

  76 CCTCCCTCTGTGTCGGTCTCCTGGACAGTCGGTCACCATCTCCTGCAC 125
     |||  |||:::||:::||  |||::: |||||||||:::|||
   8 ProSerLeuSerAlaSerValGlyAspArgValThrIleThrCysAr 24

 126 TGGAACCAGGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAAC 175
     :::||::::::::|:::    ||||||:::||||||||
  24 g...AlaSerGlnSerIleSer......AsnTyrLeuAsnTrpTyrGlnG 38

 176 ACCACCCAGGCAAAGCCCCAAACTCATGATTATGATGTCGGTAAGCGG 225
     ::  |||||||||:::|||||  :::||||||
  38 lnLysProGlyLysAlaProAsnLeuLeuIleTyrAlaAlaSerSerLeu 54

 226 GCCTCAGGGGTCTCTGATCGCTTCTCGGCTCCAAGTCTGGCAACACGGC 275
     |||||||    :::|||||||||||||  |||||||
  55 GlnSerGlyValProSerArgPheSerGlySerGlySerGlyThrAspPh 71

 276 CTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACT 325
     :::|||||||||||||||||||    ||  |||||
  71 eThrLeuThrIleSerGlyLeuGlnAlaGluAspGluAlaThrTyrTyrC 88

 326 GTTGTTCATATACAACCAGTAGCACTTTGTTATTCGGAAGAGGACCCGG 375
     ||  :::::||||  |||||    |||||||||
  88 ys......GlnGlnSerTyrSerAlaLeuThrPheGlyProGlyThrLys 102

 376 TTGACCGTC 384
     ::: :::
 103 ValAspIle 105

seq_name: sp_human:Q9UL78

seq_documentation_block:
ID   Q9UL78      PRELIMINARY;     PRT;     109 AA.
AC   Q9UL78;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]

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RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035036; AAD56272.1; -.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1
FT   NON_TER    109     109
SQ   SEQUENCE   109 AA;   11646 MW;   5F675C52EC7EE197 CRC64;

alignment_scores:
            Quality:  241.00              Length:      106
            Ratio:      2.939             Gaps:          4
Percent Similarity:  77.358      Percent Identity:  50.000

alignment_block:
US-09-019-441-1 x Q9UL78

Align seg 1/1  to: Q9UL78  from: 1  to: 109

  70 ACTCAGCCTCCC...TCTGTGTCGGTCTCCTGGACAGTCGGTCACCAT 116
     |||||| |||      :::::||  ||||||||||  ::|||||
   5 ThrGlnSerProGlyThrLeuSerLeuSerProGlyGluArgAlaThrLe 21

 117 CTCCTGCACTGGAACCAGGATGACGTTGGTGGTTATAACTATGTCTCCT 166
     :||||||    :::||||||:::||||:::     :::||||:::||
  21 uSerCysArg...AlaSerGlnSerValSerSer...SerTyrLeuAlaT 36

 167 GGTACCAACACCACCCAGGCAAAGCCCCAAACTCATGATTATGATGTC 216
     ||||||||  ||||||:::|||||:::|||  :::||:::|||||
  36 rpTyrGlnGlnLysProGlyGlnAlaProArgLeuLeuIleTyrGlyAla 52

 217 GCTAAGCGGCCTCAGGGGTCTCTGATCGCTTCTCGGCTCCAAGTCTGG 266
     :::::||||||:::|||::     ||||||||||||||  |||||
  53 SerSerArgAlaThrGlyIleProAspArgPheSerGlySerGlySerGl 69

 267 CAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTG 316
     |:::    :::|||||||||||||||  ||||| |||
  69 yThrAspPheThrLeuThrIleSerArgLeuGluProGluAspCysAlaV 86

 317 ATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTCGGAAGA 366
     |||||||  |||  ::|||  |||||||||    |||||
  86 alTyrTyrCysGlnGlnTyr...GlySerSerProLeuThrPheGlyGly 101

 367 GGGACCCGGTTGACCGTC 384
     |||||:::::||||||
 102 GlyThrLysValGluIle 107

seq_name: sp_human:Q96SA9

seq_documentation_block:
ID   Q96SA9      PRELIMINARY;     PRT;     107 AA.
AC   Q96SA9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE   VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98375893; PubMed=9712075;

```
RA   Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT   "Molecular analysis of polyreactive monoclonal antibodies from
RT   rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT   antibody v region genes.";
RL   J. Immunol. 161:2020-2031(1998).
DR   EMBL; U96396; AAB68785.1; -.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE    107 AA;  11520 MW;  4BB43E9C5B577F16 CRC64;

alignment_scores:
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                Ratio:    3.058            Gaps:        3
Percent Similarity:  74.757   Percent Identity:  50.485

alignment_block:
US-09-019-441-1 x Q96SA9

Align seg 1/1  to: Q96SA9   from: 1   to: 107

   76 CCTCCCTCTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCCTGCAC 125
      ||| |||:|||:||| |||:||||  ||||||||| |||||||||:||||
    8 ProSerLeuSerAlaSerValGlyAspArgValThrIleThrCysAr  24

  126 TGGAACCAGCGATGACGTTGGTGTTATAACTATGTCTCCTGGTACCAAC 175
      :::||:||||||||||        GlyIleSerAsnTyrLeuAlaTrpTyrGlnG 38
   24 g...AlaSerGlnSerIleSer.....SerTyrLeuAsnTrpTyrGlnG 38

  176 ACCACCCAGGCAAAGCCCCCAAACTCATGATTATGATGTCGCTAAGCGG 225
      :: ||||||||||:||||||||:||||||
   38 lnLysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeu 54

  226 GCCTCAGGGGTCTCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGC 275
      ||||||||  ||||||||||||||||||  |||:::
   55 GlnSerGlyValProSerArgPheSerGlySerGlyThrAspPh 71

  276 CTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACT 325
      ::|||||||||||| |||||    |||||  ||||
   71 eThrLeuThrIleSerSerLeuGlnProGluAspPheAlaThrTyrTyrC 88

  326 GTTGTTCATATACAACACCAGTAGCACTTTGTTATTCGGAGAGAGGACCCGG 375
      |||| ||||||  ||||||||  ||||||
   88 ys.....GlnGlnSerTyrSerThrLeuThrPheGlyGlyGlyThrLys 102

  376 TTGACCGTC 384
      ||: :::
  103 ValGluIle 105
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DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE    108 AA;  11633 MW;  B7BEDC3E41FCCA37 CRC64;

alignment_scores:
              Quality:  234.00          Length:      103
                Ratio:    3.162            Gaps:        2
Percent Similarity:  71.845   Percent Identity:  49.515

alignment_block:
US-09-019-441-1 x Q9UL70

Align seg 1/1  to: Q9UL70   from: 1   to: 108

   76 CCTCCCTCTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCCTGCAC 125
      ||| |||:|||:||| :::||||  ||  ||||| |||||||||::||
    8 ProSerLeuSerAlaSerValGlyAspArgValThrIleThrCysAr 24

  126 TGGAACCAGCGATGACGTTGGTGTTATAACTATGTCTCCTGGTACCAAC 175
      :::||:|||        GlyIleSerAsnTyrLeuAlaTrpTyrGlnG 38
   24 gAlaSerGln.......GlyIleSerAsnTyrLeuAlaTrpTyrGlnG 38

  176 ACCACCCAGGCAAAGCCCCCAAACTCATGATTATGATGTCGCTAAGCGG 225
      :: |||||||||:|||||  ::||||||
   38 lnLysProGlyLysValProLysSerLeuIleTyrAlaAlaSerThrLeu 54

  226 GCCTCAGGGGTCTCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGC 275
      ||||||||  ||||||||||||||||||  |||:::
   55 GlnSerGlyValProSerArgPheSerGlySerGlyThrAspPh 71

  276 CTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACT 325
      ::|||||||||||  |||:|||    ||  ||||
   71 eThrLeuThrIleSerSerLeuGlnProGluAspValAlaThrTyrTyrC 88

  326 GTTGTTCATATACAACACCAGTAGCACTTTGTTATTCGGAAGAGGGACCCGG 375
      |||| ||::||   :::||| |||||||
   88 ysGlnLysTyr...AsnSerAlaProArgThrPheGlyProGlyThrLys 103

  376 TTGACCGTC 384
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  104 LeuGluIle 106
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seq_name: sp_human:Q9UL70

seq_documentation_block:
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AC   Q9UL70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035044; AAD56280.1; -.
DR   HSSP; P01607; 1REI.
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Date: Sep 23, 2002 10:19 AM
About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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-LOOPEXT=0.000 -QGAPEXT=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
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-OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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Search information block:
Query: US-09-019-441-1
Query length: 390
Database: Pending_Patents_AA_Main:*
Database sequences: 3502263
Database length: 331980561
Search time (sec): 811.400000
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Sequence              Strd  Orig      ZScore    EScore  Len !  Documentation
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seq_documentation_block:
;  Sequence 2, Application US/09292053
;  GENERAL INFORMATION:
;    APPLICANT:  REFF, MITCHELL E.
;    APPLICANT:  KLOETZER, WILLIAM S.
;    APPLICANT:  NAKAMURA, TAKEHIKO
;    TITLE OF INVENTION:  GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE
;    TITLE OF INVENTION:  THEREOF AS THERAPEUTICS
;    FILE REFERENCE:  23522.0699
;    CURRENT APPLICATION NUMBER:  US/09/292,053
;    CURRENT FILING DATE:  1999-04-14
;    PRIOR APPLICATION NUMBER:  08/803,085
;    PRIOR FILING DATE:  1997-02-20
;    NUMBER OF SEQ ID NOS:  39
;    SOFTWARE:  PatentIn Ver. 2.1
;  SEQ ID NO 2
;    LENGTH: 130
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-292-053-2
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alignment_scores:
     Quality:    686.00            Length:        130
       Ratio:    5.277             Gaps:            0
Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-019-441-1 x US-09-292-053-2

Align seq 1/1 to: US-09-292-053-2   from: 1  to: 130

    1  ATGGCCTGGACTCTGCTCCTCGTCACCCTCCACTCAGGGCACAGGATC    50
       ||||||||||||||||||||||||||||||||||||||||||||||||
    1  MetAlaTrpThrLeuLeuLeuValThrLeuHisGlnGlyThrGlySe    17

   51  CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTG   100
       ||||||||||||||||||||||||||||||||||||||||||||||||
   17  rTrpAlaGlnSerAlaProThrGlnProProSerValSerGlySerProG   34

  101  GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCCATGACGTTGGTGGT  150
       ||||||||||||||||||||||||||||||||||||||||||||||||||
   34  lyGlnSerValThrIleSerCysThrGlyThrSerHisAspValGlyGly   50

  151  TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACT   200
       ||||||||||||||||||||||||||||||||||||||||||||||||
   51  TyrAsnTyrValSerTrpTyrGlnHisHisProGlyLysAlaProLysLe   67

  201  CATGATTTATGATGTCCTAAGCGGGCCTCAGGGGTCTCGATCGCTTCT   250
       ||||||||||||||||||||||||||||||||||||||||||||||||
   67  uMetIleTyrAspValAlaLysArgAlaSerGlyValSerAspArgPheS   84

  251  CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG  300
       ||||||||||||||||||||||||||||||||||||||||||||||||||
   84  erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln  100

  301  GCTGAGGACGAGGCTGATTATTACTGTGTTCATATACAACCAGTAGCAC  350
       ||||||||||||||||||||||||||||||||||||||||||||||||
  101  AlaGluAspGluAlaAspTyrTyrCysCysSerTyrThrThrSerSerTh  117

  351  TTTGTTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT  390
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  117  rLeuLeuPheGlyArgGlyThrArgLeuThrValLeuGly  130
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; Sequence 49652, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 49652
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (155)..(178)
; OTHER INFORMATION: Immunoglobulins and major histocompatibility complex proteins
; OTHER INFORMATION: domain identified by eMATRIX, accession number BL00290A, p-value=
; OTHER INFORMATION: 1.529e-14, raw score of 20.89
; NAME/KEY: DOMAIN
; LOCATION: (34)..(220)
; OTHER INFORMATION: Immunoglobulin domain identified by PFam, accession name ig,
; OTHER INFORMATION: E-value=7.2e-19, PFam score of 65.8
PCT-US01-08631-49652

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        Quality:      561.50        Length:      131
        Ratio:        4.602         Gaps:        1
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US-09-019-441-1 x PCT-US01-08631-49652     ..

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    1 MetAlaTrpAlaLeuLeuLeuLeuLeuThrLeuLeuThrGlnAspThrGlySe   17

   51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTG   100
      ||||||||||| ||||||  |||||||||||||||||||||||||||||
   17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG   34

  101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGCGTTGGTGGT   150
      |||||||:||||||||||||||||:::|||||:||||||:||
   34 lyGlnSerIleThrIleSerCysThrGlyThrGlyThrGlyAsnAspValGlySer   50

  151 TATAACTATGTCTCCTGGTACCAACACCCAGGCAAAGCCCCAAACT   200
      ||| ||||||||||||||||||||||||:::|||||||||||||||
   51 TyrAsnLeuValSerTrpTyrTyrGlnHisProGlyLysAlaProLysIl   67

  201 CATGATTTATGATGTCGCTAAGGCGGCCTCTCGATCGCTTCT   250
      ||||||:||||||::::|||||||||||||||||||||||||
   67 eMetIleTyrGluValSerLysArgProSerGlyValSerAsnArgPheS   84

  251 CTGGCTCCAAGTCGCAACACGCCCTCCCTGACCATCTCGGGCTCCAG   300
      ||||||||||||||||||||||||||||||||||||||||||||||||
   84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln   100

  301 GCTGAGGACGAGCTGATTATTACTGTGTTGTTCATATACAACCAGT...AG   347
      |||||||||||||||||:||||||||||||||||||||||| :::|||
  101 AlaGluAspGluAlaAspTyrTyrCysCysSerTyrThrSerSerArgPr   117

  348 CACTTTGTTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT   390
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  117 QAspValValPheGlyGlyGlyThrLysLeuThrValLeuGly   131

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; Sequence 82, Application PC/TUS0204175
; GENERAL INFORMATION:
; APPLICANT: diaDexus, Inc.
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Hu, Ping
; APPLICANT: Recipon, Herve
; APPLICANT: Karra, Kalpana
; APPLICANT: Cafferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes an
; FILE REFERENCE: DEX-0310
; CURRENT APPLICATION NUMBER: PCT/US02/04175
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/268,290
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/268,834
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapien
PCT-US02-04175-82

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Percent Similarity: 93.798    Percent Identity: 81.395

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US-09-019-441-1 x PCT-US02-04175-82     ..

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   54 GGCTCAGTCTGCCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTGGAC   103
      |||||||| ||||| |||||||||||||||||||||||||||||||||||
   17 pAlaGlnSerAlaLeuThrGlnSerAlaSerValSerGlySerProGlyG   34

  104 AGTCGGTCACCATCTCCTGCACTGGAACCAGCAGCGATGACGTTGGTGGTTAT   153
      ||||:||||||||||||||||:::||||||:||||||:|||||:::
   34 lnSerIleThrIleSerCysThrGlyThrSerSerHisValGlyGlyTyr   50

  154 AACATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACTCAT   203
      ||||||||||||||||||::::|||||||||||||||||||||||||
   51 AsnTyrValSerTrpTyrGlnInGlnHisProGlyLysAlaProLysLeuI   67

  204 GATTTATGATGTCGGCTAAGGCGGCCTCCTCAGGGGTCTCGATCGCTTCTCTG   253
      :||||||||::::|||||||  |||||||:||||||:||||||||||
   67 eIleTyrGluValSerGlyAsnArgProSerGlyValSerAsnArgPheSerG   84

  254 GCTCCAAGTCGGCAACACGCCCTCCCTGACCATCTCGGGCTCCAGGCT   303
      ||||||||||||||||||||||||||||||||||||||||||||||||
   84 lySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAla   100

  304 GAGGACGAGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTT   353
      ||||||||||||||||||||||||||| :::||||||
  101 GluAspGluAlaAspTyrTyrCysCysSerTyrThrArgSerThrSerHi   117

  354 GTTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT   390
      :::|||||||||||||||||||||||||||||||||||
  117 sValPheGlyThrGlyThrLysValThrValLeuGly   129

seq_name: /cgn2_6/ptodata/2/paa/US100_COMB.pep:US-10-076-747-82

seq_documentation_block:
; Sequence 82, Application US/10076747
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Hu, Ping
; APPLICANT: Recipon, Herve
; APPLICANT: Karra, Kalpana
; APPLICANT: Cafferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and E
; FILE REFERENCE: DEX-0315
; CURRENT APPLICATION NUMBER: US/10/076,747
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/268,290
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/268,834
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-076-747-82

alignment_scores:
         Quality:      560.00          Length:      129
         Ratio:         4.628          Gaps:          0
Percent Similarity:    93.798    Percent Identity:   81.395

alignment_block:
US-09-019-441-1 x US-10-076-747-82

Align seg 1/1  to: US-10-076-747-82  from: 1  to: 235

   4 GCCTGGACTCTGCTCCCGTCACCCTCCTCACTCAGGCACAGGATCCTG    53
     ||||||:::|||||:::||||||||||||||||||||||||||||||
   1 AlaTrpAlaLeuLeuPheLeuThrLeuLeuThrGlnGlyThrGlySerTr   17

  54 GGCTCAGTCTGCCCCGACTCAGCCTCCCCTGTGTCTGGGTCTCCTGGAC   103
     |||||||||    ||||||     ||||||||||||||||||||||||
  17 pAlaGlnSerAlaLeuThrGlnSerAlaSerValSerGlySerProGlyG   34

 104 AGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTAT   153
     ||||:::||||||||||||||||||||||||||::::  |||||||||
  34 lnSerIleThrIleSerCysThrGlyThrSerSerHisValGlyGlyTyr   50

 154 AACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACTCAT   203
     |||||||||||||||||:::||||||||||||||||:::||||||||::
  51 AsnTyrValSerTrpTyrGlnHisProGlyLysAlaProLysLeuIle   67

 204 GATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGATCGCTTCTCTG   253
     :|||||::||||::::::|||  ||||||||||||||||||||||||||
  67 eIleTyrGluValSerAsnProSerGlyValSerAsnArgPheSerG   84

 254 GCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCGGGCTCCAGGCT   303
     ||||||||||||||||||||||||||||||||||||||||||||||||
  84 lySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAla   100

 304 GAGGACGAGGCTGATTATTACTGTGTTCATATACAACCAGTAGCACTTT   353
     |||||||||||||||||||||||||    |||::::::
 101 GluAspGluAlaAspTyrTyrCysValHisIleGlnProValAlaLeu   117

 354 GTTATTCGGAAGAGGACCCGGTTGACCGTCCTAGGT   390
     :::||||||  ||||||||||||||||||||||
 117 sValPheGlyThrGlyThrLysValThrValLeuGly   129

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seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-08631-43242

seq_documentation_block:
; Sequence 43242, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE:   2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE:  2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 43242
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (93)..(127)
; OTHER INFORMATION: IMMUNOGLOBULIN V REGION domain identified by eMATRIX,
; OTHER INFORMATION: accession number DM00031B, p-value5.235e-12, raw score of 15.
PCT-US01-08631-43242

alignment_scores:
         Quality:      559.00          Length:      130
         Ratio:         4.620          Gaps:          0
Percent Similarity:    93.077    Percent Identity:   81.538

alignment_block:
US-09-019-441-1 x PCT-US01-08631-43242

Align seg 1/1  to: PCT-US01-08631-43242  from: 1  to: 148

   1 ATGGCCTGGACTCTGCTCCGTCACCCTCCTCACTCAGGCACAGGATC    50
     ||||||||||:::||||||||:::||||||||||||||||  ||||||
  16 MetAlaTrpAlaLeuLeuLeuLeuThrLeuLeuThrGlnAspThrGlySe   32

  51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTGTGTCGGGTCTCCTG    100
     |||||||||||||||||||||  |||||||||  ||||||||||||||
  32 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG   49

 101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT   150
     ||||||:::||::|||||||||||||||||||||:::||||||||||:::
  49 lyGlnSerIleThrIleSerCysThrGlyThrSerSerAspValGlyAsn   65

 151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACT   200
     ||||||  |||||||||||:::||||||||||||||||||||||||||
  66 TyrAsnLeuValSerTrpTyrGlnHisProGlyLysAlaProLysLe    82

 201 CATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGATCGCTTCT   250
     |::|||||||  :::|||||   ||||||||||||||||||||||||||
  82 uIleIleTyrGluGlySerLysArgProSerGlyValSerSerArgPheS   99

 251 CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCGGGCTCCAG   300
     ||||||||||||||||||||||||||||||:::||||||||||||||||
  99 erGlySerLysSerGlyAsnThrAlaSerLeuThrMetSerGlyLeuGln   115

 301 GCTGAGGACGAGGCTGATTATTACTGTGTTCATATACAACCAGTAGCAC   350
     ||||||||||||||||||||||||||||||:::::   ||||||||
 116 AlaGluAspGluAlaAspTyrTyrCysValHisIleGlnProValAlaLeu   132

 351 TTTGTTATTCGGAAGAGGGACCCCGGTTGACCGTCCTAGGT   390
     |||||||||  ||:::::
 132 rTyrValPheGlyThrGlyThrLysValThrValLeuGly   145

seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-08631-43245

seq_documentation_block:

; Sequence 43245, Application PCT/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 43245
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (168)..(191)
; OTHER INFORMATION: Immunoglobulins and major histocompatibility complex proteins
; OTHER INFORMATION: domain identified by eMATRIX, accession number BL00290A, p-value=
; OTHER INFORMATION: 1.529e-14, raw score of 20.89
PCT-US01-08631-43245

alignment_scores:
           Quality:    557.00              Length:      130
           Ratio:        4.528             Gaps:           0
Percent Similarity: 94.615      Percent Identity: 80.000

alignment_block:
US-09-019-441-1 x PCT-US01-08631-43245      ..

Align seg 1/1  to: PCT-US01-08631-43245   from: 1   to: 249

   1 ATGGCCTGACTCTGCTCCTCCGTCACCCTCCTCACTCAGGGCACAGGATC 50
     ||||||||||||||||||||||:::|||||||||||||||||||||||||||
  15 MetAlaTrpAlaLeuLeuLeuIleLeuThrLeuThrGlnGlyThrGlySe 31

  51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCCTGTCTGTGGTCTCCTG 100
     ||||||||||| ||||||||||  |||||||||::::|||||||| |||||||
  31 rTrpAlaGlnSerAlaLeuThrGlnProSerAlaSerGlySerLeuG 48

 101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT 150
     |||||||||||||||||:|||||||||||||||::::|||:|||||:||||
  48 lyGlnSerValThrPheSerCysSerGlyThrSerSerAspIleGlyAsn 64

 151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACT 200
     |||||||||||||||:|||||::::|||||||||||||||||||||||||
  65 TyrAsnTyrValSerTrpTyrArgGlnHisProGlyLysAlaProLysLe 81

 201 CATGATTATGATCGCTAAGCGGCCTCAGGGTCTCTGATCGCTTCT 250
     ::|||||::::|||||||     ||||||||     ::|||||||
  81 uMetIleTyrGluValThrLysArgProSerGlyValProAsnArgPheS 98

 251 CTGGCTCCAAGTCTGGCAACACCGGCCTCCCTGACCCATCTCTGGGCTCCAG 300
     |||||||||||||||||||||||||||||||||:::|||||||||||
  98 erGlySerLysSerGlyAsnThrAlaSerGlyLeuThrValSerGlyLeuGln 114

 301 GCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCAC 350
     |||||||||||||||||||||::::||||  !!:|||||||||||||
 115 AlaGluAspGluAlaAspTyrTyrCysSerTyrAlaGlySerAsnSe 131

 351 TTTCTTATTCGGAAGAGGGACCCCGTTGACCGTCCTAGT 390
     :||||::||||  ||||||||||||||||||||||
 131 rLeuIlePheGlyGlyGlyThrArgLeuThrValLeuGly 144

seq_name: /cgn2_6/ptodata/2/paa/US090_COMB.pep:US-09-049-672-10

seq_documentation_block:
; Sequence 10, Application US/09049672
; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THYRNOT10
; CLONE: 2872705
US-09-049-672-10

alignment_scores:
           Quality:    554.00              Length:      130
           Ratio:        4.579             Gaps:           0
Percent Similarity: 93.077      Percent Identity: 80.769

alignment_block:
US-09-019-441-1 x US-09-049-672-10      ..

Align seg 1/1  to: US-09-049-672-10   from: 1  to: 235

   1 ATGGCCTGGACTCTGCTCCTCCGTCACCCTCCTCACTCAGGGCACAGGATC 50
     |||||||:::||||||:|||||||||||:|||||||||||||||||||||||
   1 MetAlaTrpAlaLeuLeuPheLeuThrLeuThrGlnGlyThrGlySe 17

  51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCCTGTCTGTGGTCTCCTG 100
     ||||||||||| |||||||||||:||||||||||||||||||||||||||||
  17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerGlyValSerGlySerProG 34

 101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT 150
     |||||||||||||||||||||||||||||||:::|||:||||:||||:||
  34 lyGlnSerIleThrIleSerCysThrGlyThrSerSerAspValGlyGly 50

 151 TATAACTATGTCTCCTGGTACCAACACCACCACCCAGGCAAAGCCCCCAAACT 200
     ||||||||||||||||::::     |||||||||     |||||||||

```
                                                                                    301  GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC  350
                                                                                         ||||||||||||||||||||||||||||||||| |||||||||:::||||||
                                                                                    101  AlaGluAspGluAlaAspTyrTyrCysSerSerTyrThrSerSerSerTh  117

                                                                                    351  TTTG  354
                                                                                         ||||
                                                                                    117  rLeu  118

                                                                                    seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-187-385-551

                                                                                    seq_documentation_block:
                                                                                    ; Sequence 551, Application US/60187385
                                                                                    ; GENERAL INFORMATION:
                                                                                    ;   APPLICANT: Bonazzi, Vivien
                                                                                    ;   TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
                                                                                    ;   TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
                                                                                    ;   TITLE OF INVENTION: USES THEREOF
                                                                                    ;   FILE REFERENCE: CL000334
                                                                                    ;   CURRENT APPLICATION NUMBER: US/60/187,385
                                                                                    ;   CURRENT FILING DATE: 2000-03-07
                                                                                    ;   NUMBER OF SEQ ID NOS: 922
                                                                                    ;   SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                    ; SEQ ID NO 551
                                                                                    ;   LENGTH: 121
                                                                                    ;   TYPE: PRT
                                                                                    ;   ORGANISM: HUMAN
                                                                                    ;   FEATURE:
                                                                                    ;   NAME/KEY: VARIANT
                                                                                    ;   LOCATION: (1)...(121)
                                                                                    ;   OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                    US-60-187-385-551

                                                                                    alignment_scores:
                                                                                            Quality:  549.00            Length:     118
                                                                                              Ratio:    4.816             Gaps:        0
                                                                                    Percent Similarity:  96.610    Percent Identity:  88.136

                                                                                    alignment_block:
                                                                                    US-09-019-441-1 x US-60-187-385-551      from:  1  to: 121

                                                                                    Align seq 1/1  to: US-60-187-385-551   from: 1  to: 121

                                                                                      1  ATGGCCTGGACTCTGCTCCTCGCTCACCCTCCTCACTCAGGGCACAGGATC  50
                                                                                         ||||||||||||||||::||||||::||||||||||||||||||||||||||
                                                                                      1  MetAlaTrpAlaLeuLeuLeuPheLeuThrGlnGlyThrGlySe  17

                                                                                     51  CTGGGCTCAGTCGGTGCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTG  100
                                                                                         ||||||||||||||  |||||||   ||||||  ||||||||||||||||
                                                                                     17  rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG  34

                                                                                    101  GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCCAGCGATGACGTTGGTGGT  150
                                                                                         |||||||||||||||||||::|||||||||||||||::||||||||||||||
                                                                                     34  lyGlnSerIleThrIleSerCysThrGlyThrSerSerAspValGlyGly  50

                                                                                    151  TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACT  200
                                                                                         |||||||||||||||||||||||::||||||||||||||||||||||||
                                                                                     51  TyrAsnTyrValSerTrpTyrGlnHisProGlyLysAlaProLysLe  67

                                                                                    201  CATGATTATGATGTCCTAAGCGGGCCTCAGGGGTCTCGATCGCTTCT  250
                                                                                         |||||||||::||||::||||   ||||||||||::||||||||
                                                                                     67  uMetIleTyrAspValSerAsnArgProSerGlyValSerAsnArgPheS  84

                                                                                    251  CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG  300
                                                                                         |||||||||||||||  |||||||::||||||||||||||||||||||||
                                                                                     84  erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln  100

                                                                                    301  GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC  350
                                                                                         ||||||||||||||||||||||||||||||||| ||||||||:::||||||
                                                                                    101  AlaGluAspGluAlaAspTyrTyrCysSerSerTyrThrSerSerSerTh  117

                                                                                    351  TTTG  354
                                                                                         ||||
```

```
 51  TyrAsnTyrValSerTrpTyrGlnGlnSerProGlyThrAlaProLysLe  67
     ||||||||||||||||::||||::|||
201  CATGATTATGATGTCGTAAGCGGGCCTCAGGGGTCTCGATCGCTTCT  250
     |||||||||::||||::|||   ||||||||||::||||||||
 67  uMetIleTyrGluValSerAsnArgProSerGlyValSerAsnArgPheS  84

251  CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG  300
     |||||||||||||||  |||||||::||||||||||||||||||||||||
 84  erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln  100

301  GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC  350
     |||||||||||||||||| |||||||::|||| ||||||||:::|||||||
101  AlaGluAspGluAlaAspTyrTyrCysSerSerTyrValGlyAsnAsnIl  117

351  TTTGTTATTCGGAAGAGGACACCCGGTTGACCGTCCTAGGT  390
     :::::||||||  ||||||:::||||||||||||||
117  eValValPheGlyGlyThrLysLeuThrValLeuGly  130

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-186-656-1041

seq_documentation_block:
; Sequence 1041, Application US/60186656
; GENERAL INFORMATION:
;   APPLICANT: Bonazzi, Vivien
;   TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;   TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
;   TITLE OF INVENTION: USES THEREOF
;   FILE REFERENCE: CL000320
;   CURRENT APPLICATION NUMBER: US/60/186,656
;   CURRENT FILING DATE: 2000-03-03
;   NUMBER OF SEQ ID NOS: 1518
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1041
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: HUMAN
US-60-186-656-1041

alignment_scores:
        Quality:  549.00            Length:     118
          Ratio:    4.816             Gaps:        0
Percent Similarity:  96.610    Percent Identity:  88.136

alignment_block:
US-09-019-441-1 x US-60-186-656-1041      ..

Align seq 1/1  to: US-60-186-656-1041  from: 1  to: 118

  1  ATGGCCTGGACTCTGCTCCTCGCTCACCCTCCTCACTCAGGGCACAGGATC  50
     ||||||||||||||||::||||||::|||||||||||||||||
  1  MetAlaTrpAlaLeuLeuLeuPheLeuThrGlnGlyThrGlySe  17

 51  CTGGGCTCAGTCGGTGCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTG  100
     ||||||||||||||  |||||||   ||||||  ||||||||||||||||
 17  rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG  34

101  GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCCAGCGATGACGTTGGTGGT  150
     |||||||||||||||||||::|||||||||||||||::|||||||
 34  lyGlnSerIleThrIleSerCysThrGlyThrSerSerAspValGlyGly  50

151  TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACT  200
     ||||||||||||||||||||||::||||||||||||||||||||||||
 51  TyrAsnTyrValSerTrpTyrGlnHisProGlyLysAlaProLysLe  67

201  CATGATTATGATGTCGTAAGCGGGCCTCAGGGGTCTCGATCGCTTCT  250
     |||||||||::||||::|||   ||||||||||::||||||||
 67  uMetIleTyrAspValSerAsnArgProSerGlyValSerAsnArgPheS  84

251  CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG  300
     |||||||||||||||  |||||||::||||||||||||||||||||||||
 84  erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln  100
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117 rLeu 118

seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-08631-43243

seq_documentation_block:
; Sequence 43243, Application PC/TUS0108631
; GENERAL INFORMATION:
;   APPLICANT: Hyseq, Inc
;   TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;   FILE REFERENCE: 21272-049
;   CURRENT APPLICATION NUMBER: PCT/US01/08631
;   CURRENT FILING DATE:  2001-03-30
;   PRIOR APPLICATION NUMBER: 09/540,217
;   PRIOR FILING DATE:  2000-03-31
;   PRIOR APPLICATION NUMBER: 09/649,167
;   PRIOR FILING DATE:  2000-08-23
;   NUMBER OF SEQ ID NOS: 60736
;   SOFTWARE: Custom
; SEQ ID NO 43243
;   LENGTH: 151
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (86)..(120)
;   OTHER INFORMATION: IMMUNOGLOBULIN V REGION domain identified by eMATRIX,
;   OTHER INFORMATION: accession number DM00031B, p-value 5.329e-09, raw score of 15.41
PCT-US01-08631-43243

alignment_scores:
        Quality:       548.00              Length:       130
        Ratio:           4.567             Gaps:           0
Percent Similarity:     92.308      Percent Identity: 78.462

alignment_block:
US-09-019-441-1 x PCT-US01-08631-43243        ..

Algn seg 1/1  to:  PCT-US01-08631-43243  from: 1  to: 151

    1 ATGGCCTGGACTCTGCTCTGCCTCACCCTCCTCACTCAGGCCACAGGATC 50
      ||||||||:||||||||||||||||||||||||||||||||||||
    9 MetAlaTrpAlaLeuPheLeuThrLeuLeuThrGlnGlyThrGlySe 25

   51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCTCGTGTCTGGGTCTCCTG 100
      |||||||||||  |||||||||  ||||||||||||||||||||
   25 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 42

  101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT 150
      |||||||||:|||||||||||||||||||||:::|||||||||||||||:
   42 lyGlnSerIleThrIleSerThrGlyThrSerAsnAspValGlyGly 58

  151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCCAAACT 200
      ||||||||||||||||||||||||:::|||||||||||||:::||
   59 TyrAsnTyrValSerTrpTyrGlnHisHisProGlyLysAlaProGluLe 75

  201 CATGATTTATGATGTCGCTAAGCGGCCTCAGGGGTCTTCTGATCGCTTCT 250
      |:|:||:::|::||||  |||||| ||||||  |||||||
   75 uIleIlePheAspValSerAsnArgProLeuGlyValSerThrArgPheS 92

  251 CTGGCTCCAAGTCTGGCAACACGGCTCCCTCCCTGACCATCTCTGGGCTCCAG 300
      ||||||||||||  ||||||||||||||||||||||||||||  :::::
   92 erGlySerLysSerGlyIleMetAlaSerLeuThrIleSerGlyLeuGln 108

  301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC 350
      |||||||||||  |||||||||||||||||||||:::  :::::
  109 AlaGluAspGluAlaAspTyrTyrCysCysSerPheThrSerArgAsnSe 125

  351 TTTGTTATTCGGAGAGGGACCCGGTTGACGTCCTAGGT 390
      : ::|||||||  |||||||||||||||||||||
  125 rArgValPheGlySerGlyThrLysValThrValLeuGly 138

seq_name:./cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-08631-49650

seq_documentation_block:
; Sequence 49650, Application PC/TUS0108631
; GENERAL INFORMATION:
;   APPLICANT: Hyseq, Inc
;   TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;   FILE REFERENCE: 21272-049
;   CURRENT APPLICATION NUMBER: PCT/US01/08631
;   CURRENT FILING DATE:  2001-03-30
;   PRIOR APPLICATION NUMBER: 09/540,217
;   PRIOR FILING DATE:  2000-03-31
;   PRIOR APPLICATION NUMBER: 09/649,167
;   PRIOR FILING DATE:  2000-08-23
;   NUMBER OF SEQ ID NOS: 60736
;   SOFTWARE: Custom
; SEQ ID NO 49650
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (170)..(193)
;   OTHER INFORMATION: Immunoglobulins and major histocompatibility complex proteins
;   OTHER INFORMATION: domain identified by eMATRIX, accession number BL00290A, p-val
;   OTHER INFORMATION: 1.529e-14, raw score of 20.89
;   NAME/KEY: DOMAIN
;   LOCATION: (48)..(234)
;   OTHER INFORMATION: Immunoglobulin domain identified by PFam, accession name 1g,
;   OTHER INFORMATION: E-value=3e-18, PFam score of 63.8
PCT-US01-08631-49650

alignment_scores:
        Quality:       546.00              Length:       132
        Ratio:           4.439             Gaps:           1
Percent Similarity:     93.182      Percent Identity: 78.030

alignment_block:
US-09-019-441-1 x PCT-US01-08631-49650        ..

Align seg 1/1  to:  PCT-US01-08631-49650  from: 1  to: 251

    1 ATGGCCTGGACTCTGCTCTGCCTCACCCTCCTCACTCAGGCCACAGGATC 50
      ||||||||:||||||||||||||||||||||||||||||||||||
   15 MetAlaTrpAlaLeuLeuLeuLeuLeuThrLeuLeuThrGlnGlyThrGlySe 31

   51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCTCGTGTCTGGGTCTCCTG 100
      |||||||||:||||||||  ||||||||||||||||||||||||:||||
   31 rTrpAlaGlnSerAlaLeuThrGlnProSerAlaSerGlySerLeuG 48

  101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT 150
      ||||||||||:|||||||||||||||:::|||||:::|::|:::|||::
   48 lyGlnSerValThrPheSerCysSerGlyThrSerSerAspIleGlyAsn 64

  151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCCAAACT 200
      ||||||||||||||||||||||||:::||||||||||||||||:::||
   65 TyrAsnTyrValSerTrpTyrTyrArgGlnHisProGlyLysAlaProLysLe 81

  201 CATGATTTATGATGTCGCTAAGCGGCCTCAGGGGTCTTCTGATCGCTTCT 250
      |||||||||  ||||||  |||||||  ||||||||:::|||:||||||
   81 uMetIleTyrGluValThrLysArgProSerGlyValProAsnArgPheS 98

  251 CTGGCTCCAAGTCTGGCAACACGGCTCCCTCCCTGACCATCTCTGGGCTCCAG 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   98 erGlySerLysSerGlyAsnThrAlaSerLeuThrValSerGlyLeuGln 114

  301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC 350
      |||||||||||||||||||||||||||||||||||||||||||||    |
  115 AlaGluAspGluAlaAspTyrTyrCysCysSerTyrAlaGlyAspTyrTh 131

  351 T......TTGTTATTCGGAGAGGGACCCGGTTGACGTCCTAGGT 390
      |     |||::|||||||||  ||||||||||||||||||||||
  131 rProGlyValValPheGlyGlyGlyThrLysLeuThrValLeuGly 146

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-186-656-1040

seq_documentation_block:
; Sequence 1040, Application US/60186656
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERNCE: CL000320
; CURRENT APPLICATION NUMBER: US/60/186,656
; CURRENT FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 1518
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1040
; LENGTH: 120
; TYPE: PRT
; ORGANISM: HUMAN
US-60-186-656-1040

alignment_scores:
Quality:       545.00            Length:     117
Ratio:       4.823            Gaps:       0
Percent Similarity:    96.581    Percent Identity:    88.034

alignment_block:
US-09-019-441-1 x US-60-186-656-1040   ..

Align seg 1/1  to: US-60-186-656-1040  from: 1 to: 120

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  1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCCTCACTCAGGGCACAGGATC 50
    ||||||||||::||||||:::::||||||||||||||||||||||||||||
  4 MetAlaTrpAlaLeuLeuPheLeuThrLeuThrGlnGlyThrGlySe 20

 51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTG 100
    |||||||||  ||||||||   |||||||| ||||||||||||||||||
 20 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 37

101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT 150
    |||||||:::|||||||||||||||||||||:::|||||||||||||||||
 37 lyGlnSerIleThrIleSerCysThrGlyThrSerSerAspValGlyGly 53

151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCCAAACT 200
    ||||||||||||||||||||:::|||||||||||||||||||||||||||
 54 TyrAsnTyrValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLe 70

201 CATGATTTATGATGTCGGTAAGCCGGCCTCAGGGGTCTCTGATCGCTTCT 250
    |||||||||||:::|||||:::::||||||  |||||:::::|||||||
 70 uMetIleTyrAspValSerAsnArgProSerGlyValSerAsnArgPheS 87

251 CTGGCTCCAAGTCTGGCAACACGGCCTCCTGACCATCTCGGGCTCCAG 300
    ||||||||||||||||||||||||||||||||||||||||:|||||||
 87 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 103

301 GCTGAGGACGAGGCTGATTATTACTGTTGTCATATACAACCAGTAGCAC 350
    ||||||||||||||||||||||||||||:::||||||||
104 AlaGluAspGluAlaAspTyrTyrCysSerTyrThrSerSerSerTh 120

351 T 351

120 r 120
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seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-08631-49649

seq_documentation_block:
; Sequence 49649, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERNCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631

; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
SEQ ID NO 49649
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (78)..(112)
; OTHER INFORMATION: IMMUNOGLOBULIN V REGION domain identified by eMATRIX,
; OTHER INFORMATION: accession number DM00031B, p-value=7.750e-12, raw score of 15.
; NAME/KEY: DOMAIN
; LOCATION: (34)..(218)
; OTHER INFORMATION: Immunoglobulin domain identified by PFam, accession name ig,
; OTHER INFORMATION: E-value=6.1e-19, PFam score of 66.1
PCT-US01-08631-49649

alignment_scores:
Quality:       544.00            Length:     130
Ratio:       4.496            Gaps:       0
Percent Similarity:    93.077    Percent Identity:    78.462

alignment_block:
US-09-019-441-1 x PCT-US01-08631-49649   ..

Align seg 1/1  to: PCT-US01-08631-49649  from: 1 to: 235

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  1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCCTCACTCAGGGCACAGGATC 50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetAlaTrpThrLeuLeuPheLeuThrLeuThrGlnGlyThrGlySe 17

 51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTG 100
    ||||||||||  |||||||| ||||||||||||||||||||||||||||
 17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 34

101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCCATGACGTTGGTGGT 150
    |||||||:::||||||||||||||||||||:::|||:::::|||:||:
 34 lyGlnSerIleThrIleSerCysIleGlyThrSerSerAspIleGlyAla 50

151 TATAACTATGTCTCCTGGTACCAACACCACCACCCAGGCAAAGCCCCAAACT 200
    |||  :::||||||||||||||||::|||||::|||||||||||||||
 51 TyrTyrPheValSerTrpTyrGlnGlnTyrProGlyLysAlaProLysSle 67

201 CATGATTTATGATGTCGCTAAGCGGCCTCTCAGGGGTCTCTGATCGCTTCT 250
    |:::|||:::|||||| ||| :::||||:::||||||||
 67 uLeuIlePheAspValSerGlyArgProSerGlyIleSerSerArgPheS 84

251 CTGGCTCCAAGTCTGGCAACACGGCCTCCTCGACCATCTCGGGCTCCAG 300
    |||||||||||||||||||||||||||||||||||||||||||||||||
 84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100

301 GCTGAGGACGAGGCTGATTATTACTGTTGTCATATACAACCAGTAGCAC 350
    |||||||||||||||||||||||||||||:::|||||||
101 AlaGluAspGluAlaAspTyrTyrCysAlaSerTyrAlaArgSerSerTh 117

351 TTTGTTATTCCGGAAGAGGACCCGGTTGACCGTCCTAGGT 390
    |::::|||||  |||||  ||:::||||||||||||
117 rValValPheGlyGlyThrSerValThrValLeuGly 130
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seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-08631-53209

seq_documentation_block:
; Sequence 53209, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049

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; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 53209
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (78)..(112)
; OTHER INFORMATION: IMMUNOGLOBULIN V REGION domain identified by eMATRIX,
; OTHER INFORMATION: accession number DM00031B, p-value=7.750e-12, raw score of 15.41
; NAME/KEY: DOMAIN
; LOCATION: (34)..(221)
; OTHER INFORMATION: Immunoglobulin domain identified by PFam, accession name ig,
; OTHER INFORMATION: E-value=1.7e-19, PFam score of 67.8
PCT-US01-08631-53209

alignment_scores:
         Quality:   544.00                Length:    130
         Ratio:     4.496                 Gaps:        0
Percent Similarity: 93.077     Percent Identity: 78.462

alignment_block:
US-09-019-441-1 x PCT-US01-08631-53209

Align seg 1/1 to: PCT-US01-08631-53209   from: 1  to: 236

   1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCCTCACTCAGGGCCACAGGATC 50
     ||||||||||||||||||||:::|||||||||||||||||||||||||||
   1 MetAlaTrpThrLeuLeuPheLeuValThrLeuLeuThrGlnGlyThrGlySe 17

  51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTG 100
     ||||||||||||   ||||||||||| ||||||||||||||||||||
  17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 34

 101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT 150
     |||||||||   |||||| |||||||::|||:::||:::|||||
  34 lyGlnSerIleThrIleSerCysIleGlyThrSerSerAspIleGlyAla 50

 151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACT 200
     |||  :::||||||||||||||||||||||||||||:||||||
  51 TyrTyrPheValSerTrpTyrGlnInTyrProGlyLysAlaProLysLe 67

 201 CATGATTTATGATGTCGCTAAGCGGCCTCAGGGGTCTCGATCGCTTCT 250
     |:::||||:::||||| |||  ||||||||:::|||||||||:||||||
  67 uLeuIlePheAspValSerGlyArgProSerGlyIleSerSerArgPheS 84

 251 CTGGCTCCAAGTCTGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
     |||||||||||||   ||| ||||||||||||||||||||||||||
  84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100

 301 GCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCAC 350
     ||||||||||||||::: |||||||||||||:::||  ||||||||
 101 AlaGluAspGluAlaAspTyrTyrCysAlaSerTyrAlaArgSerSerTh 117

 351 TTTGTTATTCGGAAGAGGAGGGACCCCGTTGACCGTCCTAGGT 390
     |:::::|||||   ||||||  :::|||||||||
 117 rValValPheGlyGlyGlyThrSerValThrValLeuGly 130
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; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 43246
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (99)..(133)
; OTHER INFORMATION: IMMUNOGLOBULIN V REGION domain identified by eMATRIX,
; OTHER INFORMATION: accession number DM00031B, p-value=5.865e-10, raw score of 15.
PCT-US01-08631-43246

alignment_scores:
         Quality:   543.00                Length:    130
         Ratio:     4.415                 Gaps:        0
Percent Similarity: 94.615     Percent Identity: 79.231

alignment_block:
US-09-019-441-1 x PCT-US01-08631-43246

Align seg 1/1 to: PCT-US01-08631-43246   from: 1  to: 161

   1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCCTCACTCAGGGCCACAGGATC 50
     |||||||||||||||:::|||||||||||||||||||||||||||||||
  22 MetAlaTrpAlaLeuLeuLeuLeuThrLeuLeuThrGlnGlyThrGlySe 38

  51 CTGGGCTCAGTCGCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTG 100
     ||||||||||||:: |||||||||||||||||||||||||:||||
  38 rTrpAlaGlnSerAlaLeuThrGlnProProSerAlaSerGlySerProG 55

 101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT 150
     |||||||||||||||||||||:||:::||:::||||||
  55 lyGlnSerValThrIleSerCysThrGlyThrSerSerAspIleGlyTyr 71

 151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACT 200
     ||::::||||||||||||||||||||||||||||:||||||
  72 TyrAspPheValSerTrpTyrGlnGlnArgProGlyLysAlaProLysLe 88

 201 CATGATTTATGATGTCGCTAAGCGGCCTCAGGGGTCTCGATCGCTTCT 250
     |::::|||||:||||| |||  |||||||||:::|||||||||:||||||
  88 uIleIlePheGluValAsnLysArgProSerGlyValProAspArgPheS 105

 251 CTGGCTCCAAGTCTGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
     ||||||||||:::|||:||||||||||||||||||||||||||||||
 105 erGlySerLysSerAlaAsnThrAlaSerLeuThrIleSerGlyLeuGln 121

 301 GCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCAC 350
     ||||||||||||||:::|||||||||||||:::||||||:||||
 122 AlaGluAspGluAlaAspTyrTyrCysGlySerTyrAlaAlaAsnAspAs 138

 351 TTTGTTATTCGGAAGAGGAGGGACCCCGTTGACCGTCCTAGGT 390
     :  |||||||||||:::|||||||||||||
 138 nGlyLeuPheGlyArgGlyThrLysLeuThrValLeuGly 151
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seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-08631-43246

seq_documentation_block:
; Sequence 43246, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

OM of: US-09-019-441-1 to: Pending_Patents_AA_New:*     out_format : pfs

Date: Sep 23, 2002   9:59 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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 -DB=Pending_Patents_AA_New -QFMT=fastan -SUFFIX=rapn
 -GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
 -LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
 -XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
 -YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
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 -OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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Search information block:
Query: US-09-019-441-1
Query length: 390
Database: Pending_Patents_AA_New:*
Database sequences: 949130
Database length: 267991220
Search time (sec): 353.570000

score_list:
Sequence                                          Strd Orig  ZScore    EScore Len  ! Documentation
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/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-139818 +  540.00  793.77  8.1e-36
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/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-45670  +  524.00  771.53  1.6e-34
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/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-45673  +  517.00  761.30  6.1e-34
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/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-138295 +  498.00  734.07  2.1e-32
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-138293 +  495.00  729.69  3.8e-32
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-118357 +  495.00  729.62  3.8e-32
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-138297 +  494.00  728.23  4.5e-32
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-50411  +  492.50  725.30  6.6e-32
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-91484  +  492.00  725.30  6.6e-32
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-138489 +  492.00  724.09  6.6e-32
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-49731  +  491.00  723.84  7.9e-32
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-138296 +  491.00  723.84  7.9e-32
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-138453 +  491.00  723.84  7.9e-32
/cgn2_6/ptodata/1/paa/PCT_US02-16106-16 +  491.00  717.83  7.8e-32  24
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-15-882-16      +  491.00  717.83  7.8e-32  24
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-845    +  491.00  716.94  7.8e-32  2

/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-88889  +  490.50  722.97  8.7e-3
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-66381  +  490.50  722.51  8.7e-3
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-120398 +  490.50  721.44  8.7e-
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-039-785-51     +  490.50  717.01  8.6e-32
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-120890

seq_documentation_block:
;  Sequence 120890, Application US/09791537
;  GENERAL INFORMATION:
;  APPLICANT:  Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION:  THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 15305
;  SOFTWARE: PatentIn version 3.0
;  SEQ ID NO 120890
;  LENGTH: 148
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-791-537-120890

alignment_scores:
              Quality:     595.00                   Length:    130
              Ratio:         4.760                  Gaps:        0
     Percent Similarity:   96.154      Percent Identity:   86.923

alignment_block:
US-09-019-441-1 x US-09-791-537-120890
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    1 ATGGCCTGGACTCTGCCCGACTCTCCTCACCCTCCTCACTCAGGCACAGGATC   50
      |||||||||||||::||||||::|||||||||||||||||||||||||
    1 MetAlaTrpThrLeuProAspSerProHisProProHisSerAlaGlnAspHis   17
                                                              MetAlaTrpThrLeuLeuProAlaLeuLeuLeuLeuThrLeuThrGlnThrGlyLysSe

   51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCTCTGTGTCTGGGTCTCCTG  100
      |||||||::|||||||  ||||||  |  |||  ||||::|||||||||
   17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG   34

  101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGGATGACGTTGGTGGT  150
      |||||||::|||||||||||||||||  |||:::|||||||||
   34 lyGlnSerIleThrIleSerCysThrGlyThrSerSerAspValGlyGly   50

  151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACT  200
      |||||||||||||||||:||||::|||||||::|||||||||||||
   51 TyrAsnTyrValSerTrpTyrGlnGlnHisProAlaLysAlaProLysLe   67

  201 CATGATTTATGATGTCGCTAGCGGGCCTCAGGGGTCTCCTGATCGCTTCT  250
      |||||||||||::|||||||||::||||||||:::|||||||
   67 uMetIleTyrAspValSerLysArgProSerGlyValSerAsnArgPheS   84

  251 CTGGCTCCAAGTCTGGCAACACACGGCCTCCCTGACCATCTCTGGCGTCCAG  300
      ||||||||||||||||||||||||||||||||||||||||||||||||
   84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln  100

  301 GCTGAGGACGAGGCTGATTATTACTGTGTTCATATACAACCAGTAGCAC  350
      |||||||||||||||||||||||::|||||||::::||||||
  101 AlaGluAspGluAlaAspTyrTyrCysValHisIleGlnProValAlaSerSerTh  117

  351 TTTGTTATTCGGAAGAGGAGGACCCGGTTGACCGTCCTAGGT  390
      |:::::||||||    |||||:::||||||||||||||
  117 rPheValPheGlyGlyGlyThrLysLeuThrValLeuGly  130

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-82220

seq_documentation_block:

; Sequence 82220, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82220
;   LENGTH: 136
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-82220

alignment_scores:
         Quality:       579.00            Length:       130
         Ratio:         4.669             Gaps:         0
Percent Similarity:     95.385   Percent Identity:   82.308

alignment_block:
US-09-019-441-1 x US-09-791-537-82220       ..

Align seg 1/1   to: US-09-791-537-82220   from: 1  to: 136

    1 ATGGCCTGGACTCCTGCTCCCTCCGTCACCCTCCTCACTCAGGGCACAGGATC   50
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    1 MetAlaTrpAlaLeuLeuLeuLeuThrLeuLeuThrGlnGlyThrGlySe  17

   51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTG  100
      ||||||||||||  |||||||||  |||||||||::||||||||||||
   17 rTrpAlaGlnSerAlaLeuThrGlnProSerAlaSerGlySerProG  34

  101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT  150
      ||||||||||||||||||||||::||||||||||||||||||||:::||
   34 lyGlnSerValThrIleSerCysThrGlyThrSerAspValGlyAla  50

  151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACT  200
      |||||||||||||||||  |||||||||||||||||||||||||||||
   51 TyrAsnTyrValSerTrpTyrGlnHisHisProGlyLysAlaProLysLe  67

  201 CATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGATCGCCTTCT  250
      ||||||||||||:::|||||::||||||||||||||||||||:::||||||
   67 uMetMetTyrGluValSerGluArgProSerGlyValProAspArgPheS  84

  251 CTGGCTCCAAGTCGCAACACGGCCCCTCCTGACCATCCTGGGCTCCAG  300
      ||||||||||||::||:::||||||||||||||||||::||||||||
   84 erGlySerLysSerGlyAsnThrAlaSerLeuThrValSerGlyLeuGln  100

  301 GCTGAGGACGAGGCTGATTATTACTGTTCTTCATATACAACCAGTAGCAC  350
      |||||||||||||||||||||||||  |||:::|||  |:::::
  101 AlaGluAspGluAlaAspTyrTyrCysThrSerTyrAlaGlySerAsnSe  117

  351 TTTGTTATTCGGAGAGGGACCCGTTGACCGTCCTAGGT   390
      ::::||||||||||||||||::||||||||||||
  117 rPheValPheGlyThrGlyThrLysValThrValLeuGly  130

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-85829

seq_documentation_block:
; Sequence 85829, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85829
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-85829

alignment_scores:
         Quality:       570.00            Length:       129
         Ratio:         4.711             Gaps:         0
Percent Similarity:     93.798   Percent Identity:   84.496

alignment_block:
US-09-019-441-1 x US-09-791-537-85829       ..

Align seg 1/1   to: US-09-791-537-85829   from: 1  to: 130

    1 ATGGCCTGGACTCCTCCGTCACCCTCCTCACTCAGGGCACAGGATC   50
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    1 MetAlaTrpSerProLeuPheLeuPheLeuThrGlnGlyThrGlySe  17

   51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTGTGTCTGGGTCTCCTG  100
      ||||||||||||  |||||||||  |||||||||||||||||||||
   17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG  34

  101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGCGATGACGTTGGTGGT  150
      ||||||||||||||||||||||::|||||||||||||||||||||:::||||
   34 lyGlnSerIleThrIleSerCysThrGlyThrSerAspValGlyGly  50

  151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACT  200
      ||||||||||||||||||  ||||||||||:::|||||||||||||||
   51 TyrAsnTyrValSerTrpTyrGlnHisProGlyLysAlaProLysLe  67

  201 CATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGATCGCCTTCT  250
      |||||||||||||:::|||||::||||||||||||||||||:::||||||
   67 uMetIleTyrAspValSerAsnArgProSerGlyValSerAsnArgPheS  84

  251 CTGGCTCCAAGTCGCAACACGGCCCCTCCTGACCATCCTGGGCTCCAG  300
      ||||||||||||::||:::||||||||||||||||||::|||||||||
   84 erGlySerLysSerAspAsnThrAlaSerLeuThrIleSerGlyLeuGln  100

  301 GCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCAC  350
      ||||||||||||||||||||:::||||  |:::::|||::||||||||
  101 AlaGluAspGluAlaAspTyrTyrCysSerSerTyrThrSerSerSerTh  117

  351 TTTGTTATTCGGAGAGGGACCCGGTTGACCGTCCTA   387
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  117 rLeuValPheGlyLyGlyThrLysLeuThrValLeu  129

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-139061

seq_documentation_block:
; Sequence 139061, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 139061
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-139061

**Left column**

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alignment_scores:
        Quality:      569.00              Length:      130
        Ratio:          4.664             Gaps:          0
Percent Similarity:    93.846   Percent Identity:    82.308

alignment_block:
US-09-019-441-1 x US-09-791-537-139061                ..

Align seg 1/1  to: US-09-791-537-139061  from: 1  to: 235

   1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCCTCACTCAGGGCACAGGATC 50
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   1 MetAlaTrpAlaLeuLeuLeuLeuLeuThrLeuLeuThrGlnAspThrGlySe 17

  51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCTGTCTGGGTCTCCTG 100
     ||||||||| |||||| ||||||||||||||||||||
  17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 34

 101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGCGATGACGTTGGTGGT 150
     |||||||:::|||| ||||||||||||||||:::||::||||||||
  34 lyGlnSerIleThrIleSerCysThrGlyThrSerSerAspValGlySer 50

 151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCCAAACT 200
     |||||| |||||||||||::|||||||||||||||||::
  51 TyrAsnLeuValSerTrpTyrGlnHisHisProGlyLysAlaProLysIl 67

 201 CATGATTTATGATGTCGGTAAGCGGCCTCAGGGTCTCTGATCGCTTCT 250
     :|||||||:::||::|||||  |||||||||||| ||||||||
  67 eMetIleTyrGluValSerLysArgProSerGlyValSerAsnArgPheS 84

 251 CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTTCCAG 300
     |||||||||||||||||||::::|||||| ||||||||||||||||
  84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100

 301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC 350
     ||||||||||||||||||||||||::::|| ||
 101 AlaGluAspGluAlaAspTyrTyrCysCysSerTyrAlaGlySerTyrTh 117

 351 TTTGTTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
     |:::|||||||||||||||||:::|||||||||
 117 rValValPheGlyGlyThrGlyThrLysLeuThrValLeuGly 130
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-139062

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seq_documentation_block:
; Sequence 139062, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
;   SEQ ID NO 139062
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-139062
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**Right column**

Align seg 1/1  to: US-09-791-537-139062  from: 1  to: 235

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   1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCCTCACTCAGGGCACAGGATC 50
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   1 MetAlaTrpAlaLeuLeuPheLeuThrLeuThrGlnGlyThrGlySe 17

  51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCTGTCTGGGTCTCCTG 100
     |||||||| ||||| ||||||||||||||||||||||||
  17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 34

 101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGCGATGACGTTGGTGGT 150
     ||||||:::|||||::||||||||||||||:::||||||||||
  34 lyGlnSerIleThrIleSerCysThrGlySerSerAspValGlyGly 50

 151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCCAAACT 200
     |||||||||||||||||||:::||||||||||||||||||
  51 TyrAsnTyrValSerTrpTyrGlnHisHisProGlyLysAlaProLysLe 67

 201 CATGATTTATGATGTCGGTAAGCGGCCTCAGGGTCTCTGATCGCTTCT 250
     ||||||||||||||:::||  ||||||||||||||||||||
  67 uMetIleTyrAspValThrAsnArgProSerGlyValSerAsnArgPhes 84

 251 CTGGCTCCAAGTCTGGCAACACGGCCTCCTGACCATCTCTGGGCTTCCAG 300
     ||||||||||||||||||||||||||||||||||||||||
  84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100

 301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC 350
     ||||||||||||||||||  |||::::||||||
 101 ProGluAspGluAlaAspTyrTyrCysThrSerLysThrSerSerSerPh 117

 351 TTTGTTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
     ::|||||||||||||||::::||||||||||
 117 eTyrValPheGlyThrGlyThrLysValSerValLeuGly 130
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-139120

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seq_documentation_block:
; Sequence 139120, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
;   SEQ ID NO 139120
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-139120
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alignment_scores:
        Quality:      557.00              Length:      130
        Ratio:          4.528             Gaps:          0
Percent Similarity:    94.615   Percent Identity:    80.000

alignment_block:
US-09-019-441-1 x US-09-791-537-139120                ..

Align seg 1/1  to: US-09-791-537-139120  from: 1  to: 235

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   1 MetAlaTrpAlaLeuLeuPheLeuThrLeuThrGlnGlyThrGlySe 17

  51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCTGTCTGGGTCTCCTG 100
     |||||||| |||||||||||||||||||||||||||||
  17 rTrpAlaGlnSerAlaLeuThrGlnProSerAlaSerGlySerLeuG 34
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101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGCGATGACGTGGTGGT 150
    |||||||||||||||||||::||||:||:||::||||::||||
 34 lyGlnSerValThrPheSerCysSerGlyThrSerSerAspIleGlyAsn 50

151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACT 200
    ||||||||||||||||||:::||||||||||||||||
 51 TyrAsnTyrValSerTrpTyrArgGlnHisProGlyLysAlaProLysLe 67

201 CATGATTTATGATGTCGCTAAGCGGCCTCAGGGGTCTCTGATCGCTTCT 250
    ||||:||:||:::||||  ||||||   :::||||||
 67 uMetIleTyrGluValThrLysArgProSerGlyValProAsnArgPheS 84

251 CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATTCTGGGCTCCAG 300
    ||||||||||||||||||||||||||||||||||||||
 84 erGlySerLysSerGlyAsnThrAlaSerLeuThrValSerGlyLeuGln 100

301 GCTGAGGACGAGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC 350
    ||::::|||    ||||||||||||||:::::
101 AlaGluAspGluLeuIleIleThrValValSerTyrAlaGlySerAsnSe 117

351 TTTGTTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGT 390
    :|||:::||||    ||||||||||||||
117 rLeuIlePheGlyGlyGlyThrArgLeuThrValLeuGly 130

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-120441

seq_documentation_block:
; Sequence 120441, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; SOFTWARE: PatentIn version 3.0
; NUMBER OF SEQ ID NOS: 153055
; SEQ ID NO 120441
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-120441

alignment_scores:
        Quality:    547.00              Length:     119
        Ratio:      4.798               Gaps:       0
Percent Similarity:   95.798     Percent Identity:   86.555

alignment_block:
US-09-019-441-1 x US-09-791-537-120441

Align seg 1/1 to: US-09-791-537-120441    from: 1 to: 136

 34 ACTCAGGGCCACAGATCCTGGGCTGCCCGACTCAGCCTCCCTC 83
    |||||||||||||||||||||||||||||||||  |||||||
  1 ThrGlnGlyThrGlySerTrpAlaGlnSerArgLeuThrGlnProAlaSe 17

 84 TGTGTCTGGGTCTTCCTGGACAGTCGGTCACCATCTCCTGCACTGGAACCA 133
    |||||||||||||||||||||||||||::||||||||||||
 17 rValSerGlySerProGlyGlnSerIleThrIleSerCysThrGlyThrS 34

134 GCCGATGACGTTGGGTTATAACTATGTCTCCTGGTACCAACACCACCCA 183
    ||:::|||||||||||||||||||||||||::|||||
 34 erSerAspAspGlyTyrAsnTyrValSerTrpTyrArgGlnHisPro 50

184 GGCAAAGCCCCAAACTCATGATTTATGATGTCGCTAAGCGGCCTCAGG 233
    ||||||||||||||||:::||  |||||||
 51 GlyLysAlaProLysLeuMetIleTyrAspValSerAsnArgProSerGl 67

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-91653

seq_documentation_block:
; Sequence 91653, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; SOFTWARE: PatentIn version 3.0
; NUMBER OF SEQ ID NOS: 153055
; SEQ ID NO 91653
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-91653

alignment_scores:
        Quality:    546.00              Length:     130
        Ratio:      4.627               Gaps:       0
Percent Similarity:   90.769     Percent Identity:   80.769

alignment_block:
US-09-019-441-1 x US-09-791-537-91653

Align seg 1/1 to: US-09-791-537-91653    from: 1 to: 235

  1 ATGGGCTGGACTCTGCTCCTCGTCACGCTCCTCACTCAGGGCACAGGATC 50
    ||:::|||||||||||||||||||:::|||||||
  1 MetAlaTrpAlaLeuLeuLeuLeuThrLeuLeuThrGlnAspThrGlySe 17

 51 CTGGGCTCAGTCGCCGACTCAGCCTCCCTCGTGTCTGGGTCTCCTG 100
    |||||||||||||  |||||||   ||||||||||||
 17 rTrpAlaGlnSerAlaLeuThrGlnProAlaPheValSerGlySerProG 34

101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGCGATGACGTTGTGGT 150
    ||:::||:||:||||||::||||  |||||||::::||||||
 34 lyArgSerIleAlaIleSerCysThrGlyThrSerSerAspValGlySer 50

151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCCAAACT 200
    ||||||  |||||||||   :::||||||||||||
 51 TyrAsnLeuValSerTrpTyrGlnHisProGlyLysAlaProLysLe 67

201 CATGATTTATGATGTCGCTAAGCGGCCTCAGGGGTCTCTGATCGCCTTCT 250
    |||||||||  ::::||||||  |||||||
 67 uMetIleTyrGluGlySerLysArgProSerGlyValSerIleArgPheS 84

251 CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCCTCGGGCTCCAG 300
    |||||||||||||||||||||||||||||||||||||
 84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100

301 GCTGAGGACGAGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC 350
    ||::::|||    |||||||||||||::::
101

234 GGTCTCTGATCGCCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGA 283
    ||||:::||::||||||||||||||||||||||||||||
 67 yValSerAsnArgPheSerGlySerLysSerGlyAsnThrAlaSerLeuT 84

284 CCATCTCGGCTCCAGGCTGAGGACGAGCTGATTATTACTGTTGTTCA 333
    |||||:||:||:||||||||||||||::||||
 84 hrIleSerGlyLeuGlnAlaGluAspGluLeuIleIleThrValCysSerSer 100

334 TATACAACCAGTGACATTTGTTATTCGGAAGAGGGACCGGTTGACCGT 383
    ||||:::::||||||||||||  :::|||||||
101 TyrThrSerSerSerValValPheGlyGlyGlyThrArgLeuThrVa 117

384 CCTAGGT 390
    ||||||
117 lLeuGly 119

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            |||||||||||||||||||||||||||||||          :::|||||
        101 AlaGluAspGluAlaAspTyrTyrCysSerTyrGlyAspAsnSerTh 117

        351 TTTGTTATTCGGAAGAGGAGACCCGGTTGACCGTCCTAGGT 390
            |  : :||||||    ||||::||||||||||
        117 rTrpValPheGlyGlyGlyThrLysLeuThrValLeuGly 130

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-82106

seq_documentation_block:
; Sequence 82106, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT:  Debe, Derek
;   APPLICANT:  Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
;   SEQ ID NO 82106
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-82106

alignment_scores:
        Quality:    544.00               Length:      130
        Ratio:       4.496               Gaps:          0
Percent Similarity: 93.077    Percent Identity: 78.462

alignment_block:
US-09-019-441-1 x US-09-791-537-82106

Align seq 1/1  to: US-09-791-537-82106  from: 1  to: 235

1   ATGGCCTGGACTCGTCCTCGTCACCCTCCTCACTCAGGCACAGGATC  50
    ||||||||||||||||::||:|||:||||||||||||||||||||||
1   MetAlaTrpThrLeuLeuPheLeuThrLeuLeuThrGlnThrGlySe  17

51  CTGGGCTCAGTCTGCCCCGACTCAGCCTCCTCTGTGTCTGGGTCCTG  100
    |||||||||||||  ||||||||  ||||||||||||||||||||
17  rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG  34

101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT 150
    ||||||||::||||||||||||||||||||  ||||||::|||::::
34  lyGlnSerIleThrIleSerCysIleGlyThrSerSerAspIleGlyAla  50

151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCCAAACT 200
    |||  ::|||||||||  |||||  |||||||||||||||||||||||
51  TyrTyrPheValSerTrpTyrGlnInTyrProGlyLysAlaProLysLe  67

201 CATGATTTATGATGTCGCTAAGCGGCCCTCAGGGGTCTCTGATCGCTTCT 250
    |:::||::: :::||||||  |||||::::|||:::|||||
67  uLeuIlePheAspValSerGlyArgProSerGlyIleSerSerArgPheS  84

251 CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
    ||||||||||||||||||||||||||||||||||||||||||||||
84  erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100

301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC 350
    ||||||||||||||||||||||||||:||||||||||||||
101 AlaGluAspGluAlaAspTyrTyrCysAlaSerTyrAlaArgSerTh 117

351 TTTGTTATTCGGAAGAGGAGACCCGGTTGACCGTCCTAGGT 390
    |:::::||||| ||||| ::||||||||||
117 rValValPheGlyGlyGlyThrSerValThrValLeuGly 130

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-123189
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            |||||||||||||||||||||||||||||          ::|||||
        101 AlaGluAspGluAlaAspTyrTyrCysSerTyrGlyAsnSerTh 117
seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-123189

seq_documentation_block:
; Sequence 123189_Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT:  Debe, Derek
;   APPLICANT:  Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
;   SEQ ID NO 123189
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-123189

alignment_scores:
        Quality:    546.00               Length:      130
        Ratio:       4.588               Gaps:          0
Percent Similarity: 91.538    Percent Identity: 79.231

alignment_block:
US-09-019-441-1 x US-09-791-537-123189

Align seq 1/1  to: US-09-791-537-123189  from: 1  to: 130

1   ATGGCCTGGACTCGTCCTCGTCACCCTCCTCACTCAGGCACAGGATC  50
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1   MetAlaTrpAlaLeuLeuLeuLeuThrLeuLeuThrGlnThrGlySe  17

51  CTGGGCTCAGTCTGCCCCGACTCAGCCTCCTCTGTGTCTGGGTCCTG  100
    ',||||||||||||||  |||||||  ||||||  |||||||||||||
17  rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG  34

101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT 150
    |||||||||::||||||||||||||||||||||:::||||||||:::
34  lyGlnSerIleThrIleSerCysThrGlyThrSerSerAspValGlyAsn  50

151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCCAAACT 200
    ||||||   |||||||||  ||||||  |||||||||||||||||||  ||
51  TyrAsnLeuValSerTrpTyrGlnInHisHisProGlyLysAlaProAspLe  67

201 CATGATTTATGATGTCGCTAAGCGGCCCTCAGGGGTCTCTGATCGCTTCT 250
    |:::::||:::  :::||||||   ||  |||||||||:::||||||
67  uLeuLeuTyrGluAspThrLysArgProSerArgValSerAsnArgPheS  84

251 CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
    ||||||||||||||||||||||||||||||||||||||||||||
84  erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100

301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC 350
    |||||||||||||||||||||||||| |||::|||||:::|||||
101 ThrGluLeuGluAlaAspTyrTyrCysCysSerTyrAlaGlySerAsnGl 117

351 TTTGTTATTCGGAAGAGGAGACCCGGTTGACCGTCCTAGGT 390
    |||||||||| ||||||::::|||||||||||
117 yValValPheGlyGlyGlyThrLysLeuThrValLeuGly 130

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-120444

seq_documentation_block:
; Sequence 120444, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT:  Debe, Derek
;   APPLICANT:  Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
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; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 120444
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-120444

alignment_scores:
            Quality:  540.00               Length:    121
            Ratio:    4.865                Gaps:        1
Percent Similarity: 91.736    Percent Identity: 85.950

alignment_block:
US-09-019-441-1 x US-09-791-537-139818

Align seg 1/1  to: US-09-791-537-139818   from: 1  to: 137

34 ACTCAGGGCACAGATCCTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTC 83
   |||||||||||||||||||||||||||||| |||||||| ||
 1 ThrGlnGlyThrGlySerTrpAlaGlnSerAlaLeuThrGlnProArgSe 17

84 TGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCCTGCACTGGAACCA 133
   ||||||||||||||||||||||||||||||||||||||||||||
17 rValSerGlySerProGlyGlnSerValThrIleSerCysThrGlyThrS 34

134 GCGATGACGTTGGTGGTTATAAC......TATGTCTCCTGGTACCAACAC 177
   ||:::||||||||||||||       ||||||||||||||||||
34 erSerAspValGlyGlyTyrAsnTyrAspTyrValSerTrpTyrGlnHis 50

178 CACCCAGGCAAAGCCCCAAACTCATGATTTATGATGTCGGTAAGCGGGGC 227
   ||||||||||||||||||||||||||||:||:::|||||
51 HisProGlyLysAlaProLysLeuMetIleTyrAspValSerLysArgPr 67

228 CTCAGGGGTCTCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCT 277
   |||||||||||||||||||||||||||||||||||||||||||||||
67 oSerGlyValProAspArgPheSerGlySerLysSerGlyAsnThrAlaS 84

278 CCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGT 327
   |||||||||||||||:::||||||||||||:||||||||||||||||
84 erLeuThrIleSerGlyLeuGlnAlaAspAspGluAlaAspTyrTyrCys 100

328 TGTTCATATACAACCAGTAGCACTTTGTTATTCGGAAGAGGGACCCGGTT 377
   |||||::   :::    |||||::||||||:::||
101 CysSerTyrAlaGlyAsnTyrIleLeuValPheGlyGlyGlyThrLysLe 117

378 GACCGTCCTAGGT 390
   |||||||||||||
117 uThrValLeuGly 121
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-1654

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seq_documentation_block:
; Sequence 1654, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1654
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-1654

alignment_scores:
            Quality:  538.50               Length:    131
            Ratio:    4.487                Gaps:        1
Percent Similarity: 91.603    Percent Identity: 80.153

alignment_block:
US-09-019-441-1 x US-09-791-537-1654
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; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 120444
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-120444

alignment_scores:
            Quality:  540.00               Length:    119
            Ratio:    4.779                Gaps:        0
Percent Similarity: 94.958    Percent Identity: 84.874

alignment_block:
US-09-019-441-1 x US-09-791-537-120444

Align seg 1/1  to: US-09-791-537-120444   from: 1  to: 137

34 ACTCAGGGCACAGATCCTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTC 83
   |||||||||||||||||||||||||||||| |||||||| ||
 1 ThrGlnGlyThrGlySerTrpAlaGlnSerAlaLeuThrGlnProProSe 17

84 TGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCCTGCACTGGAACCA 133
   |:::|||||||||||||||||||||||||||||||||||||||||
17 rAlaSerGlySerProGlyGlnSerValThrIleSerCysThrGlyThrS 34

134 GCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCCA 183
   ||::||||||||||||||||||||||||||::|||||
34 erSerAspValGlyGlyTyrAsnTyrValSerTrpTyrGlnHisPro 50

184 GGCAAAGCCCCAAACTCATGATTTATGATGTCGGTAAGCGGGGCCTCAGG 233
   ||||||||||||||||||||||||||||:||::||||||
51 GlyLysAlaProLysLeuMetIleTyrGluValSerLysArgProSerGl 67

234 GGTCTCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGA 283
   |||| |||||||||||||||||||||||||||||||||||||||||||
67 yValProAspArgPheSerGlySerLysSerGlyAsnThrAlaSerLeuT 84

284 CCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCA 333
   ||:||||||||||||||||||||||||||||||||||||||| ||
84 hrValSerGlyLeuGlnAlaGluAspGluAlaAspTyrTyrCysCysSer 100

334 TATACAACCAGTAGCACTTTGTTATTCGGAAGAGGGACCCGGTTGACCGT 383
   |||:  ::||||||||||||||||||||||||||||||||||
101 TyrAlaGlySerAsnValValPheGlyGlyGlyThrLysLeuThrVa 117

384 CCTAGGT 390
   |||||||
117 lLeuGly 119
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-139818

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seq_documentation_block:
; Sequence 139818, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 139818
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-139818
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Align seg 1/1   to: US-09-791-537-1654    from: 1   to: 131

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  1 ATGGCCTGGACTCTGCTCCTCGTCACCTCCTCACTCAGGGCACA...GG  47
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  1 MetAlaTrpAlaLeuPheLeuThrLeuLeuThrGlnGlyThrGlyGl  17

 48 ATCCTGGGCTCAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTC  97
    ||||||||||||||||  |||||||||  ||||||||||||||||||
 17 ySerTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerP  34

 98 CTGGACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGCCGATGACGTTGGT  147
    ||||||||||::||||||||||||||::::|||:::|||
 34 roGlyGlnSerIleThrIleSerCysThrGlyThrSerSerAspIleGly  50

148 GGTTATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCCAA  197
    ||||||||||||||||||||||::||||||||||||||||||
 51 GlyTyrTyrAsnTyrValSerTrpTyrGlnHisProGlyLysAlaProLy  67

198 ACTCATGATTATGATGTCGCTAAGCGGCCTCAGGGGTCTCTGATCGCT  247
    ||||::||||||  ||::::|||  ||||||||  ||||
 67 sLeuValIleTyrAlaValSerAsnArgProSerGlyValSerHisArgP  84

248 TCTCTGGCTCCCAAGTCTGGCAACACGGCCCCCTGACCATCTCGGGCTC  297
    ||||||||||||||||||||||||||||||||||||||||
 84 heSerGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeu  100

298 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAG  347
    |||||||||||||||||||||||::::::||:|
101 GlnAlaGluAspGluAlaAspTyrTyrCysAsnSerAspAlaSerThrSe  117

348 CACTTTGTTATTCGGAAGAGGACCCGGTTGACCGTCCTAGGT  390
    ::|||||||  ||||::::||||||||||
117 rLysTrpValPheGlyGlyThrGlyThrLysLeuThrValLeuGly  131
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-37721

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seq_documentation_block:
; Sequence 37721, Application US/09791537
; GENERAL INFORMATION:
;    APPLICANT: Bionomix, Inc.
;    APPLICANT: Debe, Derek
;    APPLICANT: Danzer, Joseph
;    TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;    TITLE OF INVENTION: METHODS OF USE THEREOF
;    FILE REFERENCE: 261/210
;    CURRENT APPLICATION NUMBER: US/09/791,537
;    CURRENT FILING DATE: 2001-02-22
;    NUMBER OF SEQ ID NOS: 153055
;    SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37721
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-37721
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alignment_scores:
       Quality:   528.00              Length:   118
         Ratio:     4.757               Gaps:     0
Percent Similarity:   94.068    Percent Identity:   85.593

alignment_block:
US-09-019-441-1 x US-09-791-537-37721

Align seg 1/1   to: US-09-791-537-37721   from: 1   to: 118

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  1 ATGGCCTGGACTCTGCTCCTCGTCACCTCCTCACTCAGGGCACAGGATC  50
    ||||||||||:::||||||||::||||||||||||||||||| |||:::||
  1 MetAlaTrpAlaLeuLeuLeuThrLeuLeuThrGlnAspThrGlySe  17

 51 CTGGGCTCAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTG  100
    ||||||||||||||||||||||||  ||||||||||||||||||||
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Align seg 1/1   to: US-09-791-537-139139   from: 1   to: 131

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 17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG  34

101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGCCGATGACGTTGGT  150
    ||||||||::||||||||||||||::||||||||||||||||::::
 34 lyGlnSerIleThrIleSerCysThrGlyThrSerSerAspValGlySer  50

151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCCAAACT  200
    ||||||  |||||||||||||||||::::|||||||||||||||||
 51 TyrAsnLeuValSerTrpTyrGlnHisProGlyLysAlaProLysLe  67

201 CATGATTATGATGTCGCTAAGCGGCCTCAGGGGTCTCTGATCGCTTCT  250
    :||||||:::::||  ::||||||   |||||||||||||||||||
 67 uMetIleTyrGluGlySerLysArgProSerGlyValSerAsnArgPheS  84

251 CTGGCTCCCAAGTCTGGCAACACGGCCCCCTGACCATCTCGGGCTCCAG  300
    ||||||||||||||||||||||||||||||||||||||||||||||
 84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln  100

301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC  350
    |||||||||||||||||||||||||||||||::::|||
101 AlaGluAspGluAlaAspTyrTyrCysCysSerTyrAlaGlySerSerTh  117

351 TTTG  354
    ||||
117 rLeu  118
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-139139

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seq_documentation_block:
; Sequence 139139, Application US/09791537
; GENERAL INFORMATION:
;    APPLICANT: Bionomix, Inc.
;    APPLICANT: Debe, Derek
;    APPLICANT: Danzer, Joseph
;    TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;    TITLE OF INVENTION: METHODS OF USE THEREOF
;    FILE REFERENCE: 261/210
;    CURRENT APPLICATION NUMBER: US/09/791,537
;    CURRENT FILING DATE: 2001-02-22
;    NUMBER OF SEQ ID NOS: 153055
;    SOFTWARE: PatentIn version 3.0
; SEQ ID NO 139139
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-139139
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alignment_scores:
       Quality:   527.00              Length:   131
         Ratio:     4.504               Gaps:     1
Percent Similarity:   89.313    Percent Identity:   77.099

alignment_block:
US-09-019-441-1 x US-09-791-537-139139

Align seg 1/1   to: US-09-791-537-139139   from: 1   to: 237

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    |||||||||:::||||||||::||||||||||||||||| ||||||||||
  1 MetAlaTrpAlaLeuLeuLeuThrLeuLeuThrGlnGlyThrGlySe  17

 51 CTGGGCTCAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTG  100
    ||||||||||||  ||||||  |||||||||||||||||::||||||||||
 17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerAsnGlySerProG  34

101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGCCGATGACGTTGGT  150
    |||||||||:::||  ||||:::::||||||||||||  ||:::|||||||
 34 lyGlnLeuIleIleSerCysThrGlyProSerSerArgIleGlyAsp  50

151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCCAAACT  200
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Date: Sep 23, 2002 10:00 AM
About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

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Search information block:
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; Sequence 12, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
;   APPLICANT: CROWE, JAMES SCOTT
;   APPLICANT: LEWIS, ALAN PETER
;   TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
;   NUMBER OF SEQUENCES: 46
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
;     STREET: 555 THIRTEENTH ST. N.W.
;     CITY: WASHINGTON
;     STATE: D.C.
;     COUNTRY: U.S.
;     ZIP: 20004
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/378,939
;     FILING DATE:
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/952640
;     FILING DATE: 01-DEC-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME: ERNST, BARBARA G
;     REGISTRATION NUMBER: 30,377
;     REFERENCE/DOCKET NUMBER: 1808-118
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202) 783-6040
;     TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 12:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 235 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-378-939-12

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; Patent No. 6300064
; GENERAL INFORMATION:
;   APPLICANT:  Knappik, Achim
;   APPLICANT:  Pack, Peter
;   APPLICANT:  Ilag, Vic
;   APPLICANT:  Ge, Liming
;   APPLICANT:  Moroney, Simon
;   APPLICANT:  Plueckthun, Andreas
;   TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;   NUMBER OF SEQUENCES:  373
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  James F. Haley, Jr., Esq.  c/o Fish & Neave
;     STREET:  1251 Avenue of the Americas
;     CITY:  New York
;     STATE:  New York
;     COUNTRY:  USA
;     ZIP:  10021
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/025,769B
;     FILING DATE:  18-FEB-1998

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; Patent No. 6135941
; GENERAL INFORMATION:
;   APPLICANT:  Hillman, Jennifer L.
;   APPLICANT:  Lal, Preeti
;   APPLICANT:  Tang, Y. Tom
;   APPLICANT:  Yue, Henry
;   APPLICANT:  Au-Young, Janice
;   APPLICANT:  Corley, Neil C.
;   APPLICANT:  Guegler, Karl J.
;   APPLICANT:  Baughn, Mariah R.
;   TITLE OF INVENTION:  HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;   NUMBER OF SEQUENCES:  28
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;     STREET:  3174 Porter Drive
;     CITY:  Palo Alto
;     STATE:  CA
;     COUNTRY:  USA
;     ZIP:  94304
;   COMPUTER READABLE FORM:
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;     OPERATING SYSTEM:  DOS
;     SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
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;     FILING DATE:  HEREWITH
;     CLASSIFICATION:  536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Cerrone, Michael C
;     REGISTRATION NUMBER:  39,132
;     REFERENCE/DOCKET NUMBER:  PF-0497 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  650-855-0555
;     TELEFAX:  650-845-4166
;     TELEX:
; INFORMATION FOR SEQ ID NO: 10:
;   SEQUENCE CHARACTERISTICS:
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;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   IMMEDIATE SOURCE:
;     LIBRARY:  THYRNOT10
;     CLONE:  2872705
US-09-049-672A-10

us-09-019-441-1.rai

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; PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  EP 95 11 3021.0
;     FILING DATE:  18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
;     NAME:  James F. Haley, Jr., Esq.
;     REGISTRATION NUMBER:  27,794
;     REFERENCE/DOCKET NUMBER:  MORPHO/5
; TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (212)596-9000
;     TELEFAX:   (212)596-9090
; INFORMATION FOR SEQ ID NO:  19:
; SEQUENCE CHARACTERISTICS:
;     LENGTH:  112 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:
;     TOPOLOGY:  linear
; MOLECULE TYPE:  protein
US-09-025-769B-19

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; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
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; NUMBER OF SEQ ID NOS:  79
; SEQ ID NO 79
; LENGTH: 244
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-79

alignment_scores:
       Quality:   497.00          Length:       132
         Ratio:    4.438            Gaps:          1
Percent Similarity:  84.848   Percent Identity:  74.242

alignment_block:
US-09-019-441-1 x US-08-918-148-79         ..

Align seg 1/1   to: US-08-918-148-79   from: 1   to: 244

 19 CTCGTCACCCTCCTCACTCAGGCACAGGATCCTGGGCTCAGTCTGCCCC  68
    ::||||||||::     :::    ||||    ||    |||||   :::::
111 MetValThrValSerSerGlyGlyGlyGlySerGlyGlyGlySerGl 127

 69 G.........ACTCAGCCTCCCTCGTCTCTGGGT  94
             ||||||||||||||||  |||||
127 yGlyGlyGlySerSerTyrValLeuThrGlnProProSerValSerGlyS 144

 95 CTCCTGGACAGTCGGTCACCATCTCCTGCACTGGAACCAGCCATGACGTT 144
    ||||||||||:::|||||||||||||||||||||||||||:::|||||
144 erProGlyGlnSerIleThrIleSerCysThrGlyThrSerSerAspVal 160

145 GGTGGTTATAACTATGTCTCCTGGTACCAACACCACCACCAGGCAAAGCCCC 194
    ||||||  |||||||::||||||||:::||||||||||||||||||||||
161 GlyGlyTyrAsnTyrValSerTrpTyrGlnGlnHisProGlyLysAlaPr 177

195 CAAACTCATGATTATGATGCGCTAAGCGGCCTCAGGGGTCTCTGATC 244
    ||:::|||||||||||:   :::|||||  |||||||||||||::::
177 oLysLeuMetIleTyrGluGlySerLysArgProSerGlyValSerAsnA 194

245 GCTTCTCGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGG 294
    ||||||||||||||||:::||||||||||||||||||||||||||||||
194 rgPheSerGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGly 210

295 CTCCAGGCTGAGGACGAGGCTGATTATTACTGTTGTCATATACAACCAG 344
    |||||||||||||||||:::|||||||||||  ||||||||||||||
211 LeuGlnAlaGluAspGluAlaAspTyrTyrCysSerSerTyrThrThrAr 227

345 TAGCACTTTGTTATTCGGAAGAGGGACCGGTTGACCGTCCTAGGT 390
    |||||  ||||:::||||::|||||||||
227 gSerThrArgValPheGlyGlyThrLysLeuThrValLeuGly 242
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seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-958-201-14

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seq_documentation_block:
; Sequence 14, Application US/08958201
; Patent No. 5977319
; GENERAL INFORMATION:
; APPLICANT:   Pope, Anthony R
; APPLICANT:   Pritchard, Kevin
; APPLICANT:   Williams, Andrew J
; APPLICANT:   Johnson, Kevin S
; TITLE OF INVENTION:  Specific binding members for estradiol;
; TITLE OF INVENTION:  materials and methods
; NUMBER OF SEQUENCES:  23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Marshall O'Toole Gerstein Murray & Borun
; STREET:  6300 Sears Tower, 233 South Wacker Drive
; CITY:  Chicago
; STATE:  Illinois
; COUNTRY:  USA
; ZIP:  60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 1C/2D
US-08-958-201-14

alignment_scores:
          Quality:   466.00                    Length:        111
            Ratio:     4.614                      Gaps:          0
Percent Similarity:   90.991    Percent Identity:  80.180

alignment_block:
US-09-019-441-1 x US-08-958-201-14

Align seg 1/1  to: US-08-958-201-14  from: 1  to: 111

 58 CAGTCTGCCCCGACTCAGCCTCCCTGTCTCTGGGTCTCCTGGACAGTC 107
    ||||||| |||||||  |||||||||||||||||||||||||
  1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17

108 GGTCACCATCTCCTGCACTGGAACCAGCAGGATGACGTTGGTGGTTATAACT 157
    |::||||||||||||||||||||||||||:||||||||||||||:::|
 17 rIleThrIleSerCysThrGlyThrSerSerAspValGlyGlyTyrLysT 34

158 ATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACTCATGATT 207
    ||||||||||||||||:::||||||||||||||||||||||||
 34 yrValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuMetIle 50

208 TATGATGTCGCTAAGCGGCCTCAGGGTCTCGATCGCTTCTCTGGCTC 257
    :::||:::||||  |||||:|  |||||||||||  ||||||||||||
 51 PheGluValSerAsnArgProSerGlyValProAsnArgPheSerGlySe 67

258 CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGCGTCCAGGCTGAGG 307
    |||||||||||||||||||||||||||||||||||
 67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84

308 ACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 357
    ||||||||||||||||||||  ||| |||:::::::|
 84 spGluAlaAspTyrTyrCysSerSerLeuThrArgArgValThrValIle 100

358 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
    |||||| |||||||||||||||||||
101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111

seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-958-201-14

seq_documentation_block:
; Sequence 12, Application US/08958201
; Patent No. 5977319
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R
; APPLICANT: Pritchard, Kevin
; APPLICANT: Williams, Andrew J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Specific binding members for estradiol; materials and methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: ·.Chicago

; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: D12
US-08-958-201-12

alignment_scores:
          Quality:   462.00                    Length:        111
            Ratio:     4.574                      Gaps:          0
Percent Similarity:   90.991    Percent Identity:  79.279

alignment_block:
US-09-019-441-1 x US-08-958-201-12

Align seg 1/1  to: US-08-958-201-12  from: 1  to: 111

 58 CAGTCTGCCCCGACTCAGCCTCCCTGTCTCTGGGTCTCCTGGACAGTC 107
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  1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17

108 GGTCACCATCTCCTGCACTGGAACCAGCAGCGATGACGTTGGTGTGTTATAACT 157
    |::||||||||||||||||||||||||||:||||||||||||||:::|
 17 rIleThrIleSerCysThrGlyThrSerSerAspValGlyGlyTyrLysT 34

158 ATGTCTCCTGTACCAACACCACCACCCAGGCAAAGCCCCAAACTCATGATT 207
    ||||||||||||||||:::||||||||||||||||||||||||
 34 yrValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuMetIle 50

208 TATGATGTCGGTAAGCGGCCTCCTCAGGGTCTCGATCGCTTCTCTGGCTC 257
    :::||:::||||  |||||:|   ::||||||||||:|||||||||||
 51 PheGluValSerAsnArgProSerGlyValProAsnArgPheSerGlySe 67

258 CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGCGTCCAGGCTGAGG 307
    :::||:||||||||||||||||||||  ::||:::|||||
 67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnValGluA 84

.258 CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGCGTCCAGGCTGAGG 307
    |||||||||||||||||||||||||||:::||||||||||
 67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnValGluA 84

308 ACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 357
    ||||||||||||||||  |||  ||||:::::|
 84 spGluAlaAspTyrTyrCysSerSerLeuThrArgArgValThrValIle 100

358 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
    |||||| |||||||||||||||||||
101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-025-769B

seq_documentation_block:
; Sequence 33, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon

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100 PheGlyGlyGlyThrLysLeuThrValLeuGly 110

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-025-769B-53

seq_documentation_block:
; Sequence 53, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
;   APPLICANT: Knappik, Achim
;   APPLICANT: Pack, Peter
;   APPLICANT: Ilag, Vic
;   APPLICANT: Ge, Liming
;   APPLICANT: Moroney, Simon
;   APPLICANT: Plueckthun, Andreas
;   TITLE OF INVENTION: Protein-/(Poly)peptide libraries
;   NUMBER OF SEQUENCES: 373
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;     STREET: 1251 Avenue of the Americas
;     CITY: New York
;     STATE: New York
;     COUNTRY: USA
;     ZIP: 10021
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/025,769B
;     FILING DATE: 18-FEB-1998
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: EP 95 11 3021.0
;     FILING DATE: 18-AUG-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: James F. Haley, Jr., Esq.
;     REGISTRATION NUMBER: 27,794
;     REFERENCE/DOCKET NUMBER: MORPHO/5
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212)596-9000
;     TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 53:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 110 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-09-025-769B-53

alignment_scores:
      Quality: 465.50              Length:     111
      Ratio:   4.564               Gaps:         1
Percent Similarity: 91.892   Percent Identity: 81.982

alignment_block:
US-09-019-441-1 x US-09-025-769B-53      ..

Align seg 1/1 to: US-09-025-769B-53  from: 1  to: 110

58 CAGTCTGCCCGACTCAGCCTCCCTGTCTGGTCTCGGCTCCTGGTCTTCCTGGACAGTC 107
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1 GlnSerAlaLeuThrGlnProAlaSerValSerProGlySerProGlyGlnSe 17

108 GGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACT 157
    |:::||||||||||||||||||||||||::|||||||||::||||||||||
17 rIleThrIleSerCysThrGlyThrSerAspValGlyGlyTyrAsnT 34

158 ATGTCTCCTGGTACCAACACCACCCAGCAAAGCCCCCAAACTCATGATT 207
    |||||||||||||:::|||||||||||||||||||||||||||||||
34 yrValSerTrpTyrGlnHisProGlyLysAlaProLysLeuMetIle 50
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208 TATGATGTGCCGCTAAGCGGGCCTCCAGGGGTCTCTGATCGCTTCTCTCGGCTC 257
    ||||||||::::||| |||||||||||::::|||||||||||||||||
 51 TyrAspValSerAsnArgProSerGlyValSerAsnArgPheSerGlySe 67

258 CAAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGG 307
    |||||||||||||||||||||||::::|||||||::::|||||||||||||
 67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84

308 ACGAGGCTGATTATTACTGTGTTCATATACAACCAGTAGCACTTTGTTA 357
    ||||||||||||| |||:::: |||::|
 84 spGluAlaAspTyrTyrCysGlnGlnHisTyrThrProPro...Val 99

358 TTCCGAAGAGGACCCGGTTGACCGTCCTAGGT 390
    ||||| |||||::::|||||||||||||
100 PheGlyGlyGlyThrLysLeuThrValLeuGly 110

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-918-148-74

seq_documentation_block:
; Sequence 74, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
;  APPLICANT: Adams, Camellia
;  APPLICANT: W.
;  APPLICANT: Carter, Paul J.
;  APPLICANT: Fendly, Brian M.
;  APPLICANT: Gurney, Austin L.
;  TITLE OF INVENTION: Agonist Antibodies
;  FILE REFERENCE: P0979
;  CURRENT APPLICATION NUMBER: US/08/918,148A
;  CURRENT FILING DATE: 1997-08-25
;  NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 74
;  LENGTH: 249
;  TYPE: PRT
;  ORGANISM: artificial
US-08-918-148-74

alignment_scores:
         Quality: 452.00           Length:   132
         Ratio:    4.185           Gaps:       1
Percent Similarity:  81.818    Percent Identity:  67.424

alignment_block:
US-09-019-441-1 x US-08-918-148-74

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 19 CTCGTCACCCTCCTCACTCAGGGCACAGGATCC................... 51
    ::||||||::: ::: ||| |||||
116 MetValThrSerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGl 132

 52 .......TGGGCTCAGTCGTGCCCCGACTCAGCCTCCCTGTCTGGGT 94
    ::|||||||:::  ||||||||| |||||||||||
132 yGlyGlyGlySerGlnSerValLeuThrGlnProAlaSerValSerGlyS 149

 95 CTCCTGGACAGTGGGTCACCATTCCTGCACTGAACCAGCGATGACGTT 144
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149 erProGlyGlnSerIleThrIleSerCysThrGlyThrSerSerGlyVal 165

145 GGTGGTTATAACTATGTCTCCTGGTACCAACCACCAGGCAAAGCCCC 194
    ::||||||||||||||::: |||||||||||:::|||||
166 GlyGlyTyrAsnTyrValSerTrpTyrGlnGlnHisProGlyLysAlaPr 182

195 CAAACTCATGATTATGATGTCCTAAGCGGCCTCAGGGGTCTCGATC 244
    ||||:::||||  :::|||| ||||||| |||
182 oLysLeuIleTyrGlyAsnSerAsnArgProSerGlyValProAspA 199

245 GCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGG 294
    |||||||||||||||||||||||||||::||||||||
199 rgPheSerAlaSerLysSerGlyAsnThrAlaSerLeuThrIleSerGly 215

295 CTCCAGGCTGAGGACGAGGCTGATTATTACTGTGTTCATATACAACCAG 344
    |||||||||||||||||||||||||||||||||::::||
216 LeuGlnAlaGluAspGluAlaAspTyrTyrCysSerSerThrTyrAlaProPr 232

345 TAGCACTTTGTTATTCGGAAGAGGACCCGGTTGACCGTCCTAGGT 390
    ::||||||||| |||||::::|||||||||||
232 oGlyIleIleMetPheGlyGlyGlyThrLysLeuThrValLeuGly 247

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-049-672A-7

seq_documentation_block:
; Sequence 7, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
;  APPLICANT: Hillman, Jennifer L.
;  APPLICANT: Lal, Preeti
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: Yue, Henry
;  APPLICANT: Au-Young, Janice
;  APPLICANT: Corley, Neil C.
;  APPLICANT: Guegler, Karl J.
;  APPLICANT: Baughn, Mariah R.
;  TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;  NUMBER OF SEQUENCES: 28
;  CORRESPONDENCE ADDRESS:
;    ADDRESSE: Incyte Pharmaceuticals, Inc.
;    STREET:  3174 Porter Drive
;    CITY:  Palo Alto
;    STATE: CA
;    COUNTRY: USA
;    ZIP: 94304
; COMPUTER READABLE FORM:
;    MEDIUM TYPE: Diskette
;    COMPUTER: IBM Compatible
;    OPERATING SYSTEM: DOS
;    SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/09/049,672A
;    FILING DATE: HEREWITH
;    CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:
;    FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;    NAME: Cerrone, Michael C
;    REGISTRATION NUMBER: 39,132
;    REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 650-855-0555
;    TELEFAX: 650-845-4166
;    TELEX:
; INFORMATION FOR SEQ ID NO: 7:
;  SEQUENCE CHARACTERISTICS:
;    LENGTH: 236 amino acids
;    TYPE: amino acid
;    STRANDEDNESS: single
;    TOPOLOGY: linear
;  IMMEDIATE SOURCE:
;    LIBRARY: ADRETUT05
;    CLONE: 2492122
US-09-049-672A-7

alignment_scores:
         Quality: 442.50           Length:   132
         Ratio:    3.916           Gaps:       3
Percent Similarity:  85.606    Percent Identity:  68.939

alignment_block:
US-09-019-441-1 x US-09-049-672A-7

Align seg 1/1  to: US-09-049-672A-7  from: 1  to: 236

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;          LENGTH: 131 amino acids
;          TYPE: amino acid
;          TOPOLOGY: linear
;          MOLECULE TYPE: protein
US-08-305-683A-4

alignment_scores:
            Quality:   436.50        Length:  132
            Ratio:       3.897       Gaps:      3
Percent Similarity: 84.848  Percent Identity: 67.424

alignment_block:
US-09-019-441-1 x US-08-305-683A-4

Align seg 1/1  to: US-08-305-683A-4  from: 1 to: 131

   1 ATGGCCTGGACTCTGCTCCTCGTCCACCCTCCTCACTCAGGGCACAGGATC 50
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   1 MetAlaTrpSerProLeuLeuLeuThrLeuLeuAlaHisCysThrGlySer 17

  51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCCTGTCTGCTGGGTCTCCTG 100
     ||||||||||:::  |||||||||||||||||::::|||||::::||||
  17 rTrpAlaGlnSerValLeuThrGlnProProSerValSerGlyAlaProG 34

 101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGGGATGACGTTGGT... 147
     ||||  ||||||||||||||||||||:::||:::||||:::::||
  34 lyGlnArgValThrIleSerCysThrGlySerSerAsnIleGlyAla 50

 148 GGTTATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCCAA 197
     ||||:::|||||         :::|||  ||||||||  |||||||
  51 GlyTyrAsp...ValHisTrpTyrGlnHisLeuProGlyThrAlaProLy 66

 198 ACTCATGATTTATGATGTCGGTAAGCGGGCCTCAGGGGTCTCTGATCGCT 247
     |||||:|||||         |||    ||||||||||   ||||||
  66 sLeuLeuIleTyrGlyAspAsnArgProSerGlyValProAspArgP 83

 248 TCTCTGGCTCCCAAGTCTGGCAACACGGCCTCCCTCCTGGTCTCTGGGCTC 297
     |||||||||||||||||||:::||||||||:::|||||||||:::||||
  83 heSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleThrGlyLeu 99

 298 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTCATATACAACCAGT... 345
     ||||||||||||||||||||||||||||| ||||||  :::::|
 100 GlnAlaGluAspGluAlaAspTyrTyrCysCysHisIleGlnProGlyLe 116

 346 .AGCACTTTGTTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
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 116 uSerGlySerIlePheGlyGlyGlyThrLysLeuThrValLeuGly 131
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seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-305-683A-4

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seq_documentation_block:
; Sequence 4, Application US/08305683A
; Patent No. 5646041
; GENERAL INFORMATION:
;    APPLICANT: HARFELDT, Elisabeth
;    APPLICANT: LAKE, Philip
;    APPLICANT: NOTTAGE, Barbara
;    APPLICANT: OSTBERG, Lars G.
;    TITLE OF INVENTION: MONOCLONAL ANTIBODY TO HERPES SIMPLEX
;    TITLE OF INVENTION: VIRUS AND CELL LINE PRODUCING THE SAME
;    NUMBER OF SEQUENCES: 4
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Townsend and Townsend Khourie and Crew
;       STREET: 379 Lytton Avenue
;       CITY: Palo Alto
;       STATE: California
;       COUNTRY: US
;       ZIP: 94301
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/305,683A
;       FILING DATE: 13-SEP-1994
;       CLASSIFICATION: 424
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 07/759,279
;       FILING DATE: 13-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;       NAME: Liebeschuetz, Joe
;       REGISTRATION NUMBER: 37,505
;       REFERENCE/DOCKET NUMBER: 11823-005230
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (415) 326-2400
;       TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
;    SEQUENCE CHARACTERISTICS:
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(second column)

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seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-240-274-68

seq_documentation_block:
; Sequence 68, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;    APPLICANT: Siegel, Donald L.
;    TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;    TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;    FILE REFERENCE: 09596-42U2
;    CURRENT APPLICATION NUMBER: US/09/240,274
;    CURRENT FILING DATE: 1999-01-29
;    EARLIER APPLICATION NUMBER: 60/081,380
;    EARLIER FILING DATE: 1998-04-10
;    EARLIER APPLICATION NUMBER: 60/028,550
;    EARLIER FILING DATE: 1996-10-11
;    NUMBER OF SEQ ID NOS: 224
;    SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
;    LENGTH: 108
;    TYPE: PRT
;    ORGANISM: Homo sapiens
;    FEATURE:
;    OTHER INFORMATION: anti-Rh(D) chain R01
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US-09-240-274-68

alignment_scores:
    Quality:   421.50       Length:    106
    Ratio:    4.301       Gaps:     1
Percent Similarity: 92.453  Percent Identity: 75.472

alignment_block:
US-09-019-441-1 x US-09-240-274-68  ..

Align seg 1/1  to:  US-09-240-274-68  from: 1  to: 108

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 70 ACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTC 119
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  4 ThrGlnProSerAlaSerGlySerProGlyGlnSerValThrIleSe  20

120 CTGCACTGGAACCAGCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGT 169
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 20 rCysThrGlyAlaSerSerAspValGlyAlaTyrLysHisValSerTrpT  37

170 ACCAACACCACCCAGGCAAAGCCCCAAACTCATGATTTATGATGTCGCT 219
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 37 yrGlnGlnHisProGlyLysAlaProLysLeuLeuThrHisGluGlyThr  53

220 AAGCGGGCCTCAGGGGTCTCCTGATCGCTTCTCTGGCTCCAAGTCTGGCAA 269
    |||||||||||||||||||||||||||||||||||||||||||||||||
 54 LysArgProSerGlyValProAspArgPheSerGlySerLysSerGlyAs  70

270 CACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATT 319
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 70 nThrAlaSerLeuThrValSerGlyLeuGlnAlaGluAspGluAlaAspT  87

320 ATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTCCGGAAGAGGG 369
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 87 yrTyrCysSerPheAlaGlyAsnSer...ValIlePheGlyGlyGly 102

370 ACCCGGTTGACCGTCCTA 387
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103 ThrLysLeuThrValLeu 108
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seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-240-274

seq_documentation_block:
; Sequence 69, Application US/09240274
; Patent NO. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH:104
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain S01
US-09-240-274-69

alignment_scores:
    Quality:   413.50       Length:    106
    Ratio:    4.353       Gaps:     2
Percent Similarity: 89.623  Percent Identity: 76.415

alignment_block:
US-09-019-441-1 x US-09-240-274-69  ..

Align seg 1/1  to:  US-09-240-274-69  from: 1  to: 104

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  4 ThrGlnProSerValSerGlySerProGlyGlnSerIleThrIleSe  20

120 CTGCACTGGAACCAGCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGT 169
    ||||||||:::||||||::||||||
 20 rCysSer..........AspValGlyAsnTyrAsnLeuValSerTrpT  33

170 ACCAACACCACCCAGGCAAAGCCCCAAACTCATGATTTATGATGTCGCT 219
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 33 yrGlnGlnTyrProGlyLysAlaProLysLeuIleIleTyrGluGlySer  49

220 AAGCGGGCCTCAGGGGTCTCCTGATCGCTTCTCTGGCTCCAAGTCTGGCAA 269
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 50 LysArgProSerGlyValSerSerArgPheSerGlySerArgSerGlyAs  66

270 CACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATT 319
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 66 nThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluAspGluAlaAspT  83

320 ATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTCCGGAAGAGGG 369
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 83 yrHisCysSerTyrAlaIleSerSerArg...IlePheGlyGlyGly  98

370 ACCCGGTTGACCGTCCTA 387
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 99 ThrLysLeuThrValLeu 104
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seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-652-816A-15

seq_documentation_block:
; Sequence 15, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.8
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525004.9

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;     FILING DATE: 07-DEC-1995
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: GB 9610824.6
;     FILING DATE: 23-MAY-1996
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: PCT/GB92/02240
;     FILING DATE: 02-DEC-1992
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/244.597
;     FILING DATE: 01-JUN-1994
;  ATTORNEY/AGENT INFORMATION:
;     NAME: David W. Clough
;     REGISTRATION NUMBER: 36,107
;     REFERENCE/DOCKET NUMBER: 28111/33308
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 312-474-6300
;  INFORMATION FOR SEQ ID NO: 15:
;     SEQUENCE CHARACTERISTICS:
;     LENGTH: 111 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
; US-08-652-816A-15

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        Ratio:        4.124             Gaps:       2
Percent Similarity:  88.182      Percent Identity: 70.909

alignment_block:
US-09-019-441-1 x US-08-652-816A-15

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  1 GlnSerValLeuThrGlnProSerValSerAlaProProGlyGlnLy  17

108 GGTCACCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTTATAACT 157
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 17 sValThrIleSerCysSerGlySerThrProAsnileGlyAsn...AsnT  33

158 ATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACTCATGATT 207
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 33 yrValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuMetIle  49

208 TATGATGTCGCTAAGCGGCCTCAGGGGTCTCGATCGGTTCTCTCGGCTC 257
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 50 TyrAspValSerLysArgProSerGlyValProsAspPheSerGlySe  66

258 CAAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGCTCCAGGCTGAGG 307
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 66 rLysSerGlyAsnSerAlaSerLeuAspIleSerGlyLeuGlnSerGluA  83

308 ACGAGGCTGATTATTACTGTTGTCATATACAACCAGT...AGCACTTTG 354
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 83 spGluAlaAspTyrTyrCysAlaSerLeuSerGluPhe  99

355 TTATTCGGAAGAGGACCCGGTTGACCGTC 384
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seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-487-550-10

seq_documentation_block:
; Sequence 10, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
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;  NUMBER OF SEQUENCES: 12
;  CORRESPONDENCE ADDRESS:
;     ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
;     STREET: 699 Prince Street
;     CITY: Alexandria
;     STATE: VA
;     COUNTRY: USA
;     ZIP: 22314
;  COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/487,550
;     FILING DATE: 07-JUN-1995
;     CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;     NAME: Teskin, Robin L.
;     REGISTRATION NUMBER: 35,030
;     REFERENCE/DOCKET NUMBER: 012712-131
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 703-836-6620
;     TELEFAX: 703-836-2021
;  INFORMATION FOR SEQ ID NO: 10:
;     SEQUENCE CHARACTERISTICS:
;     LENGTH: 236 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
; US-08-487-550-10

alignment_scores:
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        Ratio:        3.738             Gaps:       2
Percent Similarity:  84.921      Percent Identity: 64.286

alignment_block:
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  7 LeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAlaAargCysGluSerVa  23

 66 CCCGACTCAGCCTCCCTGTGTCTCGGGTCTCCTGGACAGTCGGTCACCA 115
    :  ||||||||||||||||||:::||||||||::::|||||||||
 23 lLeuThrGlnProProSerValSerGlyAlaProGlyGlnLysValThrI  40

116 TCTCCTGCACTGGAACCAGCCATGACGTTGGTGGTTATAACTATGTCTCC 165
    ||||||||||||||||||::::::|||||||:::   :::
 40 leSerCysThrGlySerThrSerAsnileGlyGlyTyrAsp...LeuHis  55

166 TGGTACCAACACCACCCAGGCAAAGCCCCAAACTCATGATTTATGATGT 215
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 56 TrpTyrGlnGlnLeuProGlyThrAlaProLysLeuLeuIleTyrAspIl  72

216 CGCTAAGCGGCCTCAGGGGTCTCGATCGCTTCTCTGGCTCCAAGTCTG 265
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 72 eAsnLysArgProSerGlyIleSerAspArgPheSerGlySerLysSerG  89

266 GCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCT 315
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 89 lyThrAlaAlaSerLeuAlalleThrGlyLeuGlnThrGluAspGluAla 105

316 GATTATTACTGTTGTCATATACAACCAGT...AGCACTTTGTTATTCGG 362
    ||||||||||||  :::||| ||||| :: ::|||||
106 AspTyrTyrCysGlnSerTyrAspSerTyrLeuAsnAlaGlnValPheGl 122

363 AAGAGGGACCCGGTTGACCGTCTAGT 390
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Mon Sep 23 16:30:36 2002

122 yGlyGlyThrArgLeuThrValLeuGly 131

OM of: US-09-019-441-2 to: PIR_71:*    out_format : pfs
Date: Sep 23, 2002 10:02 AM
About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09019441/runat_23092002_095258_6306/app-query.fasta_1.1860
-DB-PIR_71 -QFMT=fastan -SUFFIX=rpr -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -LOOPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosun62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -USER=US09019441_@CGN1_1_227
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-019-441-2
Query length: 423
Database: PIR_71:*
Database sequences: 283138
Database length: 96089934
Search time (sec): 132.110000

score_list:

| Sequence | Strd | Orig | ZScore | EScore | Len | ! Documentation |
|---|---|---|---|---|---|---|
| pir2:S78055 | + | 564.00 | 863.19 | 3.8e-40 | 145 | ! Ig heavy chain precursor V-D-J |
| pir2:S13519 | + | 557.50 | 853.16 | 1.3e-39 | 147 | ! Ig heavy chain V region precurs |
| pir1:I37782 | + | 556.50 | 852.02 | 1.6e-39 | 140 | ! Ig variable region (VDJ) (clone |
| pir2:S31586 | + | 553.00 | 846.73 | 3.2e-39 | 139 | ! Ig heavy chain V region - human |
| pir2:S31676 | + | 552.00 | 845.32 | 3.9e-39 | 137 | ! Ig heavy chain V region - human |
| pir2:S31696 | + | 538.50 | 824.60 | 5.5e-38 | 139 | ! Ig heavy chain V region - human |
| pir2:S31511 | + | 535.50 | 819.17 | 1.0e-37 | 155 | ! Ig heavy chain - human |
| pir2:S31512 | + | 531.50 | 813.06 | 2.2e-37 | 155 | ! Ig heavy chain - human |
| pir2:A49045 | + | 530.50 | 812.33 | 2.7e-37 | 140 | ! Ig heavy chain V region (anti-E |
| pir2:S09711 | + | 522.50 | 799.80 | 1.3e-36 | 146 | ! Ig heavy chain V region - human |
| pir2:S09710 | + | 520.50 | 796.74 | 1.9e-36 | 146 | ! Ig heavy chain V region - human |
| pir2:A26340 | + | 518.00 | 794.59 | 3.1e-36 | 118 | ! Ig heavy chain precursor V-II r |
| pir2:B26340 | + | 514.00 | 788.62 | 6.7e-36 | 116 | ! Ig heavy chain precursor V-II r |
| pir2:E34964 | + | 511.50 | 784.74 | 1.1e-35 | 117 | ! Ig heavy chain V region - human |
| pir2:A24770 | + | 510.50 | 781.81 | 1.3e-35 | 140 | ! hypothetical hybrid Ig/T-cell r |
| pir2:S18557 | + | 510.00 | 782.52 | 1.5e-35 | 116 | ! Ig heavy chain V region precurs |
| pir2:A41287 | + | 505.00 | 773.47 | 3.9e-35 | 139 | ! Ig heavy chain precursor V-IV r |
| pir2:S31684 | + | 504.00 | 772.84 | 4.7e-35 | 124 | ! Ig heavy chain V region - human |
| pir2:S31585 | + | 495.50 | 759.09 | 2.5e-34 | 137 | ! Ig heavy chain precursor V-D-J |
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| pir2:B41287 | + | 492.00 | 753.41 | 5.0e-34 | 143 | ! Ig heavy chain precursor V-IV r |
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| pir2:S31673 | + | 486.50 | 745.76 | 1.5e-33 | 130 | ! Ig heavy chain V region - human |
| pir2:S44114 | + | 478.00 | 732.85 | 7.7e-33 | 129 | ! Ig heavy chain V region - human |
| pir2:S44114 | + | 473.50 | 725.63 | 1.9e-32 | 129 | ! Ig heavy chain V region - human |
| pir2:S31690 | + | 467.50 | 716.76 | 6.0e-32 | 130 | ! Ig heavy chain V region - human |
| pir2:PT0370 | + | 457.00 | 701.36 | 4.7e-31 | 120 | ! mu chain precursor V region |
| pir2:S30534 | + | 451.00 | 691.58 | 1.5e-30 | 130 | ! Ig heavy chain V region - human |
| pir1:GIHUH2 | + | 444.50 | 680.75 | 5.4e-30 | 146 | ! Ig heavy chain precursor V-II r |
| pir2:S30529 | + | 441.50 | 677.52 | 9.8e-30 | 123 | ! Ig heavy chain V region - human |
| pir2:S54906 | + | 441.50 | 676.84 | 9.8e-30 | 134 | ! Ig heavy chain V region - human |
| pir2:S24443 | + | 434.00 | 666.39 | 4.2e-29 | 118 | ! Ig heavy chain V region (VH4DJ) |
| pir2:S26905 | + | 433.50 | 667.08 | 4.7e-29 | 98 | ! Ig heavy chain V region (DP-70 |
| pir2:PS0341 | + | 433.50 | 664.69 | 4.7e-29 | 133 | ! Ig heavy chain V-D-J region (RA |
| pir2:S26904 | + | 430.50 | 662.51 | 8.4e-29 | 98 | ! Ig heavy chain V region (DP-69 |
| pir2:S30530 | + | 427.50 | 656.15 | 1.5e-28 | 123 | ! Ig heavy chain V region - human |
| pir2:S44113 | + | 420.50 | 645.59 | 6.0e-28 | 121 | ! Ig heavy chain V region - human |
| pir2:S31514 | + | 418.50 | 642.10 | 8.8e-28 | 128 | ! Ig heavy chain - human |
| pir2:S20780 | + | 416.00 | 638.92 | 1.4e-27 | 118 | ! Ig heavy chain V region - human |
| pir2:B23746 | + | 416.00 | 633.66 | 1.4e-27 | 231 | ! Ig Fab region IV-J(H4)-C (KAU d |
| pir2:S26903 | + | 414.50 | 638.09 | 1.9e-27 | 98 | ! Ig heavy chain V region (DP-6 |
| pir2:S47010 | + | 414.00 | 635.36 | 2.1e-27 | 126 | ! Ig heavy chain V4.21-UniqueD |
| pir2:S54226 | + | 412.00 | 631.42 | 3.1e-27 | 141 | ! Ig mu heavy chain V region p |
| pir2:S12414 | + | 410.50 | 631.98 | 4.2e-27 | 98 | ! Ig heavy chain V region (4.14 |
| pir2:S12412 | + | 410.00 | 631.14 | 4.6e-27 | 99 | ! Ig heavy chain V region (4.12 |

seq_name: pir2:S78055

seq_documentation_block:
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C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78055; S23720
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78055
A:Molecule type: mRNA
A:Residues: 1-145 <HAR>
A:Cross-references: EMBL:X54445; NID:g37817; PID:CAA38312.1; PID:g37818
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notk
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- an
patient.
A:Reference number: S23716; MUID:92031262
A:Accession: S23720
A:Molecule type: mRNA
A:Residues: 18-115 <HAW>
A:Cross-references: EMBL:X54445
A:Note: the authors translated the codon GCA for residue 67 as Arg
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F:18-145/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:32-115/Domain: immunoglobulin homology <IMM>

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              Ratio:      4.476        Gaps:        3
Percent Similarity:  84.000     Percent Identity:  74.000

alignment_block:
US-09-019-441-2 x S78055

Align seg 1/1  to: S78055  from: 1 to: 145

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      107 CCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCTGTCAGCAGTAAC 156
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      207 ACGTATCTCTGGTAGTGGTGGGGCCACCAACTACACACCCGTCCCTCAAGA 256
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       67 yGlnIleTyrHisSer...GlySerThrAsnTyrAsnProSerLeuLysS 83

      257 GTCGAGTCATCATTCACAAGACACGTCCAAGAAACCAGTTCTCCCCTGAAC 306
          ||  ||||||  ||||| ||||||||||||||||||||::::
       83 erAlaValThrIleSerValAspLysSerLysAsnGlnPheSerLeuLys 99

      307 CTGAACTCTGTGACCGCCGGACACCGCCGTGTATTACTGTGCCAGAGA 356
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                                          seq_name: pir2:I37782

                                          seq_documentation_block:
                                          Ig variable region (VDJ) (clone T23-9) - human (fragment)
                                          C;Species: Homo sapiens (man)
                                          C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
                                          C;Accession: I37782; S25476
                                          R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
                                          Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
                                          A;Title: Somatic diversification in the heavy chain variable region genes expressed b
                                          A;Reference number: A36876; MUID:94119917
                                          A;Accession: I37782
                                          A;Status: preliminary
                                          A;Molecule type: mRNA
                                          A;Residues: 1-140 <RES>
                                          A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583
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                                          F;46-128/Domain: immunoglobulin homology <IMM>

                                          alignment_scores:
                                                Quality:    556.50         Length:    145
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                                          Percent Similarity:  86.897    Percent Identity: 77.931

                                          alignment_block:
                                          US-09-019-441-2 x I37782

                                          Align seg 1/1 to: I37782  from: 1  to: 140

                                          1  ATGAAACACCTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGT  50
                                             |||||||||||||||||||||||||||||||||||||||||||||||
                                          1  MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

                                          51  CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
                                              |||||||||||||:|||||||||||||||:::||||||||||||||||||
                                          17  lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysPros  34

                                          101  CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT  150
                                               |||||||||||||:::|||||||||:||:::||||||||||   |||
                                          34   erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIle...Ser  49

                                          151  AGTAACTGGTGACCTGGATCCGGCAGCCCCAGGGAAGGGACTGGAGTG  200
                                               |||   :::||:::||||||||||||||||||||||||||||||||
                                          50   SerTyrTyrTrpIleArgGlnProProGlyLysGlyLeuGluTr  66

                                          201  GATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACACACCCGTCCC  250
                                               |||||   |||   :||:::|||||||||||:|||||||||||||||||
                                          66   pIleGlyThrTyrLeuTyrSer...GlySerThrAsnTyrAsnProSerL  82

                                          251  TCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC  300
                                               |||||||||||  ||||||  |||||| ||||||||||||||||||||
                                          82   euLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer  98

                                          301  CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC  350
                                               |||:::|||:::||||||||||||||||||||||||||||||||||||
                                          99   LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAl  115

                                          351  CAGA........GATTGGGCCCAAATAGTCGAACAACGCTAGGCT  388
                                               :::|        |||||||||||||||||||||||||||||||
                                          115  aArgHisAsnSerSerTrp........TyrGlyArgTyrPheAspT  129

                                          389  TCTGGGGCCAGGAGTCCTGGTCACCGTCTCCTCA  423
                                               :::||||||||||||||||||||||||||||||
                                          129  yrTrpGlyGlnGlyThrLeuValThrValSerSer  140

                                          seq_name: pir2:S31586

                                          seq_documentation_block:
```

```
100  LeuSerLeuSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArg..  115
     ||||||||||||||||||||||||||||:::||||||||||||||||
357  TTGGGCCAAATAGTCTGGAACAACG..............................  381
     ::::||||||:::||
116  ..........ValThrGlySerThrPhePheSerGlyTyrTyrThrArgG  129

382  ........CTAGGCTTCTGGGGCCAGGAGTCCTGGTCACCGTCTCCTCA  423
        :::  ::::|||||||||||||||:::||||||||||||||||
129  lyTyrTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer  145

seq_name: pir2:S13519

seq_documentation_block:
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S13519
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A;Reference number: S13519; MUID:91187691
A;Accession: S13519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <MOR>
A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;41-125/Domain: immunoglobulin homology <IMM>

alignment_scores:
      Quality:    557.50         Length:    144
      Ratio:        4.460         Gaps:        4
Percent Similarity:  86.806    Percent Identity: 79.167

alignment_block:
US-09-019-441-2 x S13519

Align seg 1/1 to: S13519  from: 1  to: 147

1  ATGAAACACCTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGT  50
   ||||||||||||||||||||||||||||||||||||||||||||||
8  MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  24

51  CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
    |||||||||||||:||||||||||||||||:::|||||||||||||||
24  lLeuSerGlnValGlnLeuGlnLeuGlnGluSerGlyProGlyLeuValLysPros  41

101  CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT  150
     ||||||||||||:::|||||||||:||:::||||||||||||||||||
41   erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIleSerSer  57

151  AGTAAC...TGGTGACCTGGATCCGGCAGCCCCAGGGAAGGGACTGGA  197
     |||:::   :::||:||||||||||||||||||||||||||||||||
58   SerSerTyrTyrTrpIleArgGlyTyrTrpIleArgGlnProProGlyLysGlyLeuGlI  74

198  GTGGATTGGACGTATCTCTGGTACTGGTGGGGCCACCAACTACAACCCGT  247
     ||||||||| |||:::|||   |||||||||||||||||||||||||||
74   uTrpIleGlyTyrLeuTyrSer...GlySerThrTyrTyrAsnProS  90

248  CCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC  297
     |||||||||||||||||||||||  |||||||||||||||||||||||
90   erLysSerArgValThrIleSerValAspThrSerLysAsnGlnPhe  106

298  TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTG  347
     ||||||:::|||:::|||||||||||||||||||||||||||||||||
107  SerLeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysy  123

348  TGCCAGAGAT.....TGGGCCCAAATAGTCTGGAACAACGCTAGGCTTCT  391
     |||||||         |||  :: ::||||||||||||||||||||||
123  sAlaArgProLeuLeuTrp........PheGlyGluLeuPheAspTyrT  137

seq_documentation_block:
```

A;Description: Mechanisms that generate human immunoglobulin diversity operate from t
A;Reference number: S31585
A;Accession: S31676
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137 <CUI>
A;Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

alignment_scores:
        Quality:    552.00              Length:    141
        Ratio:        4.452             Gaps:         3
Percent Similarity:  87.943    Percent Identity: 78.723

alignment_block:
US-09-019-441-2 x S31676

Align seg 1/1  to: S31676  from: 1  to: 137

  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGT  50
    |||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa 17

 51 CCTGTCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    |||||||||::||||||||||||||||||||||||||::|||||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    ||||||||||:|||||||||||||:||||||||||:::|||...Ser  49
 34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIle...Ser 49

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGAAGGACTGGAGTG 200
    |||:::||||||||||||||||||||||||||||:|||||||||||||
 50 SerTyrTyrTrpSerTrpIleArgGlnProAlaGlyLysGlyLeuGluTr 66

201 GATTGGACGTATCTTCGGTAGTGGTGGGGCCACCAACTACAAACCGTCCC 250
    ||||||||||  |||:::||||||||::::|||||||||||||||||||
 66 pIleGlyArgIleTyrThrSer...GlySerThrAsnTyrAsnProSerL 82

251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    ||||||||||||  :::||  |||||||||||||||||||||||||||
 82 euLysSerArgValThrMetSerValAspThrSerLysAsnGlnPheSer 98

301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
    |||:::||:||||||||||||||||||||||||||||||||||||||||
 99 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 115

351 CAGAGATTGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGCCCAGG 400
    ||||||      |||      :::        ||||||||||||||||||
115 aArgAspAlaProLeuMetTyrGly......MetAspValTrpGlyGlnG 130

401 GAGTCCTGGTCACCGTCTCCTCA 423
    ||:::      |||||||||||
130 lyThrThrValThrValSerSer 137

seq_name: pir2:S31696

seq_documentation_block:
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31696
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from t
A;Reference number: S31585
A;Accession: S31696
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <CUI>

---

Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31586
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31586
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <CUI>
A;Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

alignment_scores:
        Quality:    553.00              Length:    141
        Ratio:        4.424             Gaps:         2
Percent Similarity:  88.652    Percent Identity: 78.014

alignment_block:
US-09-019-441-2 x S31586

Align seg 1/1  to: S31586  from: 1  to: 139

  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGT  50
    |||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa 17

 51 CCTGTCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    ||||||::||||||||||||||||||||||||||::|||||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    ||||||||||:|||||||||||||:||||||||||:::|||...Ser  49
 34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIle...Ser 49

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGAAGGACTGGAGTG 200
    |||:::||||||||||||||||||||||||||||:|||||||||||||
 50 SerTyrTyrTrpSerTrpIleArgGlnProAlaGlyLysGlyLeuGluTr 66

201 GATTGGACGTATCTTCGGTAGTGGTGGGGCCACCAACTACAAACCGTCCC 250
    ||||||||||  |||:::||||||||::::|||||||||||||||||||
 66 pIleGlyArgIleTyrThrSer...GlySerThrAsnTyrAsnProSerL 82

251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    |||||||||||  |||:::||  |||||||||||||||||||||||
 82 euLysSerArgValThrMetSerValAspThrSerLysAsnGlnPheSer 98

301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
    |||:::||:||||||||||||||||||||||||||||||||||||||||
 99 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 115

351 CAGAGATTGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGCCCAGG 400
    ||||||      :::||  |||||||||||||||||||||||||
115 aArgGlyLeuGlyIleArgArgArgGlyAlaPheAspIleTrpGlyGlnG 132

401 GAGTCCTGGTCACCGTCTCCTCA 423
    |||      |||||||||||||
132 lyThrMetValThrValSerSer 139

seq_name: pir2:S31676

seq_documentation_block:
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992

A;Cross-references: EMBL:Z14194; NID:g30975; PIDN:CAA78563.1; PID:g30976
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

alignment_scores:
```
         Quality:  538.50          Length:     142
           Ratio:    4.308            Gaps:       4
Percent Similarity:   88.028   Percent Identity:   76.761
```

alignment_block:
US-09-019-441-2 x S31696   ..

Align seg 1/1  to: S31696  from: 1  to: 139

```
  1 ATGAAACACCTGGTTCTTCCTCCTCCTGTGGCAGCTCCCAGATGGGT  50
    ||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

 51 CCTGTCCCAGCTGCAGCTGTCGAGGAGTGCGGGCCCAGGAGTGGTGAAGCCTT 100
    ||||::|||||||||||||||||||||||||||||||::::|||||||||
 17 lLeuSerGlnValGlnLeuGlnLeuSerGlyProGlyLeuValLysProS  34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    ||||||||||||||::||||||||||||||||::|||||||||||:|||
 34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIle...Ser  49

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
    |||  :::|||||||||||||||||||||||||::|||||||||||||
 50 SerTyrTyrTrpSerTrpIleArgGlnProAlaAlaLysGlyLeuGluTr  66

201 GATTGGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACACCCCGTCC 250
    |||||||||| ||  :::||||||||||||||||||||||||||
 66 pIleGlyArgIleTyrThrSer...GlySerThrAsnTyrAsnProSerL  82

251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    ||||||||| :::||| ||||||||||||||||||||||||||
 82 euLysSerArgValThrMetSerValAspThrSerLysAsnGlnPheSer  98

301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
    |||:::|||:::||| ||||||||||||||||||||||||||||
 99 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAl  115

351 CAGAGATTGGGCCCAAATAGCTGGAACAACG...CTAGGCTTCTGGGGCC 397
    |||| :::::|| ||:|||||
115 aArgGlyLeuGlyLeuThrGlyAspLysTrpIleAspTyrTrpGlyG 132

398 AGGGAGTCCTGGTCACCGTCTCCT 421
    |||||:||| |||||||||||
132 lnGlyThrLeu.SerProSerPro 139
```

seq_name: pir2:S31511

seq_documentation_block:
A;Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>

---

A;Cross-references: EMBL:Z14194; NID:g30975; PIDN:CAA78563.1; PID:g30976
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

alignment_scores:
```
         Quality:  535.50          Length:     146
           Ratio:    4.319            Gaps:       4
Percent Similarity:   84.932   Percent Identity:   74.658
```

alignment_block:
US-09-019-441-2 x S31511   ..

Align seg 1/1  to: S31511  from: 1  to: 155

```
  1 ATGAAACACCTGGTTCTTCCTCCTCCTGTGGCAGCTCCCAGATGGGT  50
    ||||||||||||||||||||||||||||||||||||||||||||||||
 14 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  30

 51 CCTGTCCCAGCTGCAGCTGTCGAGGAGTGCGGGCCCAGGAGTGGTGAAGCCTT 100
    ||||::|||||||||||||||||||||||||||::::|||||||||
 30 lLeuSerGlnValGlnLeuGlnLeuSerGlyProGlyLeuValLysProS  47

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    ||||||||||||:::||||||||||||||||::|||||||||||:|| |||
 47 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIle...Ser  62

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
    ||| :::|||||||||||||||||||||||||::|||||||||||||||
 63 SerTyrTyrTrpSerTrpIleArgGlnProGlyLysGlyLeuGluTr  79

201 GATTGGGACGTATCTCTGTAGTGGTGGGGCCACCAACTACACCCCGTCCC 250
    ||||||  :::|||  ||||||||||||||||||||||||
 79 pIleGlyTyrIleTyrThrGlySerAlaThr...TyrAsnProProL  95

251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    ||||||||| |||||  ||||||||||||||||||||||||||
 95 euLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 111

301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
    |||:::|||:::||||||| ||||||||||||||||||||||||||
112 LeuLysValSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 128

351 CAGA..........GATTGGGCCCAAATAGCTGGAACAACGCGTAG 385
    |||| :::|| |||:::|||||
128 aArgGlyGlyIleSerSerTrpTyrAspTyrTyrGly.....MetA 143

386 GCTTCTGGGGCCAGGAGTCCTGGTCACCGTCTCCTCA 423
    ||||||||| :::|||||||||||||||
143 spValTrpGlyGlnGlyThrThrValThrValSerSer 155
```

seq_name: pir2:S31512

seq_documentation_block:
A;Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>

alignment_scores:
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         Quality:  531.50          Length:     146
           Ratio:    4.321            Gaps:       4
Percent Similarity:   84.247   Percent Identity:   73.973
```

alignment_block:

A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA a

US-09-019-441-2 x S31512

Align seg 1/1    from: 1    to: 155

```
  1 ATGAAACACCTGTCTTCCTCCTGTTCTGGCAGCTCCCAGATGGGT  50
    ||||||||||||:::|||||||||||||||||||||||||||||||
 14 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa

 51 CCTGTCCCAGCTGCAGCTGCAGAGTCGGGCCCCAGGAGTGGTGAAGCCTT  100
    |||||||||:::|||||||||||||::||||||::::||||||||||||||
 30 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS  47

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCGTCAGCAGT  150
    |||||||||:::|||||||||||||::||||||:||||||||||||||||
 47 erGluThrLeuSerLeuThrCysAlaValTyrGlyGlySerIle...Ser  62

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG  200
    ||||||||||||||||||||||||||||||||||:::|||||||||||||
 63 SerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTr  79

201 GATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACAACCCGTCCC  250
    |||   ::|||||||||||||||||||||||||||||||||||||||||||
 79 pIleGlyThrTyrLeuGlyProGlyLysGlyLeuGluTr

251 TCAAGAGTCGAGTCATCATTTCACAAGAACACGTCCAAGAACCAGTTCTCC  300
    |||||| ||    ::||||||:|||||  ||||||||:::|||||||||
 79 pIleGlyTyrTyrIleTyrTyrThrGlySerAlaThr...TyrAsnProProI  95

301 TCAAGAGTCGAGTCATCATTTCACAAGAACACGTCCAAGAACCAGTTCTCC  350
    :::||||||||| ||||||||||||||||||||:|||||||||||||||||
 95 leGlyTyrTyrIleTyrTyrThrGlySerAlaThr...TyrAsnProProI

301 CTGAACCTGAACTCTGTGACCGCCGCGACACGGCCGTGTATTACTGTGC  350
    ||:::||||||||||||||||||||||||||||||||||||||||||||||
112 LeuLysValSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAl  128

351 CAGA............GATTGGGCCCAAATAGCTGGAACAACGCTAG  385
    ||||            :::|||                    :::|||
128 aArgGlyGlyGlyLeuGlyIleSerSerTrpTyrValTyrTyrGly......MetA  143

386 GCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA  423

143 spValTrpGlyGlnGlyThrLeuValThrValSerSer  155
```

seq_name: pir2:A49045

seq_documentation_block:
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: A49045
R;Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silverma
Eur. J. Immunol. 22, 1781-1788, 1992
A;Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i bl
A;Reference number: A49045; MUID:92324290
A;Accession: A49045
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-140 <GRI>
A;Cross-references: GB:S39381; NID:g250899; PIDN:AAB22441.1; PID:g250900
A;Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBIP:108089)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

alignment_scores:
    Quality:    530.50        Length:    142
    Ratio:    4.278          Gaps:    3
Percent Similarity:  87.324    Percent Identity:  75.352

alignment_block:
US-09-019-441-2 x A49045

Align seg 1/1    from: 1    to: 140

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  1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGCCAGCTCCCAGATGGGT  50
```

seq_name: pir2:S09711

seq_documentation_block:
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S09711
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domain
A;Reference number: S09710; MUID:9262535
A;Accession: S09711
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <HUG>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>

alignment_scores:
    Quality:    522.50        Length:    149
    Ratio:    4.147          Gaps:    4
Percent Similarity:  84.564    Percent Identity:  71.812

alignment_block:
US-09-019-441-2 x S09711

Align seg 1/1    to: S09711    from: 1    to: 146

```
  1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGCCAGCTCCCAGATGGGT  50
    ||||||||||||:::||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuValAlaArgAlaProArgTrpCy  17

 51 CCTGTCCCAGCTGCAGCTGCAGAGTCGGGCCCCAGGAGTGGTGAAGCCTT  100
    |||||||||:::|||||||||||||::||||||::::||||||||||||||
 17 sLeuSerGlnValGlnLeuGlnLeuGlnSerGlyProGlyLeuValLysProS  34
```

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    ||||||||||||||:::|||||::|||||||||||||||||||||||||||
 34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerValSerSer 50

151 AGTAAC...TGGTGGACCTGGATCCGCCAGCCCCAGGGAAGGGACTGGA 197
    ||:::: .:|||||:::|||||||||||||||:|||||||||||||||| |
 51 SerGlyLeuTyrTrpSerTrpIleArgGlnProProGlyLysGlyProGl 67

198 GTGGATTGGACGTATCCTCGGTAGTGGTGGGCCACCACTACAACCCGT 247
    ||||||||| ||| ||:::|||||||||||||||||||||||||||||||
 67 uTrpIleGlyTyrIleTyrTyrSer...GlySerThrTyrAsnProS 83

248 CCCTCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTC 297
    |||||||||||||||| |||||:||||||||||||||||||||||||:||
 83 erLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPhe 99

298 TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTG 347
    |||||||||||||||| ||||||||||||||||||||||||||||||||||
100 SerLeuLysSerSerValThrAlaAlaAspThrAlaValTyrTyrCy 116

348 TGCCAGAGAT.................................TGGGGCCC 364
    |:::||
116 sThrArgProGlyTyrGlyAspThrSerValArgLysArgValTrp.... 131

365 AATAGCTGGAACAACCCTAGGCTTCTGGGCCAGGGAGTCCTGGTCACC 414
    ::::: .:::|||||||||||||||:::|:: |||||
132 ...............AsnMetAspLeuTrpGlyGlnGlyThrThrValThr 143

415 GTCTCCTCA 423
    |||||||||
144 ValSerSer 146

seq_name: pir2:A26340

seq_documentation_block:
Ig heavy chain precursor V-II region (71-2) - human
N;Alternate names: Ig heavy chain V region (DP-66)
C;Species: Homo sapiens (man)
C;Date: 05-Jun-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: A26340; S26901
R;Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.
J. Mol. Biol. 190, 529-541, 1986
A;Title: Organization and evolution of variable region genes of the human immunoglobu
A;Reference number: A26340; MUID:87061007
A;Accession: A26340
A;Molecule type: DNA
A;Residues: 1-118 <KOD>
A;Cross-references: GB:M29811; NID:g185597; PIDN:AAC99493.1; PID:g553419
A;Note: the authors translated the codon GAG for residue 25 as Gln
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups o
A;Reference number: S26885; MUID:93021117
A;Accession: S26901
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 20-118 <TOM>
A;Cross-references: EMBL:Z12366; NID:g32950; PIDN:CAA78236.1; PID:g32951
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-118/Product: Ig heavy chain V-II region 71-2 #status predicted <IMM>
F;34-118/Domain: immunoglobulin homology <IMM>

alignment_scores:
        Quality:   518.00          Length:     119
        Ratio:       4.667          Gaps:         2
Percent Similarity:  93.277    Percent Identity:  86.555

alignment_block:
US-09-019-441-2 x A26340    ..

Align seg 1/1 to: A26340  from: 1  to: 118

  1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGT 50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGT 50

seq_name: pir2:S09710

seq_documentation_block:
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S09710
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains o
A;Reference number: S09710; MUID:90262535
A;Accession: S09710
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <HUG>
A;Cross-references: GB:X52110; NID:g31447; PIDN:CAA36344.1; PIDN:CAA36344.1; PID:g31448
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>

alignment_scores:
        Quality:   520.50          Length:     153
        Ratio:       4.232          Gaps:         4
Percent Similarity:  80.392    Percent Identity:  69.935

alignment_block:
US-09-019-441-2 x S09710    ..

Align seg 1/1 to: S09710  from: 1  to: 146

  1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGT 50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuLeuValAlaAlaProArgTrpVa 17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 17 lLeuSerGlnLeuArgLeuGlnGluSerGlyProGlyLeuValLysProS 34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    |||||||||||||||||||:::|||||::|||||||||||||||||||||
 34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerValSerSer 50

151 AGTAAC...TGGTGGACCTGGATCCGCCAGCCCCAGGGAAGGGACTGGA 197
    ||:::: .:|||||:::|||||||||||||||||||||||||||||||

```
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

 51 CCTGTCCCAGCTGCAGCTGGACCTGCGGCTCGGCCCAGGAGTGGTGAAGCCTT 100
    ||||||::|||||||||||||||||||::|||::||||||||
 17 lLeuSerGlnValGlnLeuGlnLeuGluSerGlyProGlyLeuValLysProS  34

101 CGGAGACCCTGTCCCTCACCTGCGTCTGGCTCTGTGGCTCTGTCAGCAGT 150
    ||||||||||||||||||||||||::::|||||||||||||||||||||
 34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerValSerSer  50

151 ..AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGAAGGGACTGGA 197
    ||||     ::||||||||||||||||||||||||||||
 51 GlySerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGl  67

198 GTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACAACCGT 247
    ||||::|||||     |||::|||||||||||||||||||
 67 uTrpIleGlyTyrTyrIleTyrTyrSer...GlySerThrAsnTyrAsnProS  83

248 CCCTCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTC 297
    ||||||||||||     ||||||||||||||||||||
 83 erLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPhe  99

298 TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTG 347
    ||||||::||::|||||||||||||||||||||||
100 SerLeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCy  116

348 TGCCAGA 354
    ||||||||
116 sAlaArg 118

seq_name: pir2:B26340

seq_documentation_block:
Ig heavy chain precursor V-II region (71-4) - human
C;Species: Homo sapiens (man)
C;Date: 05-Jun-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: B26340
R;Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.
J. Mol. Biol. 190, 529-541, 1986
A;Title: Organization and evolution of variable region genes of the human immunoglobulin
A;Reference number: A26340; MUID:87061007
A;Accession: B26340
A;Molecule type: DNA
A;Residues: 1-116 <KOD>
A;Cross-references: GB:X05711; NID:g33602; PIDN:CAA29183.1; PID:g296660
A;Note: the authors translated the codon GAG for residue 25 as Gln
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-116/Product: Ig heavy chain V region 71-4 #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IMM>

alignment_scores:
    Quality:  514.00          Length:  118
    Ratio:    4.673           Gaps:    2
Percent Similarity: 93.220    Percent Identity: 86.441

alignment_block:
US-09-019-441-2 x B26340

Align seg 1/1  to: B26340  from: 1  to: 116

  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCAGATGGGT  50
    ||||||||::|||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

 51 CCTGTCCCAGCTGCAGCTGGACCTGCGGCTCGGCCCAGGAGTGGTGAAGCCTT 100
    ||||||::|||||||||||||||||::||||||||
 17 lLeuSerGlnValGlnLeuGlnLeuGluSerGlyProGlyLeuValLysProS  34
```

```
101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTGGTGGCTCTGTCGTCTGTCAGCAGT 150
    |||||||||||||||||||||||||||||||||||||||||||||||
 34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerVal...Ser  49

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGAAGGGACTGGAGTG 200
    |||   :::|||||||||||||||||||||||||||||||
 50 SerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTr  66

201 GATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACAACCGTCCC 250
    |||||||   |||    ||:::||||||||||||||||||||
 66 pIleGlyTyrTyrIleTyrTyrSer...GlySerThrAsnTyrAsnProSerL  82

251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    ||||||     |||||     |||||||||||||||||||
 82 euLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer  98

301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
    |||::||:||||||||||||||||||||||||||||
 99 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAl  115

351 CAGA 354
    ||||
115 aArg 116

seq_name: pir2:E34964

seq_documentation_block:
Ig heavy chain precursor V-IV region (Ab26) - human
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 23-Nov-1991 #text_change 16-Aug-1996
C;Accession: E34964
R;Sanz, I.; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
J. Immunol. 142, 4054-4061, 1989
A;Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals
A;Reference number: A92830; MUID:89235232
A;Accession: E34964
A;Molecule type: mRNA
A;Residues: 1-117 <SAN>
A;Cross-references: GB:M26997
A;Note: the authors translated the codon GCT for residue 42 as Thr
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
    Quality:  511.50          Length:  117
    Ratio:    4.693           Gaps:    1
Percent Similarity: 93.162    Percent Identity: 84.615

alignment_block:
US-09-019-441-2 x E34964

Align seg 1/1  to: E34964  from: 1  to: 117

  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCAGATGGGT  50
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  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGGCCCAGGAGTGGTGAAGCCTT 100
    ||||||::|||||||::|||::|||||||||||||||||
 17 lLeuSerGlnValGlnLeuGlnLeuGluSerGlyProGlyLeuValLysProS  34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTGGTGGCTCTGTCAGCAGT 150
    ||||||||||||||||||||||||||::::|||||||||||
 34 erGlnThrLeuSerLeuThrCysAlaValSerGlyGlySerIleSerSer  50

151 AGTAACTGGTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
    ::::|||||||||||||||||||||||||||||||||
 51 GlyAspTyrTyrTrpSerTrpIleArgGlnHisProGlyLysGlyLeuGluTr  67

201 GATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACAACCCGTCCC 250
    ||||||   |||     |||       |||||||||||||
```

```
 67 pIleGlyTyrTyrIleTyrTyrSer...GlySerThrTyrTyrAsnProSerL 83

251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    ||||||||||||| ||||| ||||||| |::||||||||||||
 83 euLysSerArgValAlaIleSerValAspThrSerAsnGlnPheSer 99

301 CTGAACCTGAACTCTGTGACCCGCCGGACGGCCGTGTATTACTGTGC 350
    |||||||||||||||||||||||||||||||||||||||||
100 LeuAsnLeuAsnSerValThrArgAlaAlaAspThrAlaValTyrTyrCysAl 116

351 C 351
    |
116 a 116
```

```
201 GATTGGACGTATCTCTGGTGTAGTGGTGGGGCCACCAACACACCCGTCCC 250
    ||||||  ||     ||   ||::::|||   |||||||||||||||
 67 pIleGlySerIleTyrHisSer...GlySerThrTyrTyrAsnProSerL 83

251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    ||||||||||||| ||||| |||||||||||||||||||||||||
 83 euLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 99

301 CTGAACCTGTCTGACCCGCCGGACACGGCCGTGTATTACTGTGC 350
    |||::::|||:::|||||||||||||||||||||||||
100 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 116

351 CAGAGATTGGGCCCAAATAGCTGGAACAACCGTAGGCTTCTGGGGCCAGG 400
    ||||       :::          :::::::|||:::||||::||
116 aArgValArgArgTyrSerSerAlaSerLysIleIlePheGlySerG 133

401 GAGTCCTGGTCACCGTC 417
    ||::::  ::::::::::
133 lyThrLeuSerIle 138
```

seq_name: pir2:A24770

seq_documentation_block:
hypothetical hybrid Ig/T-cell receptor precursor V region (SUP-T1) - human
N;Contains: Ig heavy chain precursor V-II region; T-cell receptor alpha chain J segment
C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 23-Jul-1999
C;Accession: A90873; A93378; A24770; B23373
R;Baer, R.; Chen, K.C.; Smith, S.D.; Rabbitts, T.H.
Cell 43, 705-713, 1985
A;Title: Fusion of an immunoglobulin variable gene and a T cell receptor constant gene i
A;Reference number: A90873; MUID:86079553
A;Accession: A90873
A;Molecule type: DNA
A;Residues: 1-140 <BAE>
A;Cross-references: GB:M12071; NID:g185508; PIDN:AAA52986.1; PID:g553409
A;Note: the sequence was determined from the differentiated gene
R;Denny, C.T.; Yoshikai, Y.; Mak, T.W.; Smith, S.D.; Hollis, G.F.; Kirsch, I.R.
Nature 320, 549-551, 1986
A;Title: A chromosome 14 inversion in a T-cell lymphoma is caused by site-specific recom
A;Reference number: A93378; MUID:86175073
A;Accession: A93378
A;Molecule type: DNA
A;Residues: 17-139 <DEN>
A;Note: the sequence was determined from the differentiated gene
C;Comment: This rearranged gene was isolated from a T-cell line harboring a chromosome 1
C;Genetics:
A;Map position: 14q11-q32
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; T-cell receptor
F;34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
             Quality:   510.50           Length:      139
               Ratio:     4.184             Gaps:        1
Percent Similarity:    87.770    Percent Identity:   72.662

alignment_block:
US-09-019-441-2 x A24770

Align seg 1/1  to: A24770  from: 1  to: 140

```
  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCCTCCCAGATGGGT 50
    ||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa 17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    |||||||||::::|||||||||||||||||::::|||||||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34

101 CGGAGACCCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    |||||||||||||||||||||||||||||  |||:::||||||
 34 erGluThrLeuSerLeuThrCysThrValSerGlyTyrSerIleSerSer 50

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
    ::: ::|||  |||||||||||||||||||||||||||||||||
 51 GlyTyrTyrTrpGlyTrpIleArgGlnProProGlyLysGlyLeuGluTr 67
```

OM of: US-09-019-441-2 to: SwissProt_40:*     out_format : pfs

Date: Sep 23, 2002 10:24 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2.1/USPTO_spool/US09019441/runat_23092002_095259_6394/app_query.fasta_1.1860
-DB=SwissProt_40 -QFMT=fastan -SUFFIX=rsp -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=-1 -MATRIX=blosum62
-TRANS=human40.cd1 -LIST=-45 -DOCALIGN=-200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09019441_@CGN_1_91 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-019-441-2
Query length: 423
Database: SwissProt_40:*
Database sequences: 105224
Database length: 38719550
Search time (sec): 62.410000

| Sequence | Strd | Orig | ZScore | EScore | Len | ! | Documentation |
|---|---|---|---|---|---|---|---|
| SwissProt_40:HV50_MOUSE | + | 268.00 | 425.68 | 4.3e-16 | 120 | ! | P06329 mus musculus (mous |
| SwissProt_40:HV3K_HUMAN | + | 268.00 | 425.27 | 4.3e-16 | 126 | ! | P01772 homo sapiens (huma |
| SwissProt_40:HV16_MOUSE | + | 268.00 | 424.63 | 4.3e-16 | 136 | ! | P01783 mus musculus (mous |
| SwissProt_40:HV18_MOUSE | + | 267.50 | 424.69 | 4.8e-16 | 123 | ! | P01787 mus musculus (mous |
| SwissProt_40:HV04_MOUSE | + | 266.50 | 423.53 | 5.8e-16 | 117 | ! | P01748 mus musculus (mous |

seq_name: SwissProt_40:HV2I_HUMAN

seq_documentation_block:
ID   HV2I_HUMAN     STANDARD;     PRT;     146 AA.
AC   P06331;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-II region ARH-77 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85205332; PubMed=3922855;
RA   Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT   "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT   repeat sequence in 5' flanking region.";
RL   Gene 33:181-189(1985).
DR   PIR; A02101; GIHUH2.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    146     IG HEAVY CHAIN V-II REGION ARH-77.
FT   DOMAIN        1    117     V SEGMENT.
FT   DOMAIN      118    127     D SEGMENT.
FT   DOMAIN      128    146     J SEGMENT.
FT   DISULFID     42    115     BY SIMILARITY.
FT   NON_TER     146    146
SQ   SEQUENCE   146 AA;  16228 MW;  8D7FD52BB218171F CRC64;

alignment_scores:
          Quality:   444.50              Length:    151
          Ratio:       3.735             Gaps:        7
Percent Similarity:   78.808     Percent Identity:   66.887

alignment_block:
US-09-019-441-2 x HV2I_HUMAN

Align seg 1/1 to: HV2I_HUMAN   from: 1   to: 146

```
  1 ATGAAACACCTGGTTCTTCCTCCTCGGTGGCAGCTCCCAGATGG..  48
    ||||||||||||||||||::||||||  |||  ||||||||||||
  1 MetLysHisLeuTrpPheLeuLeuLeu.TrpCysGlnLeuProAspValG 17

 49 ..GTCCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAG 96
    |||||::::||:||||||||||::: |||  |||||||||||::|||||
 17 lyValLeuSerGlnValGlnLeuGlnGlnTrpGlyAlaGlyLeuValLys 33

 97 CCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTGCTGGTGGCTCTGCAG 146
    |||||||||||||||||||||||||||:|||||||  |||||||
 34 ProSerGluThrLeuSerLeuThrCysAlaValPheGlyGlySerPhe. 49

147 CAGTAGTAACTGGTGGACCTGATCCGCCAGCCCCCAGGGAAGGGACTGG 196
    ||:: :::||:||||||||||:::||||||||||::.:::|||||||
 50 .SerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyArgGlyLeuG 66

197 AGTGGATTGGACGTATCTCTGTAGTGGTGGGCACCAACTACAACCCG 246
    ||||||||||||:: ||| |||||::::|||||:::.
 66 luTrpIleGlyGluIleAsnHisSer...GlySerThrAsnTyrLysThr 81
```

score_list:

| Sequence | Strd | Orig | ZScore | EScore | Len | ! | Documentation |
|---|---|---|---|---|---|---|---|
| SwissProt_40:HV2I_HUMAN | + | 444.50 | 702.54 | 1.3e-31 | 146 | ! | P06331 homo sapiens (human) |
| SwissProt_40:HV2F_HUMAN | + | 381.50 | 604.17 | 4.6e-26 | 129 | ! | P01824 homo sapiens (human) |
| SwissProt_40:HV46_MOUSE | + | 378.00 | 598.14 | 9.3e-26 | 137 | ! | P01822 mus musculus (mouse) |
| SwissProt_40:HV2G_HUMAN | + | 368.50 | 584.48 | 6.3e-25 | 117 | ! | P01825 homo sapiens (human) |
| SwissProt_40:HV60_MOUSE | + | 367.00 | 582.18 | 8.5e-25 | 116 | ! | P18531 mus musculus (mouse) |
| SwissProt_40:HV02_XENLA | + | 354.50 | 561.19 | 1.1e-23 | 135 | ! | P20957 xenopus laevis (afric |
| SwissProt_40:HV47_MOUSE | + | 352.50 | 559.52 | 1.6e-23 | 113 | ! | P01823 mus musculus (mouse) |
| SwissProt_40:HV61_MOUSE | + | 345.00 | 547.47 | 7.3e-23 | 116 | ! | P18532 mus musculus (mouse) |
| SwissProt_40:HV43_MOUSE | + | 344.50 | 544.87 | 8.2e-23 | 144 | ! | P01819 mus musculus (mouse) |
| SwissProt_40:HV62_MOUSE | + | 336.50 | 533.98 | 4.1e-22 | 117 | ! | P18533 mus musculus (mouse) |
| SwissProt_40:HV44_MOUSE | + | 311.00 | 493.89 | 7.3e-20 | 115 | ! | P01820 mus musculus (mouse) |
| SwissProt_40:HV45_MOUSE | + | 305.00 | 484.35 | 2.4e-19 | 116 | ! | P01821 mus musculus (mouse) |
| SwissProt_40:HV2H_HUMAN | + | 305.00 | 482.37 | 2.4e-19 | 147 | ! | P04438 homo sapiens (human) |
| SwissProt_40:HV40_MOUSE | + | 303.00 | 480.98 | 3.6e-19 | 119 | ! | P01810 mus musculus (mouse) |
| SwissProt_40:HV37_MOUSE | + | 298.00 | 473.09 | 9.9e-19 | 119 | ! | P01807 mus musculus (mouse) |
| SwissProt_40:HV01_XENLA | + | 298.00 | 471.97 | 1.0e-18 | 136 | ! | P20956 xenopus laevis (afric |
| SwissProt_40:HV3B_HUMAN | + | 295.00 | 468.72 | 1.8e-18 | 114 | ! | P01763 homo sapiens (human) |
| SwissProt_40:HV3C_HUMAN | + | 293.50 | 466.13 | 2.5e-18 | 117 | ! | P01764 homo sapiens (human) |
| SwissProt_40:HV05_CARAU | + | 293.00 | 465.41 | 2.7e-18 | 116 | ! | P19181 carassius auratus (go |
| SwissProt_40:HV38_MOUSE | + | 293.00 | 465.20 | 2.7e-18 | 119 | ! | P01808 mus musculus (mouse) |
| SwissProt_40:HV3G_HUMAN | + | 293.00 | 464.99 | 2.7e-18 | 122 | ! | P01768 homo sapiens (human) |
| SwissProt_40:HV41_MOUSE | + | 292.50 | 464.55 | 3.0e-18 | 117 | ! | P01811 mus musculus (mouse) |
| SwissProt_40:HV01_RAT | + | 288.50 | 456.62 | 6.9e-18 | 142 | ! | P01805 rattus norvegicus (rat) |
| SwissProt_40:HV2B_HUMAN | + | 287.00 | 455.66 | 9.2e-18 | 120 | ! | P01815 homo sapiens (human) |
| SwissProt_40:HV3J_HUMAN | + | 286.50 | 454.80 | 1.0e-17 | 121 | ! | P01771 homo sapiens (human) |
| SwissProt_40:HV2C_HUMAN | + | 285.50 | 453.37 | 1.2e-17 | 119 | ! | P01816 homo sapiens (human) |
| SwissProt_40:HV07_MOUSE | + | 285.00 | 451.28 | 1.4e-17 | 139 | ! | P01751 mus musculus (mouse) |
| SwissProt_40:HV3T_HUMAN | + | 283.00 | 449.64 | 2.1e-17 | 116 | ! | P01781 homo sapiens (human) |
| SwissProt_40:HV03_CAICR | + | 282.50 | 448.77 | 2.3e-17 | 117 | ! | P03982 caiman crocodilus (sp |
| SwissProt_40:HV3I_HUMAN | + | 279.50 | 443.90 | 4.2e-17 | 119 | ! | P01770 homo sapiens (human) |
| SwissProt_40:HV3H_HUMAN | + | 279.00 | 442.90 | 4.6e-17 | 122 | ! | P01769 homo sapiens (human) |
| SwissProt_40:HV3D_HUMAN | + | 277.50 | 441.03 | 6.3e-17 | 115 | ! | P01765 homo sapiens (human) |
| SwissProt_40:HV48_MOUSE | + | 277.50 | 439.50 | 6.3e-17 | 138 | ! | P03980 mus musculus (mouse) |
| SwissProt_40:HV3A_HUMAN | + | 277.00 | 439.75 | 7.0e-17 | 122 | ! | P01762 homo sapiens (human) |
| SwissProt_40:HV42_MOUSE | + | 275.50 | 437.73 | 9.4e-17 | 117 | ! | P01812 mus musculus (mouse) |
| SwissProt_40:HV39_MOUSE | + | 275.50 | 437.66 | 9.4e-17 | 118 | ! | P01809 mus musculus (mouse) |
| SwissProt_40:HV36_MOUSE | + | 274.50 | 436.22 | 1.2e-16 | 116 | ! | P01806 mus musculus (mouse) |
| SwissProt_40:HV2D_HUMAN | + | 274.50 | 435.60 | 1.2e-16 | 125 | ! | P01817 homo sapiens (human) |
| SwissProt_40:HV20_MOUSE | + | 270.00 | 428.70 | 2.9e-16 | 122 | ! | P01789 mus musculus (mouse) |
| SwissProt_40:HV22_MOUSE | + | 269.50 | 427.84 | 3.2e-16 | 123 | ! | P01791 mus musculus (mouse) |

```
247 TCCCTCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTT 296
    ||||||||||||||||||  |||||  |||||||||||||||||| ||
 82 SerLeuLysSerArgValThrIleSerLeuAspThrSerLysAsnLeuPh 98

297 CTCCCTGAACCTGAACCTGTGACCGCCCGGCGACACGGCCGTGTATTACT 346
    |||||||:::|||:::|||||||||||||||||||||||||||||||||
 98 eSerLeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrC 115

347 GTGCCAGA..........GATTGGGCCCAAATA........GCT 372
    ||||||||          |||      :::::
115 ysAlaArgGlyLeuLeuArgGlyGlyTrpAsnAspValAspTyrTyrTyr 131

373 GGAACAACGTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTC 422
    |||     ::  ||||||||||||||::::|||||||||||||||||||
132 Gly.....MetAspValTrpGlyGlnGlyThrLeuValThrValSerSe 146

423 A 423
    |
146 r 146
```

seq_name: SwissProt_40:HV2F_HUMAN

seq_documentation_block:
ID   HV2F_HUMAN   STANDARD;   PRT;   129 AA.
AC   P01824;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-II region WAH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82222235; PubMed=6806818;
RA   Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT   "Complete amino acid sequence of the delta heavy chain of human
RT   immunoglobulin D.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
CC       PROTEIN.
DR   PIR; A02099; D2HUWA.
DR   HSSP; P01825; 7FAB.
DR   GlycoSuiteDB; P01824; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   NON_TER   129   129
SQ   SEQUENCE   129 AA;   14117 MW;   D5D53D47ABE51319 CRC64;

alignment_scores:
         Quality:   381.50            Length:   130
         Ratio:     3.854             Gaps:     3
Percent Similarity: 76.154      Percent Identity: 60.769

alignment_block:
US-09-019-441-2 x HV2F_HUMAN

Align seg 1/1  to: HV2F_HUMAN   from: 1  to: 129

 58 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGAC 107
    ::||||||||||||||||||||||||:::||||||||||||||||||||||
  1 ArgLeuGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluTh 17

108 CCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGCAGCAGTAGTAAC. 156
    |||||||||  ||||||||||||||||  ::|||:::
 17 rLeuSerLeuThrCysIleValSerGlyGlyProIleArgArgThrGlyT 34

157 ..TGGTGGACCTGAGCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTGGATT 204
```

```
    :::|||  ||||||||||||||||||||||||||||
 34 yrTyrTrpGlyTrpIleArgGlnProProGlyLysGlyLeuGluTrpIle 50

205 GGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCGTCCCTCAA 254
    |||  ::   :::||  |||:::  ||||||||||||||||||||||
 51 GlyGlyValTyrTyrThr...GlySerIleTyrTyrAsnProSerLeuAr 66

255 GAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCCCTGA 304
    :::|||||| ||||||||||||||||||||||||||||||||||||
 66 gGlyArgValThrIleSerValAspThrSerArgAsnGlnPheSerLeuA 83

305 ACCTGAACTCTGTGACCGCCGGCGACACGGCCGTGTATTACTGTGCCAGA 354
    ||||:::||:::||  |||||||||||||||||||:::||||||||||||
 83 snLeuArgSerMetSerAlaAlaAspThrAlaMetTyrTyrCysAlaArg 99

355 ...............GATTGGGCCCAAATAGCTGGAACAACGCT 383
                   ||  :::          :::
100 GlyAsnProProTyrTyrTyrAspIleGlyThrThrGlySerAspAspGlyIl 116

384 AGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 423
    :::  |||||||||||||||||||||||||||||||||
116 eAspValTrpGlyGlnGlyThrThrValHisValSerSer 129
```

seq_name: SwissProt_40:HV46_MOUSE

seq_documentation_block:
ID   HV46_MOUSE   STANDARD;   PRT;   137 AA.
AC   P01822;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig heavy chain V region MOPC 315 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89238351; PubMed=2497341;
RA   Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT   "Cloning, sequencing and expression of the rearranged MOPC 315 VH
RT   gene segment.";
RL   Mol. Immunol. 26:431-434(1989).
RN   [2]
RP   SEQUENCE OF 1-31.
RX   MEDLINE=78094475; PubMed=414225;
RA   Jilka R.L., Pestka S.;
RT   "Amino acid sequence of the precursor region of MOPC-315 mouse
RT   immunoglobulin heavy chain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
RN   [3]
RP   SEQUENCE OF 1-21.
RX   MEDLINE=79148758; PubMed=428562;
RA   Schechter I., Wolf O., Zemell R., Burstein Y.;
RT   "Structure and function of immunoglobulin genes and precursors.";
RL   Fed. Proc. 38:1839-1845(1979).
RN   [4]
RP   SEQUENCE OF 19-136.
RX   MEDLINE=74170779; PubMed=4524622;
RA   Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
RT   "Amino-acid sequence of the variable region of the heavy (alpha)
RT   chain of a mouse myeloma protein with anti-hapten activity.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
RN   [5]
RP   REVISION TO 53.
RX   MEDLINE=77244979; PubMed=268248;
RA   Hood L., Margolies M.N., Givol D., Zakut R.;
RL   Unpublished results, cited by:
RA   Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
RL   Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
CC   -!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC       PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.

```
DR   EMBL; M27638; AAA61337.1; -.
DR   EMBL; X07880; CAA30727.1; -.
DR   PIR; PL0102; AVMS35.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     18
FT   CHAIN        19    137       IG HEAVY CHAIN V REGION MOPC 315.
FT   DOMAIN       19     48       FRAMEWORK-1.
FT   DOMAIN       49     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     84       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       85    116       FRAMEWORK-3.
FT   DOMAIN      117    126       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      127    137       FRAMEWORK-4.
FT   DISULFID     40    114       BY SIMILARITY.
FT   CONFLICT     15     15       G -> GG (IN REF. 1; CAA30727).
FT   CONFLICT     15     15       G -> H (IN REF. 2).
FT   CONFLICT     77     78       GY -> YG (IN REF. 4).
FT   CONFLICT    102    102       N -> D (IN REF. 4).
FT   CONFLICT    123    123       MISSING (IN REF. 4).
FT   NON_TER     137    137
SQ   SEQUENCE   137 AA;  15399 MW;  FB3828304C2B81DC CRC64;
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alignment_scores:
　　　　　Quality:　378.00　　　　　Length:　141
　　　　　Ratio:　3.287　　　　　Gaps:　3
Percent Similarity:　81.560　　　Percent Identity: 56.028

alignment_block:
US-09-019-441-2 x HV46_MOUSE　　..

Align seq 1/1 to: HV46_MOUSE   from: 1  to: 137

```
  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT 50
    ||||| |||    :::|| ||||||||::::::||  ||| || ||
  1 MetLysValLeuSerLeuLeuTyrLeuLeuThrAlaIlePro...GlyIl 16

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    :::|||::::||||||||||||||||:::||||||||||::|||||||
 16 eMetSerAspValGlnLeuGlnLeuGlnGluSerGlyProGlyLeuValLysProS 33

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    ||:::||||||||||||||||:::||| || :||||:::||
 33 erGlnSerLeuSerLeuThrCysSerValThrGlyTyrSerIleThrSer 49

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
    ::  :::|||:|||||||||||||||| |||||||::  ||||||||
 50 GlyTyrPheTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTr 66

201 GATTGGACACTATCTCTGGTAGTGGTGGGCACCAACTACAACCCGTCC 250
    ||:::||  :||:::|| ||::||||||||||||||||||
 66 pLeuGlyPheIleLys...TyrAspGlySerAsnGlyTyrAsnProSerL 82

251 TCAAGAGTCGAGTCATCATTTCACAAGACACAGTCCAAGAACCAGTTCTCC 300
    ||||::||||| |||:::||||||||| ::|||||||||
 82 euLysAsnArgValSerIleThrArgAspThrSerGluAsnGlnPhePhe 98

301 CTGAACCTGAACTCTGTGACCGCCGCGACCGCACGGCCGTGTATTACTGTGC 350
    |||::||||||||||| :::::||||| |||||||||||
 99 LeuLysLeuAsnSerValThrThrGluAspThrAlaThrTyrTyrCysAl 115
```

```
alignment_block:
US-09-441-2 x HV2G_HUMAN

Align seg 1/1  to: HV2G_HUMAN  from: 1  to: 117

 58 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGAC 107
    |||::::|||||::::|||||||||||||||::::||||||::::||
  1 GlnValGlnLeuGluGlnSerGlyProGlyLeuValArgProSerGlnTh  17

108 CCTGTCCCTCACCTGCGCTCTCTGGTGGCTCTGTCAGCAGTAGTAACT 157
    ||||||||||||::::|||||   |||||||::  |||::::::::
 17 rLeuSerLeuThrCysPheSerValSer...GlySerThrPheSerAsnAspT  33

158 GGTGGACCTGGATCCGCCAGCCCCAGGGAAGGAGGACTGGAGTGGATTGGA 207
    :::::||||||::::|||||||||||||||||||||||||  |||
 33 yrTyrThrTrpValArgGlnProProGlyArgGlyLeuGluTrpIleGly  49

208 CGTATCTCTGGTAGTGGGGGCACCACAACCCGTCCCTCAAGAG 257
    ::   |||    ::  ::|||   |||::||
 50 TyrValPheTyrHisGlyThrSerAspAspThrPro...LeuArgSe  65

258 TCGAGTCATCATTTCACAAGAACACGTCCAAGAACCAGTTCTCCCTGAACC 307
    ||||||   :::  ||||||||||||||||||::::|||
 65 rArgValThrMetLeuValAspThrSerLysAsnGlnPheSerLeuArgL  82

308 TGAACTCTGTGACCGCCGGACACGCCGTGTATTACTGTGCCAGAGAT 357
    ||:::||||||||::::||||||||||||||||||  |||||||
 82 euSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgAsn  98

358 TGGGCCAAATAGCTGGAACAACGCTAGGCTTCTGGGCCCAGGAGTCCT 407
    ||||||||||   :::     |||||||||||||
 99 ......LeuIleAlaGly...CysIleAspSerValTrpGlyGlnGlySerLe 112

408 GGTCACCGTCTCCTCA 423
    ||||||||||||||||
112 uValThrValSerSer 117

seq_name: SwissProt_40:HV60_MOUSE

seq_documentation_block:
ID   HV60_MOUSE    STANDARD;    PRT;    116 AA.
AC   P18531;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region M315 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/CJ;
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during
RT   the primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
DR   PIR; JT0509; HVMS31.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     18
FT   CHAIN        19    116       IG HEAVY CHAIN V REGION M315.
FT   DOMAIN       19     48       FRAMEWORK-1.
FT   DOMAIN       49     53       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       54     67       FRAMEWORK-2.
FT   DOMAIN       68     84       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       85    116       FRAMEWORK-3.
FT   DISULFID     40    114       BY SIMILARITY.
FT   NON_TER     116    116
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SQ  SEQUENCE  116 AA;  13095 MW;  4562E03E53DC9E10 CRC64;

alignment_scores:
         Quality:  367.00          Length:  118
           Ratio:    3.634            Gaps:    2
Percent Similarity: 85.593    Percent Identity: 62.712

alignment_block:
US-09-019-441-2 x HV60_MOUSE  ..

Align seg 1/1  to: HV60_MOUSE  from: 1  to: 116

  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT  50
    | ||||| ||||||||::::|||||||||||||  |||  |||
  1 MetLysValLeuSerLeuLeuTyrLeuLeuLeuThrAlaIlePro...GlyIl  16

 51 CCTGTCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    :||||:::::||||||||||||||||||||||::::|||||||||
 16 eLeuSerAspValGlnLeuGlnLeuGluSerGlyProGlyLeuValLysPros  33

101 CGGAGACCCTGTCCTCACCTGCGCTCTCTGGTGGCTCTGTCAGCAGT 150
    ||:::::||||||||:::|||::::|||  ||:::::|||
 33 erGlnSerLeuSerLeuThrCysSerValThrGlyTyrSerIleThrSer  49

151 AGTAACTGGTGACCTGGATCCGCCAGCCCCAGGAAGGAGGACTGAGTG 200
    :::  ::|||||||||||||||||||||  ||||||::::  |||||||
 50 GlyTyrTyrTrpAsnTrpIleArgGlnHisProGlyAsnLysLeuGluTr  66

201 GATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACACCCGTCCC 250
    :::||||   :::||||||||||||||:::||||||||||||||||
 66 pMetGlyTyrIleSer...TyrAspGlySerAsnAsnTyrAsnProSerL  82

251 TCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    ||||:::::::::  |||::::|||||||||||||||||||||||||||
 82 euLysAsnArgIleSerIleThrArgAspThrSerLysAsnGlnPhePhe  98

301 CTGAACCTGAACTCTGTGACCGCCGGACACGGCCGTGTATTACTGTGC 350
    |||:::::|||||::::::||||||||||||||||::::||||||||||
 99 LeuLysLeuAsnSerValThrThrGluAspThrAlaThrTyrTyrCysAl 115

351 CAGA 354
    ||||
115 aArg 116
```

```
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; J03632; AAA49791.1; -.
DR   PIR; B31933; B31933.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   NON_TER        1      1
FT   SIGNAL        <1     18
FT   CHAIN         19    135       IG HEAVY CHAIN V REGION XIG14.
FT   NON_TER      135    135
SQ   SEQUENCE    135 AA;   15080 MW;   EBC467105C00732E CRC64;

alignment_scores:
          Quality:   354.50               Length:     136
          Ratio:       3.252              Gaps:         4
Percent Similarity:    80.147    Percent Identity:    54.412

alignment_block:
US-09-019-441-2 x HV02_XENLA       .

Align seg 1/1  to: HV02_XENLA  from: 1  to: 135

   16 TTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTTCCCAGCTGCA  65
      ||||||||||||||||         :::||        :::|||||||||
    5 PhePheIlePheMetPhePheSerProSerCysIleLeuSerGln...Th  20

   66 GCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCC  115
      ||||||||||||||||||||:::||||||||||||||||:::|||
   20 rLeuGlnGluSerGlyProGlyThrValLysProSerGluSerLeuArgL  37

  116 TCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACC  165
      |||||||||:::||||||   :::|||||     :::
   37 euThrCysThrValSerGlyPheGluLeuSerSerTyrHis...MetHis  52

  166 TGGATCCGCCAGCCCCCAGGAAGGACTGGAGTGGATTGGACGTATCTC  215
      ||||||||:::|||::::|||||||||||||||||    |||::
   53 TrpIleArgGlnProProGlyLysGlyLeuGluTrpIleGlyValIleAl  69

  216 TGGTAGTGGTGGGGGCCACCAACCTCCCTCAAGAGTCGAGTCA  265
      :  :::||||||||  ||||||||||||||||:||||
   69 a...ThrGlyGlySerThrAlaIleAlaAspSerLeuLysAsnArgValT  85

  266 TCATTTCACAAGACACGTCCAAGAACCAGTTCTCCCTGAACCTGAACTCT  315
      ||||:::|||:::|||:||::|     |||::||:::|||::
   85 hrIleThrLysAspAsnGlyLysLysGlnValTyrLeuGlnMetAsnGly  101

  316 GTGACCGCCGCGACGGCCGTGTATTACTGTGCCAGAGATTGGGCCCA  365
      :::  |||||||||||:::||||||||||||||||||||||||
  102 MetGluValLysAspThrAlaMetTyrTyrCysAlaArgGluTyrAla..  117

  366 AATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCG  415
      :::|||    :::|||||:::||||||||||||||::||||||
  118 ....SerGlyTyrAsnPheAspTyrTrpGlyGlnGlyThrMetValThrV  133

  416 TCTCCTCA  423
      ||:::|||
  133 alThrSer  135
```

seq_name: SwissProt_40:HV47_MOUSE

```
seq_documentation_block:
ID   HV47_MOUSE     STANDARD;        PRT;    113 AA.
AC   P01823;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 36-60.
OS   Mus musculus (Mouse).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=84024551; PubMed=6414509;
RA   Juszczak E.C., Margolies M.N.;
RT   "Amino acid sequence of the heavy chain variable region from the A/J
RT   mouse anti-arsonate monoclonal antibody 36-60 bearing a minor
RT   idiotype.";
RL   Biochemistry 22:4291-4296(1983).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE
CC       MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND
CC       IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF
CC       STRAIN A/J MICE.
DR   PIR; A02098; G2MS60.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Antiarsonate antibody.
FT   NON_TER      113    113
SQ   SEQUENCE    113 AA;   12734 MW;   38DC0E0E3F5075B7 CRC64;

alignment_scores:
          Quality:   352.50               Length:     124
          Ratio:       3.525              Gaps:         4
Percent Similarity:    80.645    Percent Identity:    59.677

alignment_block:
US-09-019-441-2 x HV47_MOUSE       .

Align seg 1/1  to: HV47_MOUSE  from: 1  to: 113

   58 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGAC  107
      ||||||||||||||||||||||||||||||||:::||||||||::|||
    1 GluValGlnLeuGlnGluSerGlyProSerLeuValLysProSerGlnTh  17

  108 CCTGTCCCTCACCTGCGCTGTCTGCTGGTGGCTCTGCTGTCAGCAGTAGTAACT  157
      ||||||||||||||||||:::||    :::||    :::|||:::|
   17 rLeuSerLeuThrCysSerValThrGlyAspSerIle...ThrSerAspT  33

  158 GGTGGACCTGGATCCGGCAGCCCCCAGGGACTGGAGGGACTGGAGTGGATTGGA  207
      :::||:::||||||||    :::|||::    ||||||    :::||
   33 yrTrpAsnTrpIleArgGlnProGlyAsnLysLeuGluHisMetGly  49

  208 CGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCGTCCTCAAGAG  257
      |||||||    ||||:::||:::|    ||||||||||:::||||
   50 TyrIleSerTyrSer...GlySerThrTyrTyrAsnProSerLeuLysSe  65

  258 TCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCCCTGAACC  307
      ||||  :::|||::|||||||||||||||||||||||:::||::|
   65 rArgIleSerIleThrArgAspThrSerLysAsnGlnTyrTyrLeuGlnL  82

  308 TGAACTCTGTGACCGCCGGACACGGCCGTGTATTACTGTGCCAGAGAT  357
      ||:::|||||||:::  |||||||||||||||||:::||||||||
   82 euAsnSerValThrSerGluAspThrAlaThrTyrTyrCys.........  95

  358 TGGGGCCCAAATAGCTGAACAACACGGCTAGGCTTC......TGGGGCCAGGG  401
      ||:::|||::|||    :::|||||||    .....||||||||
   96 ........................ThrSerLeuArgPheAlaTyrTrpGlyGlnGl  106

  402 AGTCCTGGTCACCGTCTCCTCA  423
      |:::||||||||||||||||||
  106 yThrLeuValThrValSerAla  113
```

seq_name: SwissProt_40:HV61_MOUSE

```
seq_documentation_block:
ID   HV61_MOUSE     STANDARD;        PRT;    116 AA.
AC   P18532;
```

```
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 1B43 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/CJ;
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during
RT   the primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
CC   -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
DR   PIR; JT0508; HVMS1B.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     18
FT   CHAIN        19    116       IG HEAVY CHAIN V REGION 1B43.
FT   DOMAIN       19     48       FRAMEWORK-1.
FT   DOMAIN       49     53       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       54     67       FRAMEWORK-2.
FT   DOMAIN       68     84       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       85    116       FRAMEWORK-3.
FT   DISULFID     40    114       BY SIMILARITY.
FT   NON_TER     116    116
SQ   SEQUENCE    116 AA;  13158 MW;  1CB547253681FF74 CRC64;
```

alignment_scores:
```
         Quality:   345.00              Length:   118
           Ratio:    3.520                Gaps:     2
Percent Similarity:  83.051       Percent Identity:  61.017
```

alignment_block:
US-09-019-441-2 x HV61_MOUSE

Align seg 1/1  to: HV61_MOUSE  from: 1 to: 116

```
  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT 50
    ::|||  |||  ::::: |||:::||| ||:|||| |  |||||||| |||
  1 MetArgValLeuIleLeuLeuLeuCysLeuPheThrAlaPhePro...GlyIle 16

 51 CCTGTCCCAGCTGCAGAGCTGCGGCCCAGGAGTGTGAAGCCTT 100
    :||||||:::::||||||||||||||||||| ::|||||||||
 16 eLeuSerAspValGlnLeuGlnLeuGluSerGlyProAspLeuValLysPros 33

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTTCTGTCAGCAGT 150
    |::::|||||||||:::||||:::|||| |||:::||||
 33 erGlnSerLeuSerLeuThrCysThrValThrGlyTyrSerIleThrSer 49

151 AGTAACTGGTGGACCTGGATCCGGCCAGCCCCAGGGAAGGGACTGGAGTG 200
    :: |||||||||| ||| ||||||||||||||||||| ||||||
 50 GlyTyrSerTrpHisTrpIleArgGlnPheProGlyLysAsnLysLeuGluTr 66

201 GATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACCCGTCC 250
    !:::|||  ||| |||:::|  |||::|||:||||||||||||||
 66 pMetGlyTyrTyrIleHisTyrSerGlyAsn...ThrSerTyrAsnProSerL 82

251 TCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    ||||||||:: |:::||||||||||||||||||||
 82 euLysSerArgIleSerIleThrArgAspThrSerLysAsnGlnPhePhe 98

301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
    ||||||||||::: ||||||||||||||||||:::|||||||||||||||
 99 LeuGlnLeuAsnSerValThrThrGluAspThrAlaThrTyrTyrCysAl 115

351 CAGA 354
     ||||
115 aArg 116
```

seq_name: SwissProt_40:HV43_MOUSE

seq_documentation_block:
```
ID   HV43_MOUSE      STANDARD;      PRT;   144 AA.
AC   P01819;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region MOPC 141 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81012133; PubMed=6774258;
RA   Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT   "Two types of somatic recombination are necessary for the generation
RT   of complete immunoglobulin heavy-chain genes.";
RL   Nature 286:676-683(1980).
CC   -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC       DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
CC   --------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------
DR   EMBL; J00491; AAA38121.1; -.
DR   EMBL; V00768; CAA24149.1; -.
DR   PIR; A02094; G2MS14.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    144       IG HEAVY CHAIN V REGION MOPC 141.
FT   NON_TER     144    144
SQ   SEQUENCE    144 AA;  15759 MW;  8E47A7CB3706D30A CRC64;
```

alignment_scores:
```
         Quality:   344.50              Length:   146
           Ratio:    3.161                Gaps:     3
Percent Similarity:  74.658       Percent Identity:  50.685
```

alignment_block:
US-09-019-441-2 x HV43_MOUSE

Align seg 1/1  to: HV43_MOUSE  from: 1 to: 144

```
  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT 50
    ||| ||   :::||| ||::::|||||||||||||:::|| ||
  1 MetAlaValLeuAlaLeuLeuPheCysLeuAlaThrPheProSerCysIl 17

 51 CCTGTCCCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    :||||||||||||||||:::||||||||::|||::||| ||||
 17 eLeuSerGlnValGlnLeuGluSerGlyProGlyLeuValAlaProS 34

101 CGGAGACCCGTCCCTCACCTGCACTGTCTCTGGTGGCTCTGTCAGCAGT 150
    |::::|||||||:::||||:::||||||||||:::||||
 34 erGlnSerLeuSerIleThrCysThrValSerGlyPheSerLeuThrGly 50

151 AGTAACTGGTGGACCTGGATCCGCCCCAGCCCCAGGGAAGGGACTGGAGTG 200
    :: ||||||||||| ||| ||||||||||||||||||||||||||||||
```

```
  51 TyrGly...ValAsnTrpValArgGlnProProGlyLysGlyLeuGluTr 66
 201 GATTGGACGTATCTCGGTAGTGGTGGGCCACCAACTACAACCCGTCC 250
     |:::|| ||| ||::::  |||::||:::||||| :::|
  66 pLeuGlyThrIleTrpThrGlyAsn...GlySerThrAspThrAsnSerThrL 82
 251 TCAAGAGTCGAGTCATCATTCACAAGACAGTCCAAGAACCAGTTCTCC 300
     |||||||||||  :::||::|||||||||||||||::||:::
  82 euLysSerArgLeuThrIleThrIleThrLysAspAsnSerLysSerGlnValPhe 98
 301 CTGAACCTTGAACTCTGTGACCGCCGCGACCACGCCGTGTATTACTGTGC 350
     |||::||||| ::: |||||||| |||||||||||
  99 LeuLysMetAsnSerLeuGlnThrAspAspThrAlaArgTyrTyrCysAl 115
 351 CAGAGATTGGGCCCAAATAGCTGGAACA............ACGCTAG 385
     |              ||                       ||||||
 115 aSerValSerIleTyrTyrTyrGlyArgSerAspLysProPheThrLeuA 132
 386 GCTTCTGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 423
     ::|||||||||||||:::   |||||||||||||
 132 spTyrTrpGlyGlnGlyThrValSerSer 144

seq_name: SwissProt_40:HV62_MOUSE

seq_documentation_block:
ID   HV62_MOUSE       STANDARD;       PRT;    117 AA.
AC   P18533;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 733 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/CJ;
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during
RT   the primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
DR   PIR; JT0510; HVMS73.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     18
FT   CHAIN        19    117       IG HEAVY CHAIN V REGION 733.
FT   DISULFID     40    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13223 MW;  1595517827F976BE CRC64;

alignment_scores:
         Quality:  336.50                         Length:     119
         Ratio:    3.332                           Gaps:        3
Percent Similarity:  84.874      Percent Identity:   57.983

alignment_block:
US-09-019-441-2  x  HV62_MOUSE    ..

Align seg 1/1  to: HV62_MOUSE  from: 1  to: 117

   1 ATGAAACACCTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT 50
     ||||||    ::::    ||:    :::::::::||:  ||
   1 MetLysMetPheThrLeuLeuTyrLeuLeuTyrValValPro...GlyIl 16
  51 CCTTGCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
     :||||||:::::||||||||||||||||||||||||||||||:::||||||
  16 eLeuSerAspValGlnLeuGlnLeuGlnGluSerGlyProGlyLeuValLysProS 33
```

```
 101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGCTGGCTCTGTCAGCAGT 150
     ||:::||::::::||||||||:::|||:||| ||::::  :|||:::||||
  33 erGlnSerIleAlaLeuThrCysThrValThrGlyIleSerIleThrThr 49
 151 AGTAACTGG...TGGACCTGATCCGCCAGCCCCCAGGGAAGGGACTGGA 197
     ::::|||::  |||:::||||||||||||| |||| ||||
  50 GlyAsnTyrArgTrpSerTrpIleArgGlnProGlyLysGlyLeuGl 66
 198 GTGGATTGGACGTATCTCGGTAGTGGTGGGCCACCAACTACAACCCGT 247
     ||||||||||  ||| |||||  .:::|||||||||||||||||||
  66 uTrpIleGlyTyrIleTyrTyrSer...AlaIleThrSerTyrAsnPros 82
 248 CCCTCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTC 297
     |||  ||||||||||||||||||:::|||||||||||||||||||
  82 erProLysSerArgThrThrIleThrArgAspThrSerLysAsnGlnPhe 98
 298 TCCCTGAACCTGAACTCTGTGACCGCCGCGACACGGCCGTGTATTACTG 347
     ||:::|||||||::::|||||| |||||||||||||||
  99 PheLeuGluMetAsnSerLeuThrAlaGluAspThrAlaThrTyrTyrCy 115
 348 TGCCAGA 354
     |||||||
 115 sAlaArg 117

seq_name: SwissProt_40:HV44_MOUSE

seq_documentation_block:
ID   HV44_MOUSE       STANDARD;       PRT;    115 AA.
AC   P01820;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region PJ14 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81012133; PubMed=6774258;
RA   Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT   "Two types of somatic recombination are necessary for the generation
RT   of complete immunoglobulin heavy-chain genes.";
RL   Nature 286:676-683(1980).
CC   --------------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; V00767; CAA24148.1; -.
DR   PIR; A02095; HVMS14.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    115       IG HEAVY CHAIN V REGION PJ14.
FT   NON_TER     115    115
SQ   SEQUENCE   115 AA;  12447 MW;  7569DD4A4843D500 CRC64;

alignment_scores:
         Quality:  311.00                         Length:     117
         Ratio:    3.274                           Gaps:        2
Percent Similarity:  81.197      Percent Identity:   54.701

alignment_block:
```

US-09-019-441-2 x HV44_MOUSE

Align seg 1/1  to: HV44_MOUSE  from: 1  to: 115

```
   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT  50
     |||       |||  :::::::   ||||||||   |||           ::
   1 MetAlaValLeuAlaLeuLeuPheCysLeuValThrPheProSerCysIl  17

  51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGTGAAGCCTT  100
     ||||||||||::||||||||:||||||||||:::||||||||| ||||
  17 eLeuSerGlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProS  34

 101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT  150
     ||::||||||||||||||||||| |||||||||  :|::||||||||
  34 erGlnSerLeuSerIleThrCysThrValSerGlyPheSerLeuThrGly  50

 151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGAGGGACTGGAGTG  200
     ::::|||::|||||||||||||||||||||||||||||||||||
  51 TyrGly...ValAsnTrpValArgGlnProProGlyLysGlyLeuGluTr  66

 201 GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACACACCCGTCCC  250
     |::|||  |||  ||:::|||  ||||:||||||||||||||| :::|
  66 pLeuGlyMetIleTrpGlyAsp...GlySerThrAspTyrAsnSerAlaL  82

 251 TCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC  300
     ||||||||||||::  ||||||||||::|||||||||||||||||||
  82 euLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPhe  98

 301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC  350
     |||:::|||||||||  ::  ||||||||||||||||||  |||||||||
  99 LeuLysMetAsnSerLeuGlnThrAspAspThrAlaArgTyrTyrCysAl  115

 351 C 351
     |
 115 a 115
```

seq_name: SwissProt_40:HV45_MOUSE

```
seq_documentation_block:
ID   HV45_MOUSE     STANDARD;          PRT;   116 AA.
AC   P01821;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region MC101 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82075900; PubMed=6273429;
RA   Kataoka T., Nikaido T., Miyata T., Moriwaki K., Honjo T.;
RT   "The nucleotide sequences of rearranged and germline immunoglobulin
RT   VH genes of a mouse myeloma MC101 and evolution of VH genes in
RT   mouse.";
RL   J. Biol. Chem. 257:277-285(1982).
CC   -----------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------
DR   EMBL; J00502; AAA38515.1; -.
DR   PIR; A02096; G1MS10.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
```

alignment_scores:
```
              Quality:  305.00              Length: 118
                Ratio:    3.211               Gaps:    2
Percent Similarity:  80.508   Percent Identity: 52.542
```

alignment_block:
US-09-019-441-2 x HV45_MOUSE

Align seg 1/1  to: HV45_MOUSE  from: 1  to: 116

```
   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT  50
     |||       |||  :::::::   ||||||||   |||           ::
   1 MetAlaValLeuAlaLeuLeuPheCysLeuValThrPheProSerCysVa  17

  51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
     ||||||||||::||||||||:||||||||||:::||||||||:||||||||
  17 lLeuSerGlnValGlnLeuLysGluSerGlyProGlyLeuValGlnProS  34

 101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT  150
     ||::||||||||||||||||||| |||||||||  :::|||||||||
  34 erGlnSerLeuSerIleThrCysThrValSerGlyPheSerLeuThrSer  50

 151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCAGGAGAGGACTGGAGTG  200
     ::::|||::|||||||||||||||||||||  ||||||||||||||||
  51 TyrGly...ValHisTrpValArgGlnSerProGlyLysGlyLeuGluTr  66

 201 GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCCGTCCC  250
     |::|||  ::|  |||||||||  ||||:||||||||||||  :::|
  66 pLeuGly...ValIleTrpSerGlyGlySerThrAspTyrAsnAlaAlaP  82

 251 TCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC  300
     ||||||||||||||  ||||||||||||||  ::  ||||||||||||||
  82 heIleSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPhe  98

 301 CTGAACCTGAACTCTGACCGCCGCGGACACGGCCGTGTATTACTGTGC  350
     ::::|||||||||||  ||||||||||||||||||||||  |||||||||
  99 PheLysMetAsnSerLeuGlnSerAsnAspThrAlaIleTyrTyrCysAl  115

 351 CAGA 354
     ||||
 115 aArg 116
```

seq_name: SwissProt_40:HV2H_HUMAN

```
seq_documentation_block:
ID   HV2H_HUMAN     STANDARD;          PRT;   147 AA.
AC   P04438;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-II region SESS precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84298107; PubMed=6089186;
RA   Takahashi N., Noma T., Honjo T.;
RT   "Rearranged immunoglobulin heavy chain variable region (VH)
RT   pseudogene that deletes the second complementarity-determining
RT   region.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
DR   PIR; A02090; G2HUCS.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
```

DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL           1     19
FT   CHAIN           20    147       IG HEAVY CHAIN V-II REGION SESS.
FT   DOMAIN          20    118       V SEGMENT.
FT   DOMAIN         119    132       D SEGMENT.
FT   DOMAIN         133    147       J SEGMENT.
FT   NON_TER        147    147
SQ   SEQUENCE       147 AA;    16323 MW;  FCBCDB3D00FB6666 CRC64;

alignment_scores:
          Quality:        305.00        Length:    140
          Ratio:          2.798         Gaps:        4
Percent Similarity:       77.857     Percent Identity: 48.571

alignment_block:
US-09-019-441-2 x HV2H_HUMAN

Align seg 1/1 to: HV2H_HUMAN  from: 1  to: 147

  22 CTCCTCCTGGTGCAGCTCCCAGATGGGTCCTGTCCCAGCTGCAGCTGCA 71
     |||||||||:::||||| |||||||| |::||||:::::||||:::||||
   8 LeuLeuLeuLeuThrValProSerGlyValLeuSerGlnValAlaAsnLeuArg 24

  72 GGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCT 121
     :||||||||||:::||||   ||||||| :|||:||||||::||||||
  24 gGluSerGlyProAlaLeuValLysAlaThrHisThrLeuThrLeuThrC 41

 122 GCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGG...TGGACCTGG 168
     ||::: ||||| |||||||:::|| :::  ||| ::|||
  41 ysThrPheSerGlyLeuSerValAsnThrArgGlyMetSerValSerTrp 57

 169 ATCCGCCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGG 218
     ||||||||||||||||||||:|||||||||||||||||:||:
  58 IleArgGlnProProGlyLysGlyLeuGluTrpLeuAlaArgIleAspTr 74

 219 TAGTGGTGGGGCCACCAACTACACACCCGTCCCTCAAGAGTCGAGTCATCA 268
     ||:::  ||||| |||||||||||:::|||:::|
  74 pAspAspAsp...LysTyrTyrGlyThrGlyThrArgGlyLeuThrI 90

 269 TTTCCACAAGACACGTCCAAGAACCCAGTTCTCCCTGAACCTGACTCTGTG 318
     |||||:::||||||||||| ||:::||||||||||::::
  90 leSerLysAspThrSerLysAsnGlnValValLeuLysValThrAsnMet 106

 319 ACCCGCCGGACACGGCCGTGTATTACTGTGCCAGA.............. 354
     |||||||:::||||||||| ||||||||||||||||
 107 AspProAlaAspThrAlaThrTyrTyrTyrCysAlaArgMetGlnValThrMe 123

 355 ...GATTGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGG 400
     :::::||| |||||| |||:::::
 123 tValArgGluValMetIleThrSerAsnAlaPheAspIleTrpGlyGlnG 140

 401 GAGTCCTGGTCACCGTCT 418
     || :::|||||||||||
 140 ly.ThrTrpSerProSer 145

seq_name: SwissProt_40:HV40_MOUSE

seq_documentation_block:
ID   HV40_MOUSE     STANDARD;       PRT;   119 AA.
AC   P01810;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region J539.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PRELIMINARY SEQUENCE.
RX   MEDLINE=79223895; PubMed=111245;

RA   Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT   "Structural evidence for independent joining region gene in
RT   immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT   its potential role in generating diversity in
RT   complementarity-determining regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX   MEDLINE=88217852; PubMed=3449853;
RA   Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
RA   Davies D.R.;
RT   "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
RT   study at 2.6-A resolution.";
RL   Proteins 1:74-80(1986).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC       BINDS GALACTAN.
DR   PIR; A02080; AVMSJ5.
DR   PDB; 2FBJ; 15-OCT-90.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; 3D-structure.
FT   NON_TER        119    119
FT   STRAND           3      7
FT   STRAND          10     12
FT   TURN            14     15
FT   STRAND          18     25
FT   HELIX           29     31
FT   STRAND          34     39
FT   TURN            41     42
FT   STRAND          45     51
FT   TURN            53     54
FT   STRAND          58     60
FT   TURN            62     67
FT   STRAND          68     72
FT   STRAND          78     83
FT   HELIX           88     90
FT   STRAND          92    100
FT   TURN           101    103
FT   STRAND         104    108
FT   STRAND         112    116
SQ   SEQUENCE       119 AA;    13240 MW;  577B4F1DB675C1F1 CRC64;

alignment_scores:
          Quality:        303.00        Length:    122
          Ratio:          3.061       / Gaps:        3
Percent Similarity:       81.148     Percent Identity: 50.000

alignment_block:
US-09-019-441-2 x HV40_MOUSE          ..

Align seg 1/1 to: HV40_MOUSE   from: 1  to: 119

  58 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGAC 107
     :::::::|||  |||||||| ||||||||||||::|||::::|||::
   1 GluValLysLeuLeuGluSerGlyGlyGlyLeuVal GlnProGlyGlySe 17

 108 CCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACT 157
     :||:::||||::::|||||:::|||||||   |||::: |
  17 rLeuLeuSerCysAlaAlaSerGlyPheAspPhe...SerLysTyrT 33

 158 GGTGGACCTGGATCCGCCAGCCCCCAGGGGAAGGGACTGGAGTGGATTGGA 207
     |||||||||| |||||||||||||||||||||||||||||||||
  33 rpMetSerTrpValArgGlnAlaProGlyLysGlyLeuGluTrpIleGly 49

 208 CGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCCGTCCCAAGAG 257
     :::||| :::::|||:::|||||||||||||||||::||:||||
  50 GluIleHisProAspSerGlyThrIleAsnTyrThrProSerLeuLysAs 66

 258 TCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCCCTGAACC 307
     ::::: ||||||||::::|||:::::|||||| :::

```
 66  pLysPheIleIleSerArgAspAsnAlaLysAsnSerLeuTyrLeuGlnM  83

308  TGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT  357
     ::::::::||    :::  |||||||::::||||||||||||||||||||
 83  etSerLysValArgSerGluAspThrAlaLeuTyrTyrCysAlaArg...  98

358  TGGGGCCAAATAGCTGGAACAACCGCTAGGCTTCTGGGGCCAGGAGTCCT  407
     :::  ||||||    :::  ||||||:::||||||||||::::||
 99  ...LeuHisTyrTyrGlyTyrAsn...AlaTyrTrpGlyGlnGlyThrLe  113

408  GGTCACCGTCCCTCA  423
     ||||||||||||:::
113  uValThrValSerAla  118

seq_name: SwissProt_40:HV37_MOUSE

seq_documentation_block:
ID   HV37_MOUSE     STANDARD;       PRT;     119 AA.
AC   P01807;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region X44.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79223895; PubMed=111245;
RA   Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT   "Structural evidence for independent joining region gene in
RT   immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT   its potential role in generating diversity in
RT   complementarity-determining regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC       THAT BINDS GALACTAN.
DR   PIR; A02077; AVMSX4.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   NON_TER       119    119
SQ   SEQUENCE   119 AA;  13246 MW;  BC34FC8F31CD41B3 CRC64;

alignment_scores:
       Quality:   298.00              Length:    126
       Ratio:       3.072             Gaps:        3
Percent Similarity:   76.984      Percent Identity:  47.619

alignment_block:
US-09-019-441-2 x HV37_MOUSE    ..

Align seg 1/1  to: HV37_MOUSE  from: 1  to: 119

 58  CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGAC  107
     ::::::::|||  ||||||||  |||::::||::::|||  ::  ::
  1  GluValLysLeuLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySe   17

108  CCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACT  157
     :|||::||||||||::::||||||  |||||||     ::   |||
 17  rLeuLysLeuSerCysAlaAlaSerGlyPheAspPhe...SerArgTyrT   33

158  GGTGGACCTGGATCCGCCAGCCCCCAGGAAGGGACTGGAGTGGATTGGA  207
     ||   :::||::||||||  ||||||||||||||||||||||||||||||
 33  rpMetSerTrpValArgGlnAlaProGlyLysGlyLeuGluTrpIleGly   49

208  CGTATCTCTGGTAGTGGTGGGGACCACCAACTACACCCCGTCCCTCAAGAG  257
     :::||:::  ::::::::::||  ||||||||||||::::||||||||:::
```

 50  GluIleAsnProAspSerSerThrIleAsnTyrThrProSerLeuLysAs   66

258  TCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCCCTGAACC  307
     :::   |||||||||:::||:::||||||||    :::  |||:::||
 66  pLysPheIleIleSerArgAspAsnAlaLysAsnThrLeuTyrLeuGlnM   83

308  TGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGA...  354
     :::::::||    :::  |||||||::::||||||||||||||||||
 83  etSerLysValArgSerGluAspThrAlaLeuTyrTyrCysAlaArgLeu   99

355  ........GATTGGGCCCAAATAGCTGGAACAACCGCTAGGCTTCTGGGG  395
         :::::||                       :::::||||||
100  HisTyrTyrGlyTyrAla............................AlaTyrTrpGl  109

396  CCAGGAGTCCTGGTCACCGTCCCTCA  423
     ||||||:::|||||||||||||||:::
109  yGlnGlyThrLeuValThrValSerAla  118

OM of: US-09-019-441-2 to: SPTREMBL_19:*    out_format : pfs

Date: Sep 23, 2002 10:23 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_n2p.model -DEV-xlp
-Q=/cgn2_1/USPTO_spool/US0901941/runat_23092002_095259_6361/app_query.fasta_1.1860
-DB=SPTREMBL_19 -QFMT=fastan -SUFFIX=rspt -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0901941_@CGN1_1_409 -NCPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-019-441-2
Query length: 423
Database: SPTREMBL_19:*
Database sequences: 562222
Database length: 172994929
Search time (sec): 228.280000

| sp_rodent:Q924Q9 | + | 273.00 | 466.79 | 8.2e-18 | 145 | ! | Q924q9 mus musculus (mouse). |
| sp_rodent:Q924R6 | + | 272.00 | 465.60 | 1.0e-17 | 137 | ! | Q924r6 mus musculus (mouse). |
| sp_rodent:Q924Q7 | + | 272.00 | 465.07 | 1.0e-17 | 145 | ! | Q924q7 mus musculus (mouse). |
| sp_rodent:Q924Q6 | + | 272.00 | 465.07 | 1.2e-17 | 145 | ! | Q924q6 mus musculus (mouse). |
| sp_human:Q9UL92 | + | 271.00 | 464.81 | 1.2e-17 | 124 | ! | Q9u192 homo sapiens (human). |

seq_name: sp_human:Q96EY0

seq_documentation_block:
ID  Q96EY0       PRELIMINARY;       PRT;       613 AA.
AC  Q96EY0;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  UNKNOWN (PROTEIN FOR MGC-20337).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA  Strausberg R.;
RL  Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; BC011857; AAH11857.1; -.
SQ  SEQUENCE  613 AA;  67273 MW;  31214203FB8421E7 CRC64;

alignment_scores:
                Quality:   553.00              Length:     141
                Ratio:       4.389             Gaps:         2
Percent Similarity:  89.362    Percent Identity:  78.014

alignment_block:
US-09-019-441-2 x Q96EY0

Align seg 1/1 to: Q96EY0    from: 1 to: 613

```
    1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT  50
      ||||||||||||||||||||||||||||||||||||||||||||||||||
    1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

   51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
      ||||||||||||||||||||||||||||||||||||||||||||||||::
   17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyValLeuValLysPros  34

  101 CGGAGACCCTGTCCCCACCCGGCGTGTCTCGTGGCTCGTCGTCAGCAGT  150
      ||||||||||||:::||||||||||||||||||||||||||||::::
   34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIle...Ser  49

  151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG  200
      |||:::||||||::||||||||||  ||||||||||||||||||||||||
   50 SerTyrTyrTrpSerTrpIleArgGlnProAlaGlyLysGlyLeuGluTr  66

  201 GATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTACAACCCGTCCC  250
      ||||||||||||||:::||||||||||   ||| ||||||||||||||||
   66 pIleGlyArgIleTyrThrSer...GlySerThrAsnTyrAsnProSerL  82

  251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACACCAGTTCTCC  300
      ||||||||||||   :::||| ||||||||||||||||||||||||||||
   82 euLysSerArgValThrMetSerValAspThrSerLysAsnGlnPheSer  98

  301 CTGAACCTGAACTCTGTGACCGCGGACACGGCCGTGTATTACTGTGC  350
      |||:::|||:::|||||||||||||||||||||||||||||||||||
   99 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAl  115

  351 CAGAGATTGGGCCCCAAATAGCTGGACAACGCTAGGCTTCTGGGGCCAGG  400
      |||||||||||||||||      :::    ||| |||||||||||||||
  115 aSerGlnProTrpGluLeuProThrValGlyLeuPheTyrTrpGlyGlnG  132

  401 GAGTCCTGGTCACCGTCTCCTCA  423
      |||:::|||||||||||||||||
  132 lyThrLeuValThrValSerSer  139
```

score_list:

| Sequence | Strd | Orig | zScore | EScore | Len | ! | Documentation |
|---|---|---|---|---|---|---|---|
| sp_human:Q96EY0 | + | 553.00 | 935.05 | 1.6e-44 | 613 | ! | Q96ey0 homo sapiens (human). un |
| sp_human:O95973 | + | 535.00 | 917.23 | 6.4e-43 | 150 | ! | O95973 homo sapiens (human). hy |
| sp_human:Q96KX8 | + | 528.00 | 894.02 | 3.8e-42 | 496 | ! | Q96kx8 homo sapiens (human). hy |
| sp_human:Q9BU10 | + | 499.50 | 843.25 | 2.1e-39 | 597 | ! | Q9bu10 homo sapiens (human). hy |
| sp_human:Q96AA6 | + | 499.50 | 842.93 | 2.1e-39 | 618 | ! | Q96aa6 homo sapiens (human). hy |
| sp_human:Q9BQB8 | + | 497.50 | 839.81 | 3.3e-39 | 597 | ! | Q9bqb8 homo sapiens (human). un |
| sp_human:Q9UL73 | + | 424.50 | 729.29 | 2.4e-32 | 119 | ! | Q9u173 homo sapiens (human). my |
| sp_rodent:Q99M22 | + | 390.00 | 656.92 | 6.3e-29 | 479 | ! | Q99m22 mus musculus (mouse). hy |
| sp_human:Q9UL75 | + | 380.00 | 652.49 | 4.4e-28 | 122 | ! | Q9u175 homo sapiens (human). my |
| sp_human:Q91X92 | + | 355.00 | 596.65 | 1.4e-25 | 482 | ! | Q91x92 mus musculus (mouse). un |
| sp_rodent:Q99NG4 | + | 336.00 | 576.87 | 7.2e-24 | 121 | ! | Q99ng4 mus musculus (mouse). si |
| sp_human:Q96BB9 | + | 328.50 | 549.06 | 5.2e-23 | 597 | ! | Q96bb9 homo sapiens (human). hy |
| sp_human:Q9QYF0 | + | 324.50 | 548.66 | 1.1e-22 | 298 | ! | Q9qyf0 mus musculus (mouse). cn |
| sp_human:Q9UL74 | + | 312.50 | 536.67 | 1.3e-21 | 118 | ! | Q9u174 homo sapiens (human). my |
| sp_human:Q9UL88 | + | 311.50 | 533.98 | 1.6e-21 | 131 | ! | Q9u188 homo sapiens (human). my |
| sp_human:Q9UL84 | + | 300.00 | 514.86 | 2.0e-20 | 122 | ! | Q9u184 homo sapiens (human). my |
| sp_human:Q96K68 | + | 298.00 | 498.35 | 4.4e-20 | 494 | ! | Q96k68 homo sapiens (human). co |
| sp_human:Q9UL71 | + | 296.50 | 508.91 | 4.4e-20 | 121 | ! | Q9u171 homo sapiens (human). my |
| sp_human:Q9UL72 | + | 296.00 | 508.29 | 4.9e-20 | 118 | ! | Q9u172 homo sapiens (human). my |
| sp_human:Q9UL90 | + | 295.50 | 507.83 | 5.4e-20 | 113 | ! | Q9u190 homo sapiens (human). my |
| sp_human:Q9UL93 | + | 295.50 | 507.58 | 5.4e-20 | 116 | ! | Q9u193 homo sapiens (human). my |
| sp_human:Q9UL96 | + | 290.50 | 498.59 | 1.7e-19 | 121 | ! | Q9u196 homo sapiens (human). v2 |
| sp_rodent:Q924P8 | + | 290.50 | 497.23 | 1.7e-19 | 140 | ! | Q924p8 mus musculus (mouse). v2 |
| sp_rodent:Q99L31 | + | 286.50 | 479.07 | 5.2e-19 | 468 | ! | Q99131 mus musculus (mouse). si |
| sp_human:Q9HCC1 | + | 285.00 | 489.85 | 5.5e-19 | 112 | ! | Q9hcc1 homo sapiens (human). si |
| sp_rodent:Q924Q1 | + | 284.50 | 486.77 | 5.5e-19 | 142 | ! | Q924q1 mus musculus (mouse). v2 |
| sp_rodent:Q9D8L4 | + | 284.50 | 475.53 | 8.1e-19 | 473 | ! | Q9d814 mus musculus (mouse). 18 |
| sp_human:Q91WR1 | + | 283.00 | 472.66 | 1.1e-18 | 488 | ! | Q91wr1 mus musculus (mouse). hy |
| sp_rodent:Q924Q3 | + | 281.50 | 481.35 | 1.3e-18 | 146 | ! | Q924q3 mus musculus (mouse). vh |
| sp_rodent:Q924Q8 | + | 279.50 | 477.91 | 1.9e-18 | 146 | ! | Q924q8 mus musculus (mouse). vh |
| sp_rodent:Q99KA4 | + | 279.00 | 465.79 | 2.8e-18 | 487 | ! | Q99ka4 mus musculus (mouse). hy |
| sp_rodent:Q924Q4 | + | 278.00 | 475.65 | 3.7e-18 | 141 | ! | Q924q4 mus musculus (mouse). vh |
| sp_rodent:Q924R0 | + | 277.00 | 473.80 | 3.4e-18 | 143 | ! | Q924r0 mus musculus (mouse). vh |
| sp_human:Q9Y509 | + | 277.00 | 473.54 | 3.4e-18 | 147 | ! | Q9y509 homo sapiens (human). vh |
| sp_rodent:Q91XE1 | + | 276.50 | 461.63 | 4.8e-18 | 480 | ! | Q91xe1 mus musculus (mouse). vh |
| sp_rodent:Q924R4 | + | 276.00 | 471.95 | 4.8e-18 | 145 | ! | Q924r4 mus musculus (mouse). vh |
| sp_rodent:Q924R2 | + | 275.50 | 471.42 | 4.7e-18 | 140 | ! | Q924r2 mus musculus (mouse). vh |
| sp_rodent:Q924R8 | + | 274.50 | 469.31 | 5.9e-18 | 146 | ! | Q924r8 mus musculus (mouse). vh |
| sp_human:Q9UL91 | + | 274.00 | 470.44 | 6.3e-18 | 118 | ! | Q9u191 homo sapiens (human). my |
| sp_rodent:Q924P9 | + | 274.00 | 468.64 | 6.5e-18 | 143 | ! | Q924p9 mus musculus (mouse). v3 |

seq_name: sp_human:095973

seq_documentation_block:
```
ID   095973       PRELIMINARY;      PRT;    150 AA.
AC   095973;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   VH4 HEAVY CHAIN VARIABLE REGION PRECURSOR (FRAGMENT).
GN   IGM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT   "Clonal proliferation of IgM secreting B cell in the synovium of
RT   Behcet's patient with arthritis.";
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF103795; AAC79084.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Signal.
FT   SIGNAL        1     19
FT   CHAIN        20   >150
FT   NON_TER      150  150       POTENTIAL.
SQ   SEQUENCE    150 AA;  16315 MW;  85564E04938AA7C9 CRC64;
```

VH4 HEAVY CHAIN VARIABLE REGION.

alignment_scores:
```
          Quality:   535.00           Length:    142
          Ratio:       4.280           Gaps:        3
Percent Similarity:  88.028    Percent Identity:  75.352
```

alignment_block:
US-09-019-441-2 x 095973

Align seg 1/1  to: 095973   from: 1  to: 150

```
   1 ATGAAACACCTGTGGTTCTTCCTCCTCGCTGGTGGCAGCTCCAGATGGGT 50
     ||||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetLysHisLeuTrpPhePheLeuLeuLeuAlaValAlaAlaProArgTrpVa 17

  51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
     ||||||||||||||||||||||||||||||||||||:::||||||
  17 lLeuSerGlnLeuGlnLeuGlnGluSerGlyProGlyLeuValLysPros 34

 101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
     |||||||||||||||:|:||||||||||||:::||||||||||||||
  34 erGluThrLeuSerLeuCysThrValSerGlyGlySerIleSerSer 50

 151 AGTAAC...TGGTGGACCTGATCCGCCAGCCCCCAGGGAAGGGACTGGA 197
     ::|||   ||||||||||||||:|||||||||||||||||||
  51 ThrAsnTyrTyrTrpGlyTrpIleArgGlnProProGluLysGlyLeuGl 67

 198 GTGGATTGGACGTATCTCTGGTAGTGGTGGGGACCACCAACTACAACCGT 247
     ||||||||:::|||||||||||     |||||||||||||
  67 uTrpIleGlySerLeuHisAsnSer...GlySerAspTyrTyrAsnProS 83

 248 CCCTCAAGAGTCGAGTCATCATTCACAAGAACAGTCCAAGAACCAGTTC 297
     ||||||||||||:::||   ||||||||||||||||
  83 erLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPhe 99

 298 TCCCTGAACCTGAACTGTGACCGCCGGACACGGCCCGTGTATTACTG 347
     |||||||||:||::||| |||| ||||||||||||||||
 100 SerLeuArgLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCy 116

 348 TGCCAGAGATTGGGCCCAAATAGCTGGAACAACGCTGGAACAACG 397
```

---

```
116 sAlaArg.........LeuGlyMetGlyAlaPheAspPheTrpGlyH 129
    |||||||              ::::::  ||||||||
398 AGGGAGTCCTGGTCACCGTCCTCA 423
    :::||:::::||||||||||||
129 isGlyThrMetValThrValSerSer 137
```

seq_name: sp_human:Q96KX8

seq_documentation_block:
```
ID   Q96KX8       PRELIMINARY;      PRT;    496 AA.
AC   Q96KX8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 53.4 KDA PROTEIN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LUNG;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC016369; AAH16369.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   496 AA;  53391 MW;  D34692984904OD69 CRC64;
```

alignment_scores:
```
          Quality:   528.00           Length:    144
          Ratio:       4.224           Gaps:        3
Percent Similarity:  86.806    Percent Identity:  75.000
```

alignment_block:
US-09-019-441-2 x Q96KX8

Align seg 1/1  to: Q96KX8   from: 1  to: 496

```
   1 ATGAAACACCTGTGGTTCTTCCTCCTCGCTGGTGGCAGCTCCAGATGGGT 50
     ||||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetLysHisLeuTrpPhePheLeuLeuLeuAlaValAlaAlaProArgTrpVa 17

  51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
     |||||||||||||||||||||||||||||||||||:::||||||
  17 lLeuSerGlnLeuGlnLeuGlnGluSerGlyProGlyLeuValLysSers 34

 101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
     |||||||||||||||:|:||||||||||||:::||||||||||||||
  34 erGluThrLeuSerLeuThrCysValSerGlyGlySerIleSerSer 50

 151 AGTAAC...TGGTGGACCTGATCCGCCAGCCCCCAGGGAAGGGACTGGA 197
     :|:::|   |||||||||||||||:|||||||||||||||||||||
  51 SerSerTyrTyrTrpGlyTrpIleArgGlnProProGlyLysGlyLeuGl 67

 198 GTGGATTGGACGTATCTCTGGTAGTGGT...GlyIleThrTyrTyrAsnProS 247
     ||||||||:::|||||||||||     ||||||||||||
  67 uTrpIleAlaAsnThrTyrTyrSer...GlyIleThrTyrTyrAsnProS 83

 248 CCCTCAAGAGTCGAGTCATCATTCACAAGAACACGTCCAAGAACCAGTTC 297
     |||||||||||:::||   |||||||||||::::::
  83 erLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnLeu 99

 298 TCCCTGAACCTGAACTGTGACCGCCGGACACGGCCCGTGTATTACTG 347
     |||||||||:||::||| |||| |||||||||||||||
 100 SerLeuLysValArgSerValThrAlaAlaAspThrAlaValTyrPheCy 116

 348 TGCCAGAGATTGGGCTTYr.....CTAGGCTTCT 391
     ||||||       :::||   :::||
 116 sAlaArgHisGlyTyrSerArgSerGlyArgThrGlyAlaIleAspTyrT 133

 392 GGGGCCAGGAGGAGTCCTGGTCACCGTCCTCA 423
```

```
         ||||||||||||:::||||||||||||
    133  rpGlyGlyGlnGlyThrLeuValThrValSerSer 143

seq_name: sp_human:Q9BU10

seq_documentation_block:
ID   Q9BU10          PRELIMINARY;          PRT;      597 AA.
AC   Q9BU10;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 65.3 KDA PROTEIN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LYMPH, LYMPHOMA;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002963; AAH02963.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE  597 AA;  65274 MW;  2DAFA8FB7E055851 CRC64;

alignment_scores:
            Quality:    499.50          Length:     146
            Ratio:      4.061           Gaps:         3
 Percent Similarity:    84.247    Percent Identity:  70.548

alignment_block:
US-09-019-441-2 x Q9BU10

Align seg 1/1  to: Q9BU10  from: 1  to: 597

   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT  50
     ||||||||||||||||||||||||||:::||||||||||||||||||||||
   1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

  51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
     |||||||||||:::|||||||||:::|||  ||:::::|||:::||||||
  17 lLeuSerGlnLeuGlnLeuGlnTrpGlyAlaGlyLeuLeuLysProS  34

 101 CGGAGACCCTGTCCCTCACCTGCGTCTCTGGTGGCTCTGTCAGCAGT  150
     ||||||||||:::|||||||||||  |||  ||:::||||||||||
  34 erGluThrLeuSerLeuThrCysValTyrGlyGlySerPhe...Ser  49

 151 AGTAACTGGTGGACCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTG  200
     |||  :::|||||||||:::||  |||||||||||||||||||||||||
  50 GlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTr  66

 201 GATTGGACGTATCTCTGGTAGTGGTGGGGGCACCAACCCGTCCC  250
     |||:::::|||:::||  |||::::::|||||||||||||||||||
  66 pIleGlyGluIleAsnHisSer...GlySerThrAsnTyrAsnProSerL  82

 251 TCAAGAGTCGAGTCATCATTCACAGAACACGTCCAAGAACCAGTTCTCC  300
     ||||||||||:::|||  ||:::||||||||:::|||||||||||||
  82 euLysSerArgValThrIleSerValAspThrSerLysSerGlnLeuSer  98

 301 CTGAACCTGAACTCTGTGACCGCCGCGACACGCCCGTATTACTGTGC  350
     |||||||||:::|||||||  ||||:::||||||||||||||||||||
  98 LeuLysLeuSerSerValAsnAlaAlaAspThrAlaValTyrTyrCysAl  115
```

```
         |||:::|||:::|||:::||||||||||||||||||||||||||
    99  LeuLysLeuSerSerValAsnAlaAlaAspThrAlaValTyrTyrCysAl  115

   351 CAGAGATTGGGCCCAAATAGCTGGACAACGCTAGGC............  387
       ||||                                 |||    ||||
   115 aArgValIleThrArgAlaSerProGlyThrAspGlyArgGlyMetA  132

   388 ..TTCTGGGGCCAGGGAGTCCTGGTCACCGTCCTCCTCA  423
       ||||||||||||||||:::    ||||||||||||||||
   132 spValTrpGlyGlnGlyThrThrValThrValSerSer  144

seq_name: sp_human:Q96AA6

seq_documentation_block:
ID   Q96AA6          PRELIMINARY;          PRT;      618 AA.
AC   Q96AA6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 67.8 KDA PROTEIN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LYMPH, AND LYMPHOMA;
RA   Strausberg R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC017356; AAH17356.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE  618 AA;  67758 MW;  96DBD4C7C696E0A6 CRC64;

alignment_scores:
            Quality:    499.50          Length:     146
            Ratio:      4.061           Gaps:         3
 Percent Similarity:    84.247    Percent Identity:  70.548

alignment_block:
US-09-019-441-2 x Q96AA6

Align seg 1/1  to: Q96AA6  from: 1  to: 618

   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT  50
     ||||||||||||||||||||||||||:::||||||||||||||||||||||
   1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

  51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
     |||||||||||:::|||||||||:::|||  ||:::::|||:::||||||
  17 lLeuSerGlnLeuGlnLeuGlnTrpGlyAlaGlyLeuLeuLysProS  34

 101 CGGAGACCCTGTCCCTCACCTGCGTCTCTGGTGGCTCTGTCAGCAGT  150
     ||||||||||:::|||||||||||  |||  ||:::||||||||||
  34 erGluThrLeuSerLeuThrCysValTyrGlyGlySerPhe...Ser  49

 151 AGTAACTGGTGGACCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTG  200
     |||  :::|||||||||:::||  |||||||||||||||||||||||||
  50 GlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTr  66

 201 GATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACCCGTCCC  250
     |||:::::|||:::||  |||::::::|||||||||||||||||||
  66 pIleGlyGluIleAsnHisSer...GlySerThrAsnTyrAsnProSerL  82

 251 TCAAGAGTCGAGTCATCATTCACAGAACACGTCCAAGAACCAGTTCTCC  300
     ||||||||||:::|||  ||:::||||||||:::||||||||||||
  82 euLysSerArgValThrIleSerValAspThrSerLysSerGlnLeuSer  98

 301 CTGAACCTGAACTCTGTGACCGCCGCGACACGCCCGTATTACTGTGC  350
     |||||||||:::|||||||  ||||:::||||||||||||||||||||
  99 LeuLysLeuSerSerValAsnAlaAlaAspThrAlaValTyrTyrCysAl  115

 351 CAGAGATTGGGCCCAAATAGCTGGACAACGCTAGGC............  387
```

```
201 GATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACAACCCGTCCC 250
    |||||||:::||:: |||  ||| ||||||||||||||||||
 66 pIleGlyGluIleAsnHisSer...GlyIleThrAsnTyrAsnProSerL 82

251 TCAAGAGTGCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    |||||||||||  ||||||||||||||||||||:::||::::||:::|||
 82 euLysSerArgValThrIleSerValAspThrSerLysGlnLeuSer 98

301 CTGAACCTGAACTCTGTGACCGCCGCGACACGGCCGTGTATTACTACTGTGC 350
    |||:::||:: ||||||::|||||||||||||||||||||||||||
 99 LeuLysLeuSerSerValAsnAlaAlaspThrAlaValTyrTyrCysAl 115

351 CAGAGATTGGGCCCAAATAGCTGGAACAACGTAGGC.............. 387
    ||||  |||  ||::::||  :::  ||
115 aArgValIleThrArgAlaSerProGlyThrAspGlyArgTyrGlyMetA 132

388 ..TTCTGGGGCCAGGAGTCCTGGTCACCGTCTCCTCA 423
    |||||||||||||::::|||||||||||||||
132 spValTrpGlyGlnGlyThrThrValSerSer 144
```

seq_name: sp_human:Q9UL73

seq_documentation_block:
```
ID   Q9UL73        PRELIMINARY;        PRT;     119 AA.
AC   Q9UL73;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035041; AAD56277.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1
FT   NON_TER     119
SQ   SEQUENCE   119 AA;   13219 MW;   1BDB86B6420EA0BE CRC64;
```

alignment_scores:
```
      Quality:   424.50              Length:    124
      Ratio:       4.043              Gaps:        4
Percent Similarity:  84.677    Percent Identity:  70.968
```

alignment_block:
US-09-019-441-2 x Q9UL73

Align seg 1/1 to: Q9UL73 from: 1 to: 119
```
 58 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGAC 107
    ||:::||||||::|||||::||||||:::|||||||||:|||||||||||
  1 GlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluTh 17

108 CCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACT 157
    ||||||||||||||:::||||||||||||||||||||||||
 17 rLeuSerLeuThrCysThrValSerGlyGlySerIle...CysSerTyrT 33

158 GGTGGACCTGGATCCGCCAGCCCCCAGGAAGGGACTGGAGTGGATTGGA 207
    :::|||:::||||||||||||||||||||||||||||||||||
```

---

```
115 aArgValIleThrArgAlaSerProGlyThrAspGlyArgTyrGlyMetA 132
    |||                           |||    |||

388 ..TTCTGGGGCCAGGAGTCCTGGTCACCGTCTCCTCA 423
    |||||||||||||::::|||||||||||||||
132 spValTrpGlyGlnGlyThrThrValSerSer 144
```

seq_name: sp_human:Q9BQB8

seq_documentation_block:
```
ID   Q9BQB8        PRELIMINARY;        PRT;     597 AA.
AC   Q9BQB8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=RHABDOMYOSARCOMA;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LYMPHOMA;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006180; AAH06180.1; -.
DR   EMBL; BC001872; AAH01872.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGC1; 4.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ   SEQUENCE   597 AA;   65300 MW;   2DAFAD50A6375851 CRC64;
```

alignment_scores:
```
      Quality:   497.50              Length:    146
      Ratio:       4.078              Gaps:        3
Percent Similarity:  83.562    Percent Identity:  70.548
```

alignment_block:
US-09-019-441-2 x Q9BQB8

Align seg 1/1 to: Q9BQB8 from: 1 to: 597
```
  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT 50
    ||||||||||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa 17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    ||||||||||||||||||::::|||||||||::|||  ||||||||||||
 17 lLeuSerGlnLeuGlnLeuGlnGluSerGlyProGlyLeuLeuLysProS 34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    |||||||||||||||:::|||||||||||
 34 erGluThrLeuSerLeuThrCysAlaValSerGlyValTyrGlyGlySerPhe...Ser 49

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
    ::::|||:::||::||||||||||||||||||||||
 50 GlyTyrTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTr 66
```

```
 33 yrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTrpIleGly 49
    |||||||:::|||||||||||||||||||||::|||||||||
 16 eLeuSerAspValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 33

208 CGTATCCTCGGTAGTGGTGGGGCCACCAACTACAACCCGTCTCCTCAAGAG 257
    |||   || |||:|||||||||||::||||||||||||
101 CGGAGACCCTGTCCCTCACCTGCGTGTCTCTCGGTGGCTCTGTCAGCAGT 150

 50 TyrIleTyrTyrSer...GlySerThrAsnTyrThrProSerLeuLysSe 65
    ||||||:::||||||||||||:::||||||||||
 33 erGlnSerLeuThrCysSerValThrGlyTyrSerIleThrSer 49

258 TCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCCCTGAACC 307
    |||||||  |||||  |||  |||||||||||||:::|
 65 rArgValThrIleSerValAspArgSerLysAsnGlnPheSerLeuLysL 82

308 TGAACTCTGTGACCGCCGCGGACGACGGCCGTGTATTACTGTGCCAGA... 354
    ||:::|||:|||||||||||||||||||||:||||
 82 euThrSerLeuThrAlaAlaAspThrAlaValTyrPheCysAlaArgLeu 98

355 ..GATTGGGGCCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGG 401
    ::|||||:                 ::|||||||||
 99 SerAsnTrpGlyProTyr........TyrPheAspTyrTrpGlyGlnGl 112

402 AGTCCTGGTCACCGTCTCCTCA 423
    |::||||||||||||||||||
112 yThrLeuValThrValSerSer 119
```

seq_name: sp_rodent:Q99M22

seq_documentation_block:
ID  Q99M22        PRELIMINARY;         PRT;        479 AA.
AC  Q99M22;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  HYPOTHETICAL 52.0 KDA PROTEIN.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC  TISSUE.;
RA  Strausberg R.;
RL  Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; BC002091; AAH02091.1; -.
DR  HSSP; P01810; 2FBJ.
DR  InterPro; IPR003599; Ig.
DR  InterPro; IPR003597; Ig_c1.
DR  InterPro; IPR003600; Ig_like.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; ig; 4.
DR  SMART; SM00409; IG; 3.
DR  SMART; SM00407; IGc1; 3.
DR  SMART; SM00406; IGv; 1.
DR  SMART; SM00410; IG_like; 1.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW  Hypothetical protein.
SQ  SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;

alignment_scores:
        Quality:      390.00              Length:       146
        Ratio:         3.421              Gaps:           4
Percent Similarity:  78.082      Percent Identity:  56.164

alignment_block:
US-09-019-441-2 x Q99M22

Align seg 1/1 to: Q99M22 from: 1 to: 479

```
  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCAGATGGGT 50
    |||||| |||  :::::::  ||||||||:::|||    ::  ||
  1 MetLysValLeuSerLeuLeuTyrLeuLeuThrAlaIlePro...GlyIl 16

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
```

```
 :||||||:::||||||||||||||||||||||||||||||||||||||
 16 eLeuSerAspValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 33

101 CGGAGACCCTGTCCCTCACCTGCGTGTCTCTCGGTGGCTCTGTCAGCAGT 150
    ||||||||||||||||||||||||||||||||||||||:||||||
 33 erGlnSerLeuThrCysSerValThrGlyTyrSerIleThrSer 49

151 AGTACTGGTGGACCTGGATCCCGCAGCCCCAGGGAAGGGACTGGAGTG 200
    :::  ::||||||||||||||  ||||||  ||||:|  |||||
 50 GlyTyrTyrTrpAsnTrpIleArgGlnPheProGlyAsnGlyLeuGluTr 66

201 GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCCGTCCC 250
    |::||| |||:| ||:::              ||||||||||||||||||
 66 pMetGlyTyrIleAsn...TyrAspGlySerAsnAsnTyrAsnProSerL 82

251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    |||||::||:::  :||||||||||:||||||||||||||||||||
 82 euLysAsnArgIleSerIleThrArgAspThrSerLysAsnGlnPhePhe 98

301 CTGAACCTGAACTCTGTGACCGCCGCGGACGACGGCCGTGTATTACTGTGC 350
    ||||:|||||||||||::|||||||||||||||||:::|||||||||||
 99 LeuLysLeuAsnSerValThrThrGluAspThrAlaThrThrTyrTyrCysAl 115

351 CAGAGATTGGGCCCCAAATAGCTGGAACAACGCTAGGCTTC.......... 390
    |         :::    |||:::
115 a...............SerArgGlyTyrSerTrpPheP 123

391 ....TGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 423
    ||||||||||||||||||||||||||||||||
123 roAsnTrpGlyGlnGlyThrLeuValThrValSerAla 135
```

seq_name: sp_human:Q9UL75

seq_documentation_block:
ID  Q9UL75        PRELIMINARY;         PRT;        122 AA.
AC  Q9UL75;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE  (FRAGMENT).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=98277139; PubMed=9614934;
RA  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA  Young D.C.;
RT  "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT  fetus.";
RL  Clin. Immunol. Immunopathol. 87:184-192(1998).
DR  EMBL; AF035039; AAD56275.1; -.
DR  HSSP; P01825; 7FAB.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; ig; 1.
DR  SMART; SM00406; IGv; 1.
FT  NON_TER      1      1
FT  NON_TER    122    122
SQ  SEQUENCE 122 AA; 13719 MW; 56CB0612586A6529 CRC64;

alignment_scores:
        Quality:      380.00              Length:       124
        Ratio:         3.762              Gaps:           4
Percent Similarity:  81.452      Percent Identity:  64.516

alignment_block:
US-09-019-441-2 x Q9UL75

Align seg 1/1 to: Q9UL75 from: 1 to: 122

```
 58 CAGCTGCAGCTGCAGGAGTCGGGGCCCAGGAGTGGTGAAGCCTTCGGAGAC 107
    |||::|||||||||:::||||||||||::|||||||||||:::||
  1 GlnValGlnLeuGlnGlnSerGlyProGlyLeuValLysProSerGlnTh 17

108 CCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCTGTCAGCAGT...AGTA 154
    |||||::|||||:::|||| ||||||| |||
 17 rLeuSerLeuThrCysAlaIleSerGlyAspSerValSerSerAsnSerA 34

155 ACTGGTGGACCTGGATCCGCCAGCCCCAGGGAAGGGACTGGAGTGGATT 204
    |||::|||||||||||:::|||||||||||:::|||||
 34 laAlaTrpAsnTrpIleArgGlnSerProSerArgGlyLeuGluTrpLeu 50

205 GGACGT...ATCTCTGGTAGTGTGGGGCCACCAACTACAACCCGTCCCT 251
    |||||      :::||||||||| ||:::||
 51 GlyArgThrTyrTyrArgSerLysTrpTyrArgAspTyrArgValSerVa 67

252 CAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCCC 301
    :||||||||:::  |||:::  ||||||||||||||
 67 lLysSerArgIleThrIleAsnProAspThrSerLysAsnGlnPheSerL 84

302 TGAACCTGAACTGTGACCGCGCGGACACGGCCGTGTATTACTGTGCC 351
    ||:::|||||||| |||||||||||||||
 84 euGlnLeuAsnSerValThrProGluAspThrAlaValTyrTyrCysAla 100

352 AGAGATTGGGCCCAAATAGCTGGAACACACGCTAGGCTTCTGGGGCCAGGG 401
    |||||  |||   :::|||||||||||
101 ArgAsp...LeuGluLeuGly...GlnPheAspTyrTrpGlyGlnGl 115

402 AGTCCTGGTCACCGTCTCCTCA 423
    |::::||||||||||||||
115 yThrLeuValThrValSerSer 122

seq_name: sp_rodent:Q91X92

seq_documentation_block:
ID   Q91X92       PRELIMINARY;        PRT;    482 AA.
AC   Q91X92;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   UNKNOWN (PROTEIN FOR MGC:18822).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011181; AAH11181.1; -.
SQ   SEQUENCE   482 AA;  51865 MW;  312E01F9C1BC7F3C CRC64;

alignment_scores:
        Quality:   355.00                 Length:      141
        Ratio:     3.198                  Gaps:        4
Percent Similarity:  78.723   Percent Identity:  53.901

alignment_block:
US-09-019-441-2 x Q91X92

Align seg 1/1  to: Q91X92  from: 1  to: 482

  1 ATGAAACACCTGGTGTTCTTCCTCCTGCTCCTGGTGCCAGCTCCCAGATGGT 50
    |||  |||   ||||||||:::  |||||||:: ||||:::||
  1 MetAlaValLeuAlaLeuLeuLeuCysLeuValThrPheProSerCysAl 17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    ||||||||:::|||||||:::||||||||| :::|||
 17 aLeuSerGlnValGlnLeuGlnLeuGlnGluSerGlyProLeuValAlaProSer 34
```

```
101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCTGTCAGCAGT 150
    ||:::|||||||::::|||||| :::|||||| :::||||||
 34 erGlnSerLeuSerIleThrCysThrValSerGlyPheAlaLeuThrSer 50

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCAGGGAAGGGACTGGAGTG 200
    :::|||:||||||||||||||||||||||||||||||||||
 51 TyrAla...IleSerTrpValArgGlnProProGlyLysGlyLeuGluTr 66

201 GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCCGTCCC 250
    |:::|||   :::|||||||||||||||||||||
 66 pLeuGly...ValIleTrpThrGlyGlyValThrAsnTyrAsnSerAlaL 82

251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    ||||||||||  |||:::::::|||
 82 euLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPhe 98

301 CTGAACCTGAACTGTGACGCCGCGGACACGGCCGTGTATTACTGTGC 350
    |||:::||||||| :: |||||||||||||||
 99 LeuLysMetAsnSerLeuGlnThrAsnAspThrAlaArgTyrTyrCysAl 115

351 CAGAGATTGGGCCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGG 400
    ||||||  :::::  || :::||||||||
115 aArgAsp...SerAsnTyrGluGly...AlaMetAspTyrTrpGlyGlnG 130

401 GAGTCCTGGTCACCGTCTCCTCA 423
    |:::||||||||||||||
130 lyThrSerValThrValSerSer 137

seq_name: sp_rodent:Q99NG4

seq_documentation_block:
ID   Q99NG4       PRELIMINARY;        PRT;    121 AA.
AC   Q99NG4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SINGLE CHAIN FV (FRAGMENT).
OS   Mus musculus (Mouse).
OG   Plasmid pHEN1.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=98169018; PubMed=9510199;
RA   Hawlisch H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,
RA   Bautsch W., Kola A., Klos A., Koehl J.;
RT   "Site-Directed C3a-Receptor Antibodies from Phage Display Libraries.";
RL   J. Immunol. 160:2947-2958(1998).
DR   EMBL; AJ222590; CAA10890.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
KW   Plasmid.
FT   NON_TER        1      1
FT   NON_TER      121    121
SQ   SEQUENCE   121 AA;  13255 MW;  D293E4EBC8C59D5B CRC64;

alignment_scores:
        Quality:   336.00                 Length:      122
        Ratio:     3.360                  Gaps:        2
Percent Similarity:  81.967   Percent Identity:  54.918

alignment_block:
US-09-019-441-2 x Q99NG4
```

```
Align seg 1/1   to: Q99NG4   from: 1 to: 121

   58 CAGCTGCAGCTGCAGGAGTTCGGGCCCAGGAGTGTGAAGCCTTCGGAGAC 107
      |||::||||||::|||||||||||||||||||  ||||||||::|||
    1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSe 17

  108 CCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACT 157
      :||||:::|||||:|||||||||  ::|||:|||
   17 rLeuSerIleThrCysThrValSerGlyPheProLeu...ThrSerHisG 33

  158 GGTGGACCTGGATCCGCCAGCCCCCAGGAAGGACTGGAGTGGATTGGA 207
      ::|||:::|||||||||||||||:::|||
   33 lyValSerrpValArgGlnProProGlyLysGlyLeuGluTrpLeuGly 49

  208 CGTATTCTTGGTAGTGGTGGTGGGCCACCAACTACAAACCCTCCCTCAAGAG 257
      |||  |||:|||:||||::  :|||||
   50 ValIleTrpGlyAspGlyAsn...ThrLysTyrHisSerAlaLeuIleSe 65

  258 TCGAGTCATCATTCACAGAACACGTCCAAGAACCAGTTCTCCCTGAACC 307
      ||||:::  |||||:||||:::|||||||||  |||:::|
   65 rArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeuLysL 82

  308 TGAACTCTGTGACCGCCGGGACACGGCCGTGTATTACTGTGCCAGAGAT 357
      ||||:::  ::: ||||||||||||||||
   82 euAsnSerLeuGlnThrGluAspThrAlaThrTyrTyrCysAlaArgHis 98

  358 TGGGCCCAAATAGCTGGAACAACCTAGGCTTCTGGGGCCAGGAGTCCT 407
      |||||||||||||   ::|||||||||||
   99 TyrTyrLysTyrAlaAsnTyrAlaMetAspTyrTrpGlyGlnGlyThrSe 115

  408 GGTCACCGTCTCCTCA 423
      ||||||||||||||
  115 rValThrValSerSer 120
```

seq_name: sp_human:Q96BB9

seq_documentation_block:
```
ID   Q96BB9        PRELIMINARY;      PRT;    597 AA.
AC   Q96BB9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 65.0 KDA PROTEIN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015760; AAH15760.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   597 AA;   65039 MW;   4FCA3AD8ECE263D9 CRC64;
```

alignment_scores:
```
        Quality:   328.50
        Ratio:       3.221
Percent Similarity:   72.340        Percent Identity:   51.064
```

alignment_block:
US-09-019-441-2 x Q96BB9

Align seg 1/1   to: Q96BB9   from: 1 to: 597

```
   13 TGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGTCCTGTCCCAGCT 62
      |||:::|||      |||||||     ::  ||   :::||
    7 TrpLeuPhe......LeuValAlaIleLeuLysGlyValGlnCysGluVa 21

   63 GCAGCTGCAGGAGTTCGGGCCCAGGAGTGTGAAGCCTTCGGAGACCCTGT 112
```

---

```
   21 lGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuA 38

  113 CCCTCACCTGCGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGG 162
      |||::||||||   |||   :::|||   ||   ..Met 53
   38 rgLeuSerCysAlaAlaSerGlyPheSerPheSerTyrAla...Met 53

  163 ACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGACGTAT 212
      ::||::||||  |||||||||||||||||||::::|||
   54 AsnTrpValArgGlnAlaProGlyLysGlyLeuGluTrpValSerAlaIl 70

  213 CTCTGGTAGTGGTGGGGGCCACCAACTACAAACCCGTCCCTCAAGAGTCGAG 262
      ||||||||||||:::|||  |||:::|||
   70 eSerGlySerGlyGlySerThrTyrTyrAlaAspSerValLysGlyArgP 87

  263 TCATCATTCACAAGACACGTCCAAGAACCAGTTCTCCCTGAACCTGAAC 312
      |||   ||:::|||||   |||:::|||||||||
   87 heThrIleSerArgAspAsnSerArgAspThrLeuTyrLeuGlnMetAsn 103

  313 TCTGTGCCGCCGGGACACGCCGTGTATTACTGTGCCAGAGATTGGGGC 362
      |||:::   |||   ||||||||||||||||||
  104 SerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLysAspProAr 120

  363 CCAAATAGCTGGA..........ACAACGCTAGGCTTCTGGGGCCAGG 400
      :::::            ::||||||||||
  120 gGlyTyrSerAlaSerGlyAsnTyrThrArgGluAspTyrTrpGlyGlnG 137

  401 GAGTCCTGGTCACCGTCTCCTCA 423
      ||:::|||||||||||||
  137 lyThrLeuValThrValSerSer 144
```

seq_name: sp_rodent:Q9QYF0

seq_documentation_block:
```
ID   Q9QYF0        PRELIMINARY;      PRT;    298 AA.
AC   Q9QYF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CN 8 SCFV.
GN   CN 8.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=SPLEEN;
RX   MEDLINE=20183931; PubMed=10706631;
RA   Shinohara N.; Demura T., Fukuda H.;
RT   "Isolation of a vascular cell wall-specific monoclonal antibody
RT   recognizing a cell polarity by using a phage display subtraction
RT   method.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR   EMBL; AB036341; BAA88633.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 2.
SQ   SEQUENCE   298 AA;   31867 MW;   E0F96B8A17004317 CRC64;
```

alignment_scores:
```
        Quality:   324.50          Length:  144
        Ratio:       2.897          Gaps:      4
Percent Similarity:   77.778     Percent Identity:   48.611
```

alignment_block:
US-09-019-441-2 x Q9QYF0

Align seg 1/1   to: Q9QYF0   from: 1 to: 298

```
alignment_block:
US-09-019-441-2 x Q9UL74

Align seg 1/1 to: Q9UL74  from: 1  to: 118

 85 GGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGGCTGTCTCTGG 134
    ||:::|||||||||||||::||||||||||||||||||||||||:::||||     17
  1 GlyLeuValLysProSerGlnThrLeuSerLeuThrCysAlaIleSerG1

135 TGGCTCTGTCAGCAGT...AGTAACTGGTGACCTGGACCTGGATCCCGCCCAGCCCC 181
    ||:::          |||:::          ||||:::                    34
 17 yAspSerValSerSerAsnSerAlaAlaTrpAsnCysIleArgProValP

182 CAGGGAAGGGACTGGAGTGGATTGGACGTATCTCT...GGTAGTGGTGGG 228
    ||:::::|||||:::||||                   |||                 50
 34 roSerArgGlyLeuGluTrpLeuGlyArgThrThrTyrArgSerLysTrp

229 GCCACCAACTACAACCCGTCCCTCAAGAGTCGAGTCATCATTCACAAGA 278
    :::::||                |||||:::    ||    ||                67
 51 TyrAsnAspThrAlaValSerValLysSerArgIleThrIleAsnProAs

279 CACGTCCAAGAACCAGTTCTCCCTGAACCTGAACTCTGTGACCGCCGGCGG 328
    ||||||||||||||||||||||||||||||              ||           84
 67 pThrSerLysAsnGlnPheSerLeuGlnLeuAsnSerValThrProGluA

329 ACACGGCCGTGTATTACTGTGCCAGA.........GATTGGGCCCAAATA 369
    |||||||||||||||||||||||||             :::|||            100
 84 spThrAlaValTyrTyrCysAlaSerThrTrpLeuAsnTrpGlyTyrGlu

370 GCTGGAACAACGCTAGGCTTCTGGGGCCCAGGGAGTCCTGGTCACCGTCTC 419
    :::::      |||:::||||||||||||||||||||                   117
101 LysAspAspAlaPheAspIleTrpGlyGlnGlyThrMetValThrValSe

420 CTCA 423
     |||                                                    118
117 rSer
```

seq_name: sp_human:Q9UL88

seq_documentation_block:
ID   Q9UL88        PRELIMINARY;     PRT;    131 AA.
AC   Q9UL88;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035026; AAD56262.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      131    131
FT   NON_TER      131    131
SQ   SEQUENCE   131 AA;  14142 MW;  96E7D668E375DEA0 CRC64;

alignment_scores:
            Quality:  311.50                     Length:   132

---

```
  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCA........GCTCC 41
    ::|||   |||   :::    ::|||||||:::                   34
 18 ValLysLeuLeuPheAlaIleProLeuValProPheTyrAlaAl

 42 CAGATGGGTCCTGTCCCAGCTGCAGCTGCAGGAGTCGGGGCCCAGGAGTGG 91
    :::         :::::|||:::|||:::::|||||:||:::|||        51
 34 aGlnProAlaMetAlaGlnValLysLeuGlnLnSerGlyGlyGlyLeuV

 92 TGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTCTTGGTGGCTCT 141
    ||||||:::         :::|||:::|||||||:::::||||  ||||||  66
 51 aLysProGlyGlySerLeuLysLeuSerCysAlaAlaSer...GlySer

142 GTCAGCAGTAGTAACTGGTGACGTATCTCTGGTGGTGGGGCACCAGGAAGGG 191
    |||         |||:::::||||   |||:::||||||              83
 67 AspPheSerArgTyrTrpMetSerTrpValArgGlnAlaProGlyLysGl

192 ACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCACCAACTACA 241
    ||||||||||||||||:::::      |||:::||||  :::||||       100
 83 yLeuGluTrpIleGlyIleIleAsnProAspSerSerThrIleAsnTyrT

242 ACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAAC 291
    :::||||||||||||:::        |||:::::||||||             116
100 hrProSerLeuLysAspLysPheIleIleSerArgAspAsnAlaLysAsn

292 CAGTTCTCCCTGAACCTGTGACGCGCGGACACGGCCGTGTA 341
    :::         ||||||||:::|||  |||||||:::||            133
117 ThrLeuTyrLeuGlnMetSerLysValArgSerGluAspThrAlaLeuTy

342 TTACTGTGCCAGAGATTGGGCCCAAATAGCTGGAACAACCCTAGGCTTCT 391
    |||||||||||   ||||||||        :::||||                147
133 rTyrCysAlaArg.....AlaSerTyrArgGlyHisSer...AlaTyrT

392 GGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 423
    ||||||||||||:::    ||||||||||                       157
147 rpGlyGlnGlyThrThrValThrValSerSer
```

seq_name: sp_human:Q9UL74

seq_documentation_block:
ID   Q9UL74        PRELIMINARY;     PRT;    118 AA.
AC   Q9UL74;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035040; AAD56276.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    118    118
SQ   SEQUENCE   118 AA;  13028 MW;  C6EAD38BB6930485 CRC64;

alignment_scores:
            Quality:  312.50                     Length:   118
            Ratio:      3.511                     Gaps:       3
Percent Similarity: 75.424                Percent Identity: 57.627

OM of: US-09-019-441-2 to: A_Geneseq_032802:*    out_format : pfs

Date: Sep 23, 2002 10:06 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US0901941/runat_23092002_095257_6281/app_query.fasta_1.1860
-DB=A_Geneseq_032802 -QFMT=fastan -SUFFIX=rag -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.500
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0901941_@CGN_1_175 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-019-441-2
Query length: 423
Database: A_Geneseq_032802:*
Database sequences: 747574
Database length: 111073796
Search time (sec): 193.710000

/SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2000.DAT:AAY64684 +  495.50  881.39  4.5e
/SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2000.DAT:AAY64674 +  494.00  877.81  6.5e
/SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1995.DAT:AAR66343 +  494.00  877.98  7.8e
/SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2001.DAT:AAG62159 +  492.50  863.37  1.2e

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2001.DAT:AAB36206

seq_documentation_block:
ID   AAB36206 standard; protein; 473 AA.
XX
AC   AAB36206;
XX
DT   15-FEB-2001 (first entry)
DE   Human immune system associated protein HISAP-4.
XX
KW   Human; immune system associated protein; HISAP-4; immune disorder;
KW   infection; autoimmune disease; cancer.
XX
OS   Homo sapiens.
XX
PN   US6135941-A.
XX
PD   24-OCT-2000.
XX
PF   27-MAR-1998;   98US-0049672.
XX
PR   27-MAR-1998;   98US-0049672.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
PI   Hillman JL, Au-Young J;
XX
DR   WPI; 2001-030926/04.
DR   N-PSDB; AAC66522.
XX
PT   New human immune system associated proteins (HISAP) and polynucleotides
PT   encoding the HISAP, useful for diagnosing, treating or preventing
PT   immune or cell proliferative disorders or infections -
XX
PS   Claim 1; Column 53-56; 54pp; English.
XX
CC   The present invention provides the coding and protein sequences for a
CC   number of human immune system associated proteins (HISAPs). These can be
CC   used in the diagnosis and treatment of various autoimmune disorders,
CC   infections and cell proliferation diseases. The diseases include AIDS,
CC   adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC   Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC   gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC   erythematosus, arteriosclerosis, cirrhosis and cancer.
XX
SQ   Sequence   473 AA;

alignment_scores:
Quality:             559.00        Length:            144
Ratio:               4.333         Gaps:              3
Percent Similarity:  89.583        Percent Identity:  78.472

alignment_block:
US-09-019-441-2 x AAB36206

Align seg 1/1  to: AAB36206  from: 1  to: 473

  1 ATGAAACACCTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT   50
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  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
    |||||||||||||||||||||||||||||||::|||||||:::|||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProVa  34

score_list:

| Sequence | Strd | Orig | ZScore | EScore | Len | Documentation |
|---|---|---|---|---|---|---|
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| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2000.DAT:AAY56728 | + | 558.00 | 992.70 | 2.7e-47 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1997.DAT:AAW14927 | + | 555.50 | 976.63 | 6.4e-47 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1997.DAT:AAW14925 | + | 555.50 | 976.63 | 6.4e-47 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1997.DAT:AAW14926 | + | 552.50 | 982.93 | 9.5e-47 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1997.DAT:AAW32477 | + | 552.50 | 982.93 | 9.5e-47 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1998.DAT:AAW43430 | + | 552.50 | 982.86 | 9.6e-47 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1993.DAT:AAR31948 | + | 550.50 | 967.50 | 2.0e-46 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1997.DAT:AAW01822 | + | 550.50 | 967.50 | 2.0e-46 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1998.DAT:AAW63765 | + | 548.50 | 975.84 | 2.4e-46 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1997.DAT:AAW35284 | + | 548.50 | 975.84 | 2.4e-46 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1997.DAT:AAW14922 | + | 548.50 | 975.84 | 2.4e-46 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1998.DAT:AAW53988 | + | 544.00 | 955.65 | 9.1e-46 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2001.DAT:AAB90607 | + | 542.50 | 965.11 | 9.4e-46 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1998.DAT:AAW57446 | + | 542.50 | 952.02 | 1.3e-45 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2000.DAT:AAY96290 | + | 539.50 | 959.67 | 1.9e-45 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1995.DAT:AAR66732 | + | 536.00 | 953.48 | 4.2e-45 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2000.DAT:AAY99556 | + | 534.00 | 949.90 | 6.6e-45 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2000.DAT:AAY82628 | + | 530.00 | 930.22 | 2.3e-44 | | |
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| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2000.DAT:AAB26884 | + | 526.00 | 923.69 | 5.6e-44 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1996.DAT:AAR93553 | + | 524.50 | 920.99 | 7.9e-44 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1997.DAT:AAW01818 | + | 524.50 | 920.99 | 7.9e-44 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1998.DAT:AAW63761 | + | 521.00 | 926.86 | 1.3e-43 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2000.DAT:AAY64677 | + | 520.50 | 913.96 | 2.0e-43 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2000.DAT:AAY44721 | + | 519.50 | 923.76 | 1.9e-43 | | |
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| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1995.DAT:AAR66348 | + | 514.00 | 915.88 | 6.3e-43 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1993.DAT:AAR42689 | + | 513.00 | 915.88 | 7.9e-43 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1995.DAT:AAR66346 | + | 513.00 | 913.92 | 7.9e-43 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1995.DAT:AAR66329 | + | 510.00 | 908.72 | 1.6e-42 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1995.DAT:AAR66298 | + | 508.50 | 903.23 | 2.4e-42 | | |
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| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2000.DAT:AAY56713 | + | 505.00 | 898.03 | 5.4e-42 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1995.DAT:AAY64676 | + | 504.50 | 897.34 | 5.7e-42 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1997.DAT:AAW24536 | + | 498.50 | 886.12 | 2.3e-41 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2000.DAT:AAY56706 | + | 497.00 | 883.79 | 3.2e-41 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2000.DAT:AAY56707 | + | | | | | |

CC    antibody.
XX
SQ    Sequence    141 AA;

alignment_scores:
        Quality:    558.00        Length:    142
        Ratio:    4.394        Gaps:    2
Percent Similarity:  89.437    Percent Identity: 77.465

alignment_block:
US-09-019-441-2 x AAY56728

Align seg 1/1    to: AAY56728    from: 1    to: 141

  1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGCAGCTCCCAGATGGGT  50
    |||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa  17

 51 CCTGTCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
    ||||||||||||||||||||||||:::||||||||||||||||||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyValValLysProS  34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT  150
    |||||||||||||||||||||||||::||||||||::::...||
 34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerPhe...Ser  49

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGACTGGAGTG  200
    ::::::||||||||||||||||||||||||||||||||||||||||||||
 50 ThrTyrTyrTrpTrpAsnTrpIleArgGlnProProGlyLysGlyLeuGluTr  66

201 GATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACACCCGTCCC  250
    ||||||    ||::::||::||    ||||||        ||||||||||
 66 pIleGlyTyrIleGlyGlyGlyGlyAlaArgProAsnTyrAsnSerSerL  83

251 TCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC  300
    |||||||||        ::||||    |||:::||||||||||||||||||
 83 euLysSerArgIleThrLeuSerLeuLysLeuSerAlaSerLysAsnGlnPheSer  99

301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC  350
    ||||||||||||||||::||||||||||||||||||||||||||||||||
100 LeuAsnLeuAsnSerValThrAlaAlaAspThrAlaValTyrTyrCysAl  116

351 CAGAGATTGGGCCCCAAATAGCTGGAACA...ACGCTAGGCTTCTGGGGCC  397
    |||||||        ||::::::    ...:::::::    ||||||||||
116 aArgAspArgGlyTyrGlyAlaSerAsnAspAlaPheAspPheTrpGlyG  133

398 AGGGAGTCCTGTCCACCGTCTCCTCA  423
    |||::::    |||||||||||||||
133 lnGlyLeuArgValThrValSerSer  141

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1997.DAT:AAW14927

seq_documentation_block:
ID    AAW14927 standard; protein; 467 AA.
XX
AC    AAW14927;
XX
DT    18-OCT-1997 (first entry)
XX
DE    Human gamma-4PE heavy chain.
XX
KW    CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW    cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW    leukaemia; lymphoma; graft-versus-host disease; asthma;
KW    transplant rejection; HIV; therapy; CE9 gamma 4PE.
XX
OS    Homo sapiens.
XX
FH    Key    Location/Qualifiers
FT    Misc-difference 248
FT    /note= "site of S229P mutation"
FT    Misc-difference 255

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101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT  150
    |||||||||||||||||||||||||||||||||||||||||::::::||
 34 erGluThrLeuSerLeuThrCysAlaValSerGlySerIleThrSer  50

151 AGTAAC...TGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGACTGGA  197
    ::::::    ||::::||||||||||||||||||||||||||||||||||
 51 GlyGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGl  67

198 GTGGATTGGACGTATCTCTGGTGGTGGTGGGCCACCAACTACAACCCGT  247
    ||||||||    ||    ||::::||    ||||||||||||||||||||
 67 uTrpIleGlyTyrIleTyrTyrSer...GlySerThrLeuTyrAsnProS  83

248 CCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC  297
    |||||||||||||||||||||||||||||||||||||||||||||||||
 83 erLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPhe  99

298 TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTG  347
    |||||||||||||||||::::||||||||||||||||||||||||||||
100 SerLeuAsnLeuAsnSerValThrAlaAlaAspThrAlaValTyrTyrCy  116

348 TGCCAGAGATTGGGCCCCAAATAGCTGGAACAACCGTAGGCTTC......T  391
    |||||||||    :::    :::    ||    :::::||    |
116 sAlaArgAspTrpAlaProLysTrpLeuArgGlyLeuAsnTyrGlyMetAspValT  133

392 GGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA  423
    ||||||||||||::::||||||||||||||||
133 rpGlyGlnGlyThrLeuValThrValSerSer  143

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2000.DAT:AAY56728

seq_documentation_block:
ID    AAY56728 standard; protein; 141 AA.
XX
AC    AAY56728;
XX
DT    15-FEB-2000 (first entry)
XX
DE    Amino acid sequence of Cynomologous VH cDNA clone 2-5.
XX
KW    Complementary determining region; antibody; primate; immunogenicity;
KW    Old World ape; Old World monkey; antigen-binding affinity.
XX
OS    Macaca cynomolgus.
XX
PN    WO955369-A1.
XX
PD    04-NOV-1999.
XX
PF    28-APR-1999;    99WO-US09131.
PR    28-APR-1998;    98US-0083367.
XX
PA    (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI    Taylor AH;
XX
DR    WPI; 2000-023265/02.
DR    N-PSDB; AAZ39331.
XX
PT    Antibodies containing donor complementarity determining regions and
PT    non-human primate acceptor frameworks, having reduced immunogenicity in
PT    humans -
XX
PS    Example 3; Page 79; 123pp; English.
XX
CC    The invention provides an antibody (Ab) comprising donor CDRs
CC    (complementarity determining regions) derived from a non-human antigen-
CC    specific donor antibody, and an acceptor framework from a non-human
CC    primate. The Abs are prepared by grafting CDRs from a non-human antigen-
CC    specific donor antibody onto homologous Old World ape or monkey acceptor
CC    frameworks. The Abs have reduced immunogenicity and are better tolerated
CC    in humans (because of the close similarity between the human and primate
CC    proteins), but retain the full antigen-binding affinity of the donor

```
 84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100

301 CTGAACCTGAACTCTGACCGCCGGGACACGGCCGTGTATTACTGTGC 350
    |||::||||:||:::|||||||||||||||||||||||||||||||||
101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 117

351 CAGAGAT...............TGGGCCAAATAGCTGGAACAACGC 382
    |  :::                 |||
117 aSerAsnIleLeuLysTyrLeuHisTrp.................L 127

383 TAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCCTCA 423
    ||  ::||||||||||||||||||||||||||||||||||
127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSerSer 140
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seq_name: /SID1/gcgdata/hold-geneseq/geneseq-embl/AA1997.DAT:AAW14925

seq_documentation_block:
ID   AAW14925 standard; Protein; 467 AA.
XX
AC   AAW14925;
XX
DT   18-OCT-1997  (first entry)
XX
DE   Human gamma-4 heavy chain.
XX
KW   CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW   cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW   leukaemia; lymphoma; graft-versus-host disease; asthma;
KW   transplant rejection; HIV; therapy; CE9 gamma 4.
XX
OS   Homo sapiens.
XX
PN   WO9709351-A1.
XX
PD   13-MAR-1997.
XX
PF   05-SEP-1996;  96WO-US14324.
XX
PR   06-SEP-1995;  95US-0523894.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Hanna N, Newman RA, Reff ME;
XX
DR   WPI; 1997-201913/18.
DR   N-PSDB; AAT62868.
XX
PT   Chimeric antibody comprising monkey variable domains and human
PT   constant domains - affects CD4-mediated immune functions, esp.
PT   useful for treatment of autoimmune disease, e.g. rheumatoid
PT   arthritis
XX
PS   Claim 6; Page 82-84; 155pp; English.
XX
CC   3 Polypeptides (AAW14925-27) respectively comprise the heavy chain
CC   regions of human gamma-4, gamma-4E carrying an L236E mutation in
CC   the hinge region, and gamma-4PE carrying L236E and S229P mutations.
CC   They can be incorporated into novel monoclonal and chimeric
CC   antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in
CC   which the human IgG4 Fc binding domain framework is combined with
CC   the antigen binding domains (see also AAW14922-23) of macaque anti-
CC   human CD4 monoclonal antibody E9.1. These antibodies show high
CC   affinity to human CD4, have little or no immunogenicity in humans
CC   and show reduced or absence of effector function. They can be used
CC   to treat autoimmune diseases such as rheumatoid arthritis.
XX
SQ   Sequence   467 AA;

alignment_scores:
          Quality:   555.50             Length:    147
            Ratio:     4.480              Gaps:      2
Percent Similarity:  84.354    Percent Identity:  74.830
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FT                /note= "site of L236E mutation"
XX
PN   WO9709351-A1.
XX
PD   13-MAR-1997.
XX
PF   05-SEP-1996;  96WO-US14324.
XX
PR   06-SEP-1995;  95US-0523894.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Hanna N, Newman RA, Reff ME;
XX
DR   WPI; 1997-201913/18.
DR   N-PSDB; AAT62870.
XX
PT   Chimeric antibody comprising monkey variable domains and human
PT   constant domains - affects CD4-mediated immune functions, esp.
PT   useful for treatment of autoimmune disease, e.g. rheumatoid
PT   arthritis
XX
PS   Claim 6; Page 91-93; 155pp; English.
XX
CC   3 Polypeptides (AAW14925-27) respectively comprise the heavy chain
CC   regions of human gamma-4, gamma-4E carrying an L236E mutation in
CC   the hinge region, and gamma-4PE carrying L236E and S229P mutations.
CC   They can be incorporated into novel monoclonal and chimeric
CC   antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in
CC   which the human IgG4 Fc binding domain framework is combined with
CC   the antigen binding domains (see also AAW14922-23) of macaque anti-
CC   human CD4 monoclonal antibody E9.1. These antibodies show high
CC   affinity to human CD4, have little or no immunogenicity in humans
CC   and show reduced or absence of effector function. The gamma-4E and
CC   -4PE mutations confer activity enhanced stability and eliminate
CC   depleting activity. The antibodies can be used to treat autoimmune
CC   diseases such as rheumatoid arthritis.
XX
SQ   Sequence   467 AA;

alignment_scores:
          Quality:   555.50             Length:    147
            Ratio:     4.480              Gaps:      2
Percent Similarity:  84.354    Percent Identity:  74.830

alignment_block:
US-09-019-441-2 x AAW14927      ..

Align seq 1/1  to: AAW14927   from: 1  to: 467

  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT 50
    |||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuLeuValAlaAlaProArgTrpVa 17

 51 CCTGTGCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    |||||||||::||||||||||||||||||||||||||||:::||||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    |||||||||||||||||||||||::|||||||||||||:::|||:::
 34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly 50

151 AGTAACTGGTGGACCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTG 200
    |||||||||||||||||||||||||||||||||||||||||||||||||
 51 SerAsnTrpTrpThrTrpIleArgGlnSerProGlyLysGlyLeuGluTr 67

201 GATTGGACGTATCTCTGGTAGTGGTGGGACGCACCAACTACAACCCGTCC 250
    |||||||| |||||||||||:::|||||:::||||||||||||||||||
 67 pIleGlyTyrIleTyrGlySerGlyGlyThrHisTyrAsnProSerL 84

251 TCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    ||:::::||||| |||||| ||||||||||||||||||||||
```

```
alignment_block:
US-09-019-441-2 x AAW14925

Align seg 1/1  to: AAW14925  from: 1  to: 467

   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGTTGTGGCAGCTCCCAGATGGGT  50
     |||||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetLysHisLeuTrpPhePheLeuLeuLeuLeuLeuValAlaAlaProArgTrpVa  17

  51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
     |||||||||:::||||||||||||||||||||||||||||:::||||||||
  17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyValLysProS  34

 101 CGGAGACCCCTGTCCCTCACCTGCGCTCTCTGTGGCTCTGTCAGCAGT  150
     ||||||||||||||||||||:::|||||||||||||:::|||::||
  34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly  50

 151 AGTAACTGGTGGAACTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTG  200
     :::  ::||:: |||||||||  |||||||||||||||||||||||||
  51 AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr  67

 201 GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCCGTCCC  250
     ||||||  ||| ||||||||||||||||||||||||||||||||||||
  67 pIleGlyTyrIleTyrGlyGlyGlyGlyThrAsnTyrAsnProSerL  84

 251 TCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC  300
     ||:|::::||||| |||||||  ||||||||||||||||||||||||
  84 euAsnAsnArgValSerIleAspThrSerLysAsnLeuValSerSer  140

 301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC  350
     ||:|::||:|||||||||||||||||||||||||||||||||||||||
 101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl  117

 351 CAGAGAT.................TGGGCCCAAATAGCTGGAACAACGC  382
     | :::              |||
 117 aSerAsnIleLeuLysTyrLeuHisTrp..............L  127

 383 TAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA  423
     ||:||||||||||||||||||||||||||||||||||||||
 127 euLeuTyrTrpGlyGlnGlyGlyValLeuValThrValSerSer  140
```

```
alignment_scores:
    Quality:  555.50                    Length:     147
    Ratio:      4.480                    Gaps:         2
Percent Similarity: 84.354    Percent Identity: 74.830

alignment_block:
US-09-019-441-2 x AAW14926

Align seg 1/1  to: AAW14926  from: 1  to: 467

   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGTTGTGGCAGCTCCCAGATGGGT  50
     |||||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetLysHisLeuTrpPhePheLeuLeuLeuLeuLeuValAlaAlaProArgTrpVa  17

  51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
     |||||||||:::||||||||||||||||||||||||||||:::||||||||
  17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyValLysProS  34

 101 CGGAGACCCCTGTCCCTCACCTGCGCTCTCTGTGGCTCTGTCAGCAGT  150
     ||||||||||||||||||||:::|||||||||||||:::|||::||:
  34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly  50

 151 AGTAACTGGTGGAACTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTG  200
     :::  ::||:: |||||||||  |||||||||||||||||||||||||
  51 AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr  67

 201 GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCCGTCCC  250
     ||||||  ||| ||||||||||||||||||||||||||||||||||||
  67 pIleGlyTyrIleTyrGlyGlyGlyGlyThrAsnTyrAsnProSerL  84

 251 TCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC  300
     ||:|::::||||| |||||||  ||||||||||||||||||||||||
  84 euAsnAsnArgValSerIleAspThrSerLysAsnLeuPheSer  100

 301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC  350
     ||:|::||:|||||||||||||||||||||||||||||||||||||||
 101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl  117

 351 CAGAGAT.................TGGGCCCAAATAGCTGGAACAACGC  382
     | :::              |||
 117 aSerAsnIleLeuLysTyrLeuHisTrp..............L  127

 383 TAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA  423
```

```
          ||    ::|||||||||||||||||||||||||||||||
      127 euLeuTyrTrpGlyGlyValLeuValThrValSerSer 140

seq_name: /SIDS1/gcgdata/hold-geneseqp-embl/AA1997.DAT:AAW32477

seq_documentation_block:
ID   AAW32477 standard; Protein; 140 AA.
XX
AC   AAW32477;
XX
DT   16-JAN-1998  (first entry)
XX
DE   Anti-CD4 cynomolgus monkey immunoglobulin heavy chain variable region.
XX
KW   Anti-CD4 antibody; cynomolgus monkey; immunoglobulin; Ig;
KW   chimpanzee; chimeric antibody; human therapy; Old World monkey;
KW   antigen binding region; tumour.
XX
OS   Macaca fascicularis.
XX
PN   US5658570-A.
XX
PD   19-AUG-1997.
XX
PF   25-JUL-1991;  91US-0735064.
XX
PR   10-JUL-1992;  92US-0912292.
PR   25-JUL-1991;  91US-0735064.
PR   23-MAR-1992;  92US-0856281.
PR   25-JAN-1995;  95US-0379072.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Hanna N, Newman RA, Raab RW;
XX
DR   WPI; 1997-424183/39.
DR   N-PSDB; AAT91564.
XX
PT   Chimeric antibodies for human therapy - comprising human or
PT   chimpanzee immunoglobulin constant region and an Old World monkey
PT   antigen-binding region
XX
PS   Example 3; Fig 13; 46pp; English.
XX
CC   A new chimeric antibody (Ab) has been developed comprising a human or
CC   chimpanzee immunoglobulin (Ig) constant region and an Old World monkey
CC   antigen (Ag)-binding region. The present sequence represents an anti-CD4
CC   cynomolgus monkey Ig heavy chain variable region. An anti-CD4 antibody
CC   (Ab) comprising the light- and heavy-chain variable regions encoded by
CC   DNA corresponding to the present sequence, and that of AAT91565, is also
CC   new. The Abs are useful for human therapy, especially of tumours. Old
CC   world monkeys are sufficiently different from humans to allow Abs
CC   against human Ags, even relatively conserved Ags such as CD4 and CD54,
CC   to be raised in these monkeys, and are sufficiently similar to humans to
CC   avoid host anti-Ab immune responses when the Abs are introduced into
CC   humans.
XX
SQ   Sequence  140 AA;

alignment_scores:
     Quality:    552.50         Length:      147
     Ratio:        4.456         Gaps:          2
Percent Similarity: 84.354   Percent Identity: 74.150

alignment_block:
US-09-019-441-2 x AAW32477    ..

Align seg 1/1  to: AAW32477   from: 1  to: 140

    1 ATGAAACACCTGTGTTCTTCCTCCTCGGTGGCAGCTCCCAGATGGT 50
      |||||||||||||||||||||||||||||||||||||||||||||||
    1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa 17
```

```
   51 CCTGTCCCAGCTGCAGCTGCGAGGAGTCGGGCCCAGGAGTGTGAAGCCTT 100
      |||||||::::|||||||||||||||||::|||||||:::||||||||||
   17 lLeuSerGlnValGlnLeuGlnLeuGlnAlaGlyProGlyLeuValLysProS 34

  101 CGGAGACCCGTGTCCCTCACCTGGCTGTCTGGTGGCTCTGTCAGCAGT 150
      |||||||||||||::|||||||::|||||||||||||||::||||::::
   34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly 50

  151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
      ::::  ::::||| |||||||||||   |||||||||||||||||||||||
   51 AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr 67

  201 GATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACAACCCGTCCC 250
      |||||| ||| |||::::||||||||||::||||||||||||||||||||
   67 pIleGlyTyrIleTyrGlySerGlyGlyGlyThrAsnTyrAsnProSerL 84

  251 TCAAGAGTCGAGTCATCATTTCACAGACACGTCCAAGAACCAGTTCTCC 300
      |:::::||||| |||||| ||||||||||||| ||||||  |||||
   84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100

  301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
      |||::||::|||||||||||||||||||||||||||||||||||||||||
  101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 117

  351 CAGAGAT.............TGGGCCCAAATAGCTGGAACAACGC 382
      | :::                  |||
  117 aSerAsnIleLeuLysTyrLeuHisTrp................L 127

  383 TAGGCTTCTGGGGCCAGGAGTCCTGTCACCGTCCTCCTCA 423
      ||  ::|||||||||||||||||||||||||||||||||||
  127 euLeuTyrTrpGlyGlyValLeuValThrValSerSer 140
```

seq_name: /SIDS1/gcgdata/hold-geneseqp-embl/AA1998.DAT:AAW43430

```
seq_documentation_block:
ID   AAW43430 standard; Protein; 140 AA.
XX
AC   AAW43430;
XX
DT   05-MAY-1998  (first entry)
XX
DE   Monkey anti-CD4 heavy chain variable region protein sequence.
XX
KW   Primer; PCR; amplification; leader sequence; human; monkey; baboon;
KW   macaque; immunoglobulin; heavy chain variable region; chimpanzee; hybrid;
KW   lymphoma; AIDS; autoimmune disease; inflammatory disease; transplant;
KW   tumour; antibody.
XX
OS   Macaca cynomolgus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /note= "signal peptide"
FT   Protein         20..140
FT                   /note= "mature protein"
XX
PN   US5693780-A.
XX
PD   02-DEC-1997.
XX
PF   07-JUN-1995;  95US-0481869.
XX
PR   10-JUL-1992;  92US-0912292.
PR   25-JUL-1991;  91US-0735064.
PR   23-MAR-1992;  92US-0856281.
PR   25-JAN-1995;  95US-0379072.
PR   07-JUN-1995;  95US-0481869.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Hanna N, Newman RA, Raab RW;
XX
```

DR   WPI; 1998-031820/03.
DR   N-PSDB: AAV05695.
XX
PT   Nucleic acid encoding hybrid antibody - comprising monkey
PT   antigen-binding region and human or chimp constant region
XX
PS   Example 3; Fig 13; 46pp; English.
XX
CC   This sequence represents the heavy chain variable region from an
CC   anti-human CD4 immunoglobulin raised in cynomolgus monkeys. The coding
CC   sequence was PCR amplified and used in the construction of a recombinant
CC   antibody comprising: (i) an Old World monkey Ig antigen-binding region;
CC   and (ii) a human or chimpanzee Ig constant region. The hybrid antibodies
CC   can be used as passive or active therapeutic agents against human
CC   diseases, e.g. B-cell lymphoma, AIDS, autoimmune and inflammatory
CC   diseases, transplant rejection or tumours, or for producing therapeutic
CC   and diagnostic conjugates. Although evolutionary distant monkeys are
CC   used to raise antibodies against human antigens, they are sufficiently
CC   similar that they produce antibodies similar to human antibodies, such
CC   that when the monkey antibodies are introduced into humans, no host
CC   anti-antibody response is stimulated.
XX
SQ   Sequence   140 AA;

alignment_scores:
        Quality:  552.50            Length:    147
          Ratio:    4.456             Gaps:      2
Percent Similarity:  84.354     Percent Identity: 74.150

alignment_block:
US-09-019-441-2 x AAW43430

Align seg 1/1  to: AAW43430  from: 1  to: 140

   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGTGGCAGCTCCCAGATGGGT  50
     |||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

  51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
     |||||||||||||||||||||||::::|||||||||||||:::|||||||
  17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyValValLysProS  34

 101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCGTCAGCAGT 150
     ||||||||||||||||||||||:::::|||||||||||::||:|||
  34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly  50

 151 AGTAACTGGTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
     :::|||  ||||||||||  |||||||||||||||||||||||||
  51 AspTyrTyrTrpTrpSerTrpIleArgGlnSerProGlyLysGlyLeuGluTr  67

 201 GATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTACAACCCGTCCC 250
     ||||| ||| |||::||||||||||||||||||||||||||||||||||||
  67 pIleGlyTyrIleTyrGlySerGlyGlyGlyHisTyrAsnProSerL  84

 251 TCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
     ||:::::|||||  ||||| |||||||||||||||||||  |||||
  84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100

 301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
     ||  :::|||||||||||||||||||||||||||||||||||||||||
 101 LeuLysLeuAsnSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 117

 351 CAGAGAT..........TGGGCCCAAATAGCTGGAACAACGC 382
     |   :::       |||
 117 aSerAsnIleLeuLysTyrLeuHisTrp...............L 127

 383 TAGGCTTCTGGGGGCCAGGAGTCCTGGTCACCGTCCTCCTCA 423
     ||  ::::|||||||||||||||||||||||||||||||||||
 127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSerSer 140

---

seq_documentation_block:
ID   AAR31948 standard; Protein; 141 AA.
XX
AC   AAR31948;
XX
DT   08-JUN-1993  (first entry)
XX
DE   Anti-CD4 VH peptide.
XX
KW   PCR; amplify; clone; heavy; light; chain; variable; region; lambda;
KW   immortalised B-cell; vector; TCAE 6; human; IgG1; constant; antigen;
KW   recombinant; antibody; chimpanzee; Ig; Ag; old world monkey; eczema;
KW   immunoglobulin; therapeutic; rheumatoid arthritis.
XX
OS   Simian sp.
XX
PN   WO9302108-A.
XX
PD   04-FEB-1993.
XX
PF   24-JUL-1992;      92WO-US06194.
XX
PR   25-JUL-1991;      91US-0735064.
PR   23-MAR-1992;      92US-0856281.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Hanna N,  Newman RA,   Raab RW;
XX
DR   WPI; 1993-058729/07.
DR   N-PSDB: AAQ35903.
XX
PT   Recombinant antibodies including Old World monkey portion and
PT   human portion - used for treatment of auto-immune diseases,
PT   infectious diseases, AIDS, tumours, diabetes, proliferative
PT   diseases, intestinal inflammations and allergies, etc.
XX
PS   Disclosure; Page 53-54; 92pp; English.
XX
CC   The sequences given in AAR31948-49 represent the Simian anti CD4 VH
CC   and V-lambda sequences respectively. The DNA encoding these peptides
CC   were derived using the primer sequences given in AAQ35901-02. The
CC   amplification products were sequentially cloned into the vector
CC   TCAE 6, which contains human IgG1 and human lambda constant regions.
CC   The amplified sequences could be used in the production of a
CC   recombinant antibody, comprising a human, chimpanzee or old world
CC   monkey immunoglobulin (Ig) constant region and an antigen (Ag)
CC   binding portion of an old world monkey Ig variable region, where the
CC   old world monkeys may be the same or different. The recombinant
CC   antibody may be used as a therapeutic agent for the treatment of
CC   rheumatoid arthritis, eczema and immunological disorders.
XX
SQ   Sequence   141 AA;

alignment_scores:
        Quality:  552.50            Length:    147
          Ratio:    4.456             Gaps:      2
Percent Similarity:  84.354     Percent Identity: 74.150

alignment_block:
US-09-019-441-2 x AAR31948

Align seg 1/1  to: AAR31948  from: 1  to: 141

   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGTGGCAGCTCCCAGATGGGT  50
     |||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  18

  51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
     |||||||||||||||||||||||::::|||||||||||||:::|||||||
  18 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyValValLysProS  35

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:AAR31948

```
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of the primatised
CC   antibody in e.g. CHO cells.  Primatised 7C10 and 7B6 anti-B7.1
CC   antibodies have also been produced (see also AAW01817-20).  The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence   476 AA;

alignment_scores:
         Quality:  550.50              Length:      153
         Ratio:      4.476             Gaps:          2
Percent Similarity:  80.392      Percent Identity: 71.242

alignment_block:
US-09-019-441-2 x AAW01822

Align seg 1/1  to: AAW01822  from: 1  to: 476

    1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT 50
      ||||||||||||||||||||||||||||||||||::|||:::||
    1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa 17

   51 CCTGTCCCAGCTGCAGCTGCGAGGAGTCGGCCCCAGGAGTGGTGAAGCCTT 100
      ||||||||||:||||||||||||||||||||||:::||||||
   17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34

  101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
      |||||||||||||||||||||||||::||:::||
   34 erGluThrLeuSerLeuThrCysAlaValSerGlyGlySerIleSerGly 50

  151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
      |||   ||||||:|||||||||||||||||||
   51 GlyTyrTyrGlyTrpGlyTrpIleArgGlnProProGlyLysGlyLeuGluTr 67

  201 GATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACAACCCGTCCC 250
      ||||   ||  :::|||||:::|| ||  ||||||||||||||||
   67 pIleGlySerPheTyrSerSerGlyAsnThrTyrTyrAsnProSerL 84

  251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTCTCC 300
      ||||||||:::|||  ||||| |||||||||||||||||||||
   84 euLysSerGlnValThrIleSerThrArgThrSerLysAsnGlnPheSer 100

  301 CTGAACCTGAACTCTGTGACCGCCGGACACGGCCGTGTATTACTGTGC 350
      |||:::||||||:||||||||||||||||||||||||
  101 LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValThrTyrTyrCysVa 117

  351 CAGAGAT..............................TGGGCCC 364
      :|||||                              |||
  117 lArgAspArgLeuPheSerValValGlyMetValTyrAsnTrpPheA 134

  365 AAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACC 414
      ||||:::|||  ||||||||||  |||||||||||||||||
  134 spVal..................TrpGlyProGlyLeuValThr 143

  415 GTCTCCTCA 423
      |||||||||
  144 ValSerSer 146
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:AAW63765

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  101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
      |||||||||||||||||||||||||||:::||:::||:||:
   35 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly 51

  151 AGTAACTGGTGGACCTGGATCTCTGCCCCAGGGAAGGGACTGGAGTG 200
      :::  ::||||  ||||||:||||||||||||
   52 AspTyrTyrTrpPheTrpIleSerGlnArgProGlyLysGlyLeuGluTr 68

  201 GATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACAACCCGTCCC 250
      |||||   ||  :::|||||:::|| ||  ||||||||||||||||||
   68 pIleGlyTyrIleTyrGlyGlyGlyThrAsnTyrAsnProSerL 85

  251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
      ||:::::||::|||  ||||| ||||||||||||||||:   ||||
   85 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 101

  301 CTGAACCTGAACTCTGTGACCGCCGGACACGGCCGTGTATTACTGTGC 350
      |||::::||||:||||||||||||||||||||||||||
  102 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValThrTyrTyrCysAl 118

  351 CAGAGAT...................TGGGCCAAATAGCTGGAACAACGC 382
      :||                       ||
  118 aSerAsnIleLeuLysTyrLeuHisTrp.................L 128

  383 TAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 423
      ||  :::|||||||||||||||||||||||||||
  128 euLeuTyrTrpGlyGlnGlyValLeuValThrValSerSer 141
```

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:AAW01822

```
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation.
XX
OS   Macaca fascicularis.
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997;   97WO-US19906.
XX
PR   08-NOV-1996;   96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   N-PSDB; AAV35489.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 5b; 87pp; English.
XX
CC   This sequence represents a primatized form of the antibody 16C10 heavy
CC   chain from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence 476 AA;

alignment_scores:
    Quality:    550.50           Length:       153
    Ratio:        4.476          Gaps:           2
Percent Similarity: 80.392       Percent Identity: 71.242

alignment_block:
US-09-019-441-2 x AAW63765   ..

Align seg 1/1   to: AAW63765   from: 1   to: 476

  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT 50
    |||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa 17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    ||||||||||::|||||||||||||||||||||||||::|||||||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyValLysProS 34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    |||||||||||||||||||||||||||||||||||::|||::|||:::||
 34 erGluThrLeuSerLeuThrCysAlaValSerGlyGlySerIleSerGly 50
```

```
151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
    |||  |||||||||||||||||||||||||||||||||||||||||||||
 51 GlyTyrGlyTrpGlyTrpIleArgGlnProProGlyLysGlyLeuGluTr 67

201 GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCCGTCCC 250
    ||||||  :::   ::||||||:::::||     :|||||||||||:|||
 67 pIleGlySerPheTyrSerSerSerGlyAsnThrTyrTyrAsnProSerL 84

251 TCAAGAGTGGAGTCATCATTCACAAGAACACGTCCAAGAACCAGTTCTCC 300
    |||||||||:::||| ||||| |||||||||||| |||||||||||||||
 84 euLysSerGlnValThrIleSerThrArgAspThrSerLysAsnGlnPheSer 100

301 CTGAACCTGAACTCTGTGACCGCCGCGACACGGCCGTGTATTACTGTGC 350
    |||:::||||||:::|||::::||||||||||||||||||||||||:::|
101 LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyrTyrCysVa 117

351 CAGAGAT..............................TGGGCCC 364
    :||||||                            ||||||
117 lArgAspArgLeuPheSerValValGlyMetValTyrAsnAsnTrpPheA 134

365 AAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACC 414
    ::::                   |||||  |||||||||||||||||||||
134 spVal.......................TrpGlyProGlyValLeuValThr 143

415 GTCTCCTCA 423
    |||||||||
144 ValSerSer 146

seq_name:  /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1997.DAT:AAW35284

seq_documentation_block:
ID   AAW35284 standard; protein; 139 AA.
XX
AC   AAW35284;
XX
DT   18-FEB-1998  (first entry)
XX
DE   Monkey anti-human CD4 antibody heavy chain variable region.
XX
KW   Old World monkey; immunoglobulin; Ig; heavy chain; CD4;
KW   variable region; chimeric antibody;
KW   B cell lymphoma; infectious disease; AIDS; autoimmune disease;
KW   inflammatory disease; transplant rejection; imaging reagent;
KW   vaccine; immunogen; immunotherapy; anti-idiotypic response;
KW   immunosuppression; treatment; prevention; proliferative disease;
KW   hyperproliferative disease; immunologically mediated disease;
KW   rheumatoid arthritis; lupus erythematosus;
KW   systemic lupus erythematosus; SLE; Hashimoto's thyroiditis;
KW   multiple sclerosis; myasthenia gravis; type 1 diabetes; uveitis;
KW   nephrotic syndrome; psoriasis; atopical dermatitis;
KW   contact dermatitis; eczematous dermatitides; seborrheic dermatitis;
KW   Lichen planus; Pemplugus; bullous pemphigus; Epidermolysis bullosa;
KW   urticaria; angioedemas; vascullitides; erythema;
KW   cutaneous eosinophilia; alopecia areata;
KW   reversible obstructive airways disease; intestinal inflammation;
KW   intestinal allergy; Coeliac disease; proctitis; eosinophilia;
KW   gastroenteritis; mastocytosis; Crohn's disease; ulcerative colitis;
KW   food related allergy; migraine; rhinitis; eczema;
KW   non-immunogenic.
XX
OS   Cebus apella.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= sig_peptide
FT   Peptide         20..139
FT                   /label= mat_peptide
XX
PN   US5681722-A.
XX
PD   28-OCT-1997.
XX
PF   07-JUN-1995;   95US-0478039.
```

```
  1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaAlaProArgTrpVa  17

 51 CCTGTCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGTGAAGCCTT   100
    ||||||||::||||||||::||||||||:::||||||:::|||||||||
 17 lLeuSerGlnValGlnLeuGlnGluAlaGlyProGlyLeuValLysProS  34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    |||||||||||||||||||||||::||||||||::|||||:::||::::|
 34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly  50

151 AGTAACTGGTGGAGCTGGATCCGGCAGCCCCCAGGAAGGACTGGAGTG   200
    :::  :::||| ||||||||| ||||||| |||||:::||||||||||
 51 AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr  67

201 GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACACACCGTCC  250
    |||||| ||| |||||::||||||||||:::||||||||||||||||||
 67 pIleGlyTyrIleTyrGlySerGlyGlyGlyThrAsnTyrAsnProSerL  84

251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC  300,
    ||:||||||||| ||| || |||| ||||||||||||||| |||||||
 84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100

301 CTGAACCTGAACTCTGACCGCCCGGACGACACGGCCGTGTATTACTGTGC 350
    ||:::|||::||||||||||||||||||||||||||||||||||||||||
101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 117

351 CAGAGAT................TGGGGCCAAATAGCTGGAACAACGC   382
    |  :::|                || ||
117 aSerAsnIleLeuLysTyrLeuHisTrp...............L      127

383 TAGGCTTCTGGGCCAGGAGTCCTGGTCACCGTCTCC              420
    |  :::||||||||||||||||||||||||||||
127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSer            139
```

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1997.DAT:AAW14922

```
seq_documentation_block:
ID  AAW14922 standard; Protein; 139 AA.
XX
AC  AAW14922;
XX
DT  18-OCT-1997 (first entry)
XX
DE  Monkey anti-CD4 heavy chain variable domain.
XX
KW  CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW  cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW  leukaemia; lymphoma; graft-versus-host disease; asthma;
KW  transplant rejection; HIV; therapy; CE9.1.
XX
OS  Macaca cynomolgus.
XX
FH  Key           Location/Qualifiers
FT  Peptide       1..19
FT                /label= Sig_peptide
FT  Protein       20..120
FT                /label= Mat_protein
XX
PN  WO9709351-A1.
XX
PD  13-MAR-1997.
XX
PF  05-SEP-1996;  96WO-US14324.
XX
PR  06-SEP-1995;  95US-0523894.
XX
PA  (IDEC-) IDEC PHARM CORP.
XX
PI  Hanna N,  Newman RA,  Reff ME;
XX
DR  WPI: 1997-201913/18.
DR  N-PSDB; AAT62865.
XX
```

```
XX
PR  10-JUL-1992;  92US-0912292.
PR  25-JUL-1991;  91US-0735064.
PR  23-MAR-1992;  92US-0856281.
PR  25-JAN-1995;  95US-0379072.
PR  07-JUN-1995;  95US-0478039.
XX
PA  (IDEC-) IDEC PHARM CORP.
XX
PI  Hanna N,  Newman RA,  Raab RW;
XX
DR  WPI: 1997-535052/49.
DR  N-PSDB; AAT95167.
XX
PT  Production of humanised antibodies containing monkey variable region
PT  - used for the treatment of B cell lymphoma, autoimmune disease,
PT  inflammatory disease and infection, e.g. by HIV
XX
PS  Example 3; Columns 107-108; 84pp; English.
XX
CC  The present sequence is a monkey anti-human CD4 antibody
CC  heavy chain variable region, which was used in the development of
CC  a novel method for producing a chimeric antibody (Ab), comprising
CC  the variable region of an Old World monkey (OWM) Ab and the
CC  constant region of a human Ab. The method comprises amplifying DNA
CC  from the OWM using a primer complementary to the 5' leader sequence
CC  of the OWM Ab gene and fusing the resulting variable region coding
CC  sequence with a human constant region coding sequence.
CC  The chimeric Ab may be used as a passive or active therapeutic for
CC  B cell lymphoma, infectious, e.g. AIDS, autoimmune and inflammatory
CC  diseases and transplant rejection. The Ab can be used in its native
CC  form or as part of an Ab/chelate, Ab/drug or Ab/toxin complex.
CC  Additionally, a whole Ab, or a fragment (Fab2, Fab, Fv) may be used
CC  as an imaging reagent or as a potential vaccine or immunogen in
CC  active immunotherapy to generate anti-idiotypic responses.
CC  An anti-CD4 recombinant Ab, or a fragment can also be used to
CC  induce immunosuppression and can therefore be used to treat or
CC  prevent resistance to, or rejection of transplanted organs or
CC  tissues, autoimmune, inflammatory, proliferative and
CC  hyperproliferative diseases, cutaneous manifestations of
CC  immunologically mediated diseases (e.g. rheumatoid arthritis, lupus
CC  erythematosus, systemic lupus erythematosus, Hashimoto's
CC  thyroiditis, multiple sclerosis, myasthenia gravis, type 1
CC  diabetes, uveitis, nephrotic syndrome, psoriasis, atopical
CC  dermatitis, contact dermatitis and further eczematous dermatitides,
CC  seborrheic dermatitis, Lichen planus, Pemplugus, bullous pemphigus,
CC  Epidermolysis bullosa, urticaria, angioedemas, vasculitides,
CC  erythema, cutaneous eosinophilias, alopecia areata), reversible
CC  obstructive airways disease, intestinal inflammations and
CC  allergies (e.g. Coeliac disease, proctitis, eosinophilia
CC  gastroenteritis, mastocytosis, Crohn's disease and ulcerative
CC  colitis) and food related allergies (e.g. migraine, rhinitis and
CC  eczema).
CC  The Ab of the invention is non-immunogenic and therefore does not
CC  induce a human anti-Ab response. It also has a relatively long
CC  half-life and a full effector function with human cells and
CC  complement.
XX
SQ  Sequence  139 AA;
```

```
alignment_scores:
         Quality:   548.50               Length:   146
         Ratio:     4.459                Gaps:     2
Percent Similarity:  84.247   Percent Identity:  73.973

alignment_block:
US-09-019-441-2 x AAW35284   ..

Align seg 1/1  to: AAW35284  from: 1 to: 139

  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT  50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
PT   Chimeric antibody comprising monkey variable domains and human
PT   constant domains - affects CD4-mediated immune functions, esp.
PT   useful for treatment of autoimmune disease, e.g. rheumatoid
PT   arthritis
XX
PS   Claim 3; Page 76; 155pp; English.
XX
CC   2 Polypeptides (AAW14922 and AAW14923) respective comprise the heavy
CC   and light chain variable domains of a cynomolgus monkey anti-human
CC   CD4 monoclonal antibody.  DNA sequences (AAT62865-66) encoding these
CC   antigen binding domains were cloned from the anti-CD4 hybridoma
CC   cell line E9.1.  Novel monoclonal and chimeric antibodies, such as
CC   CE9.1 (AAW14924), comprise the monkey antigen binding domains fused
CC   to monkey or human constant domain sequences, pref. the human Kappa
CC   or lambda light chain constant domain sequence and the human gamma
CC   1 or gamma 4 (see also AAW14924) constant domain or a mutated gamma 4
CC   heavy chain (see also AAW14926-27).  These recombinant antibodies
CC   exhibit high affinity to human CD4 and have little or no
CC   immunogenicity in humans.  They can be used to treat autoimmune
CC   diseases such as rheumatoid arthritis.
XX
SQ   Sequence   139 AA;
XX

alignment_scores:
       Quality:   548.50           Length:      146
       Ratio:       4.459           Gaps:          2
Percent Similarity:  84.247    Percent Identity: 73.973

alignment_block:
US-09-019-441-2 x AAW14922        ..

Align seg 1/1  to: AAW14922  from: 1  to: 139

   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT 50
     ||||||||||:::||||||||||||||||||||||||||||||||||||||
   1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa 17

  51 CCTGTCCCAGCTGCAGCTGCAGGAGTGCGGCCCAGGAGTGTGAAGCCTT 100
     ||||||||||||:::||||||||||||::|||||||||::||||||||||
  17 lLeuSerGlnValGlnLeuGlnGluAlaGlyProGlyLeuValLysProS 34

 101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCGTGGCTCTGTCAGCAGT 150
     ||||||||||||||||||||::||||:::||:|::|||::::::||:|||
  34 erGluThrLeuSerLeuThrCysSerValSerGlyLySerIleSerGly 50

 151 AGTAACTGGTGGAACCTGGATCCGCCAGCCCCCAGGAAGGGACTGGAGTG 200
     :::  :||||||||||:|||||||||||||||| |||||||||||||||||
  51 AspTyrTyrTrpPheTrpTrpAsnProGlyLysGlyLeuGluTr 67

 201 GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCACTACAACCCGTCCC 250
     |||||| ||| |||:|||:||||::::|||||||||||||||||||||||
  67 pIleGlyTyrIleTyrGlySerGlyGlyGlyThrThrThrSerProSerL 84

 251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAAACCAGTTCTCC 300
     |:::::||||| ||||||  ||||||||||||||||||||||||||:|||
  84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100

 301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
     |||::||||:::|||||||||||||:|||:||||||||||||||||:||||
 101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 117

 351 CAGAGAT...............TGGGGCCAAATAGCTGGAACAACGC 382
     ||:::  :                  |||||||||||||||||
 117 aSerAsnIleLeuLysTyrLeuHisTrp.................L 127

 383 TAGGCTTCTGGGGCCAGGAGTCCTGGTCACCGTCTCC 420
       ||  :::||||||||||||||||||||||||||||||
 127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSer 139
```

seq_name: /SID51/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:AAW53988

seq_documentation_block:

```
ID   AAW53988 standard; Protein; 139 AA.
XX
AC   AAW53988;
XX
DT   29-JUL-1998  (first entry)
XX
DE   Anti-CD4 antibody VH domain.
XX
KW   Anti-CD4 antibody; monkey; human; therapy; variable heavy domain;
KW   Old World monkey; constant domain; eczema; immuno-modulated disease;
KW   rheumatoid arthritis.
XX
OS   Primate sp.
XX
PN   US5750105-A.
XX
PD   12-MAY-1998.
XX
PF   07-JUN-1995;          95US-0476349.
XX
PR   10-JUL-1992;          92US-0912292.
PR   25-JUL-1991;          91US-0735064.
PR   23-MAR-1992;          92US-0856281.
PR   05-DEC-1995;          95US-0379072.
PR   07-JUN-1995;          95US-0476349.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Hanna N,  Newman RA,   Raab RW;
XX
DR   WPI; 1998-296690/26.
DR   N-PSDB; AAV23760.
XX
PT   Improved method for antibody treatment - uses an antibody comprising
PT   an Old World monkey variable region and a human constant domain .
XX
PS   Claim 9; Fig 13; 84pp; English.
XX
CC   This sequence is the variable heavy domain of an anti-CD4 antibody
CC   (Ab).  This sequence can be used in the method of the invention for
CC   treating a subject, where the treatment comprises administration of an
CC   Ab. The method comprises the administration of an antibody which has an
CC   Old World monkey (e.g. baboon or macaque) variable region which binds to
CC   an antigen (Ag) (or Ag binding portion), and a human constant domain. The
CC   method is useful for the treatment of eczema and immuno-modulated
CC   diseases and especially rheumatoid arthritis. The recombinant antibodies
CC   used are sufficiently different from native monkey antibodies to allow
CC   human antigens to raise these antibodies, but similar enough to human
CC   antibody so there is no immune response to the antibodies in humans.
CC   Compared to antibodies used in therapy in prior art, these antibodies do
CC   not induce human anti-antibodies on repeated administration. They also
CC   have longer half-lives and do not have a lack of effector function with
CC   human cells.
XX
SQ   Sequence   139 AA;

alignment_scores:
       Quality:   548.50           Length:      146
       Ratio:       4.459           Gaps:          2
Percent Similarity:  84.247    Percent Identity: 73.973

alignment_block:
US-09-019-441-2 x AAW53988        ..

Align seg 1/1  to: AAW53988  from: 1  to: 139

   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT 50
     ||||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa 17

  51 CCTGTCCCAGCTGCAGCTGCAGGAGTGCGGCCCAGGAGTGTGAAGCCTT 100
     |||||||||||||||||||||||||||::|||||||||||||||||||||
```

```
     17  lLeuSerGlnValGlnLeuGlnGluAlaGlyProGlyLeuValLysPros  34

    101  CGGAGACCCTGTCCCTCACCTGCGTGTCTCGGTGGCTCTGGTCAGCAGT  150
         |||||||||||||||||::|||||||||||||||||||||::|||::|
     34  erGluThrLeuSerLeuThrCysSerValSerGlySerIleSerGly   50

    151  AGTAACTGGTGGACCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTG  200
         :::   ::|||   ||||||||||||||||  |||||||||||||||
     51  AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr   67

    201  GATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTACAACCCGTCCC  250
         ||||||   ||| |||||||||||||:::||||||||||||||||||||
     67  pIleGlyTyrIleTyrGlySerGlyGlyGlyThrAsnTyrAsnProSerL   84

    251  TCAAGAGTCCAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC  300
         ||::::::|||||  |||||  ||||||||||||||||  |||||
     84  euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer  100

    301  CTGAACCTGAACTCTGTGACCGCCGGACACGGCGTGTATTACTGTGC  350
         |||::|||:::|||||||||||||||||||||||||||||||||||
    101  LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl  117

    351  CAGAGAT..............TGGGCCCAAATAGCTGGAACAACGC  382
         ::|                   ||
    117  aSerAsnIleLeuLysTyrLeuHisTrp.............L  127

    383  TAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC  420
         ||  ::|||||||||||||||||||||||||||||||
    127  euLeuTyrTrpGlyGlnGlyValLeuValThrValSer  139
```

seq_name: /SIDS1/gcgdata/hold-geneseqp-embl/AA2001.DAT:AAB90607

seq_documentation_block:
ID    AAB90607 standard; Protein; 487 AA.
XX
AC    AAB90607;
XX
DT    01-JUN-2001  (first entry)
XX
DE    Human secreted protein, SEQ ID NO: 145.
XX
KW    Human; secreted protein; immunomodulatory; antisclerotic;
KW    dermatological; antiinflammatory; anti-HIV; cytostatic; cardiant;
KW    vascular; anti-angiogenic; ophthalmological; neuroprotectant;
KW    nootropic; anticonvulsant; antialzheimers; antiparkinsonian;
KW    antimicrobial; vulnerary; vaccine; gene therapy; cancer;
KW    protein coordinate data; infection.
XX
OS    Homo sapiens.
XX
PN    WO200121658-A1.
XX
PD    29-MAR-2001.
XX
PF    22-SEP-2000; 2000WO-US26013.
XX
PR    24-SEP-1999;  99US-0155709.
XX
PA    (HUMA-) HUMAN GENOME SCI INC.
XX
PI    Ni J, Baker KP, Birse CE, Ebner R, Fiscella M, Komatsoulis GA;
PI    Lafleur DW, Moore PA, Olsen HS, Rosen CA, Ruben SA, Soppet DR;
PI    Young PE, Wei P, Florence KA;
XX
DR    WPI; 2001-235311/24.
DR    N-PSDB; AAF97947.
XX
PT    Nucleic acids encoding 32 human secreted polypeptides, useful for
PT    preventing, diagnosing and/or treating e.g. cancers, Parkinson's
PT    disease and diabetic retinopathy -
XX
PS    Claim 11; Page 821-823; 890pp; English.
XX

CC    The present sequence is one of 32 novel human secreted polypeptides. The
CC    nucleic acid molecules and polypeptides may be used in the prevention,
CC    diagnosis and treatment of diseases such as immune disorders (e.g.
CC    multiple sclerosis, systemic lupus erythematosus and human
CC    immuno-deficiency virus (HIV) infections), hyperproliferative disorders
CC    (e.g. cancers and Gaucher's disease), cardiovascular diseases
CC    (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary
CC    arteriosclerosis), angiogenic disorders (e.g. corneal graft
CC    neovascularisation and diabetic retinopathy), neurological disorders
CC    (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease),
CC    infectious diseases and/or for promoting wound healing, regeneration
CC    and/or chemotaxis. The nucleic acid molecules may be used to produce the
CC    secreted polypeptides. They may also be used as DNA probes in diagnostic
CC    assays to detect and quantitate the presence of similar nucleic acid
CC    sequences in samples. The polypeptides may be used as antigens in the
CC    production of antibodies and in assays to identify modulators of
CC    their expression and activity.
XX
SQ    Sequence  487 AA;

alignment_scores:
         Quality:   544.00         Length:      148
         Ratio:       4.283        Gaps:          3
Percent Similarity:  85.811    Percent Identity: 74.324

alignment_block:
US-09-019-441-2 x AAB90607       ..

Align seg 1/1  to: AAB90607      from:  1  to: 487

```
      1  ATGAAACACCTGTGGTTCTTCCTCCTCCTCTGGTGGCAGCTCCCAGATGGT  50
         |||||||||||||||||||||||||||||||||||||||||||||||||
      1  MetLysHisLeuTrpPhePheLeuLeuLeuLeuTrpTrpGlnLeuProAsp

     51  CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
         |||||||||||||::||||||||||||||||||||::||::||||||||
     17  lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysPros   34

    101  CGGAGACCCTGTCCCTCACCTGCGTGTCTCGGTGGCTCTGTCAGCAGT  150
         |||||||||||||||||||||||||||||||||||||||::::||||||
     34  erGluThrLeuSerLeuThrCysValSerThrValSerGlySerIleSerSer   50

    151  AGTAACTGGTGGACCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGA  197
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    198  GTGGATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTACAACCCGT  247
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     67  uTrpIleGlyTyrIleSer...TyrAsnGlyValThrTyrTyrAsnPros   83

    248  CCCTCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTC  297
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seq_documentation_block:
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AC    AAW57446;

Mon Sep 23 16:30:42 2002

us-09-019-441-2.rag

Page 12

XX
DT   10-AUG-1998 (first entry)
XX
DE   Anti-CD4 antibody variable heavy (VH) region.
XX
KW   Anti-CD4 antibody; antigen-binding; treatment; chimeric; human;
KW   monkey; rheumatoid arthritis; psoriatic arthritis.
XX
OS   Chimeric - Macaca cynomolgus.
OS   Chimeric - Homo sapiens.
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FH   Key            Location/Qualifiers
FT   Misc-difference 138
FT                  /note= "encoded by GTC"
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PN   US5756096-A.
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PD   26-MAY-1998.
XX
PF   07-JUN-1995;   95US-0476237.
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PR   07-JUN-1995;   95US-0476237.
PR   25-JUL-1991;   91US-0735064.
PR   23-MAR-1992;   92US-0856281.
PR   10-JUL-1992;   92US-0912292.
PR   25-JAN-1995;   95US-0379072.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Hanna N, Newman RA, Raab RW;
XX
DR   WPI; 1998-321461/28.
DR   N-PSDB; AAV31428.
XX
PT   Treatment of rheumatoid and psoriatic arthritis - comprises
PT   administration of chimeric human-monkey anti-CD4 antibody
XX
PS   Disclosure; Fig 13; 47pp; English.
XX
CC   This represents the heavy chain variable region (VH) of the cynomolgus
CC   monkey anti-CD4 antibody. The antibody comprises antigen-binding
CC   sequences from an Old World monkey antibody and human constant domain
CC   sequences. The antibody specifically binds to CD4 and can be used in the
CC   treatment of rheumatoid or psoriatic arthritis.
XX
SQ   Sequence  139 AA;

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Date: Sep 23, 2002 10:19 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

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; GENERAL INFORMATION:
;    APPLICANT: Hillman, Jennifer L.
;    APPLICANT: Lal, Preeti
;    APPLICANT: Tang, Y. Tom
;    APPLICANT: Yue, Henry
;    APPLICANT: Au-Young, Janice
;    APPLICANT: Corley, Neil C.
;    APPLICANT: Guegler, Karl J.
;    APPLICANT: Baughn, Mariah R.
;    TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;    NUMBER OF SEQUENCES: 28
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Incyte Pharmaceuticals, Inc.
;       STREET: 3174 Porter Drive
;       CITY: Palo Alto
;       STATE: CA
;       COUNTRY: USA
;       ZIP: 94304
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Diskette
;       COMPUTER: IBM Compatible
;       OPERATING SYSTEM: DOS
;       SOFTWARE: FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/049,672
;       FILING DATE: HEREWITH
;       CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;       NAME: Cerrone, Michael C
;       REGISTRATION NUMBER: 39,132
;       REFERENCE/DOCKET NUMBER: PF-0497 US
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 650-855-0555
;       TELEFAX: 650-845-4166
;       TELEX:
; INFORMATION FOR SEQ ID NO:  4:
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;       LIBRARY: PANCTUT01
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; US-09-049-672-4

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Sequence 12, Application US/09612914
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;   APPLICANT:  Hanna, Nabil
;   APPLICANT:  Newman, Roland A.
;   APPLICANT:  Reff, Mitchell E.
;   TITLE OF INVENTION:  Recombinant Anti-CD4 Antibodies for Human
;   TITLE OF INVENTION:  Therapy
;   NUMBER OF SEQUENCES:  59
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;     STREET:  699 Prince Street
;     CITY:  Alexandria
;     STATE:  VA
;     COUNTRY:  USA
;     ZIP:  22314-3187
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/612,914
;     FILING DATE:  10-JUL-2000
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/523,894
;     FILING DATE:  06-SEP-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Teskin, Robin L.
;     REGISTRATION NUMBER:  35,030
;     REFERENCE/DOCKET NUMBER:  012712-165
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  703-836-6620
;     TELEFAX:  703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
;   SEQUENCE CHARACTERISTICS:
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;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-09-612-914-12

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Percent Similarity:  84.354      Percent Identity: 74.830

alignment_block:
US-09-019-441-2 x US-09-612-914-12

Align seq 1/1  to: US-09-612-914-12  from: 1  to: 467

  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTCGTGGCAGCTCCCAGATGGGT  50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    ||||||||::||||||||||||||||||||:||||::||:||||||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS  34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    |||||||||||||||||||||:::||||||||||||||||::|||:::
 34 erGluThrLeuSerLeuThrCysServalSerGlyGlySerIleSerGly  50

151 AGTAACTGGTGGACCTGGATCCGGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
    :::  ::||||| |||||||||||||||||||||||||||||||||||||
 51 AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr  67

201 GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCCGTCCC 250
    |||||| ||| |||||||::||||||||||::||||||||||||||||
 67 pIleGlyTyrIleTyrGlySerGlyGlyGlyGlyThrAsnTyrAsnProSerL  84
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  SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/612,914
;     FILING DATE:  10-JUL-2000
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/523,894
;     FILING DATE:  06-SEP-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Teskin, Robin L.
;     REGISTRATION NUMBER:  35,030
;     REFERENCE/DOCKET NUMBER:  012712-165
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  703-836-6620
;     TELEFAX:  703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  467 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-09-612-914-10

alignment_scores:
       Quality:  555.50                Length:     147
       Ratio:    4.480                 Gaps:         2
Percent Similarity:  84.354      Percent Identity: 74.830

alignment_block:
US-09-019-441-2 x US-09-612-914-10

Align seq 1/1  to: US-09-612-914-10  from: 1  to: 467

  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTCGTGGCAGCTCCCAGATGGGT  50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    ||||||||::||||||||||||||||||||:||||::||:||||||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS  34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    |||||||||||||||||||||:::||||||||||||||||::|||:::
 34 erGluThrLeuSerLeuThrCysServalSerGlyGlySerIleSerGly  50

151 AGTAACTGGTGGACCTGGATCCGGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
    :::  ::||||| |||||||||  |||||||||||||||||||||||||
 51 AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr  67

201 GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCCGTCCC 250
    |||||| ||| |||||||::||||||||||::||||||||||||||||
 67 pIleGlyTyrIleTyrGlySerGlyGlyGlyGlyThrAsnTyrAsnProSerL  84

251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    ||.:::::||||| |||||| ||||||||||  |||||
 84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100

301 CTGAACCTGAACTCTGTGACCGCCGGACACGGCCGTGTATTACTGTGC 350
    |||.::||||||||||||||||||||||||||||||||||||||||||
101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValThrTyrTyrCysAl 117

351 CAGAGAT.........TGGGCCCAAATAGTCGGAACAACGC 382
    |||||||                             |||
117 aSerAsnIleLeuLysTyrLeuHisTrp..............L 127

383 TAGGCTTCTGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 423
    ||||||||||||||||||||||||||||||||||||||||
127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSerSer 140

seq_name:  /cgn2_6/ptodata/2/paa/US096_COMB.pep:US-09-612-914-12

seq_documentation_block:
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251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTC 300
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 84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100

301 CTGAACCTGAACTCTGTGACCGCCGCGGACAGGCCGTGTATTACTGTGC 350
    ||::::::||||:::|||||||||||||||||||||||||||
101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 117

351 CAGAGAT.............TGGGCCCAAATAGCTGGAACAACGC 382
    :: :::
117 aSerAsnIleLeuLysTyrLeuHisTrp.............L 127

383 TAGGCTTCTGGGCCAGGAGTCCTGGTCACCGTCTCCTCA 423
    || :::||||||||||||||||||||||||
127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSerSer 140

seq_name: /cgn2_6/ptodata/2/paa/US096_COMB.pep:US-09-612-914A-8

seq_documentation_block:
; Sequence 8, Application US/09612914A
; GENERAL INFORMATION:
;    APPLICANT: Hanna, Nabil
;              Newman, Roland A.
;              Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
;                    Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
;    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;    STREET: 699 Prince Street
;    CITY: Alexandria
;    STATE: VA
;    COUNTRY: USA
;    ZIP: 22314-3187
; COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/09/612,914A
;    FILING DATE: 10-Jul-2000
;    CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: US 08/523,894
;    FILING DATE: 06-SEP-1995
; ATTORNEY/AGENT INFORMATION:
;    NAME: Teskin, Robin L.
;    REGISTRATION NUMBER: 35,030
;    REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 703-836-6620
;    TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH: 467 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;    MOLECULE TYPE: protein
;    SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-612-914A-8

alignment_scores:
    Quality:      555.50       Length:     147
    Ratio:          4.480       Gaps:          2
Percent Similarity:  84.354   Percent Identity:  74.830

alignment_block:
US-09-019-441-2 x US-09-612-914A-8     ..
Align seg 1/1  to: US-09-612-914A-8   from: 1  to: 467
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  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGT 50
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  1 MetLysHisLeuTrpPhePheLeuLeuLeuLeuValAlaAlaProArgTrpVa 17

 51 CCTGTCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    ||:::||||||||||||||||||||||||||||::::||||||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    ||||||||||||||||||||||||||||||||:::||||::|||:
 34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly 50

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
    :::  ::||| ||||||||||  |||||||||||    ||||||||||
 51 AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr 67

201 GATTGGACGTATCTGTGGTAGTGGTGGGGCCACCAACTACAACCCGTCCC 250
    ||||||  |||||||||||||||||||||||||||||||||||||||
 67 pIleGlyTyrIleTyrGlySerGlyGlyGlyThrAsnTyrAsnProSerL 84

251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    ||:::::||||  ||||||||||||||||||||||||||||::::|||
 84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100

301 CTGAACCTGAACTCTGTGACCGCCGCCGGACAGGCCGTGTATTACTGTGC 350
    |||::::|||||:::||||||||||||||||||||||||||||||||
101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 117

351 CAGAGAT.............TGGGCCCAAATAGCTGGAACAACGC 382
    |:  :::                                   ||
117 aSerAsnIleLeuLysTyrLeuHisTrp.............L 127

383 TAGGCTTCTGGGCCAGGAGTCCTGCTCACGTCTCCTCA 423
    || :::|||||||||||||||||||||||||
127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSerSer 140
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seq_name: /cgn2_6/ptodata/2/paa/US096_COMB.pep:US-09-612-914A-10

seq_documentation_block:
; Sequence 10, Application US/09612914A
; GENERAL INFORMATION:
;    APPLICANT: Hanna, Nabil
;              Newman, Roland A.
;              Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
;                    Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
;    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;    STREET: 699 Prince Street
;    CITY: Alexandria
;    STATE: VA
;    COUNTRY: USA
;    ZIP: 22314-3187
; COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/09/612,914A
;    FILING DATE: 10-Jul-2000
;    CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: US 08/523,894
;    FILING DATE: 06-SEP-1995
; ATTORNEY/AGENT INFORMATION:
;    NAME: Teskin, Robin L.
;    REGISTRATION NUMBER: 35,030
;    REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 703-836-6620
;    TELEFAX: 703-836-2021
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INFORMATION FOR SEQ ID NO: 10:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 467 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: protein
  SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-612-914A-10

alignment_scores:
    Quality:    555.50              Length:      147
    Ratio:        4.480              Gaps:          2
Percent Similarity:  84.354    Percent Identity: 74.830

alignment_block:
US-09-019-441-2 x US-09-612-914A-10

Align seg 1/1  to: US-09-612-914A-10  from: 1  to: 467     .

  1  ATGAAACACCTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGT   50
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  1  MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa   17

 51  CCTGTCCCAGCTGCAGGAGTGCAGGAGTGGGCCCAGGAGTGGTGAAGCCTT  100
     |||||||:::|||||||||||||||||||:||||||||
 17  lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS   34

101  CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT  150
     |||||||||||||||||||::|||||:::||:::||:::
 34  erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly   50

151  AGTAACTGGTGGACCTGGATCCCCAGCCCCAGGGAAGGACTGGAGTG  200
     :::  :::||| ||||||||||  |||||||||||||||||
 51  AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr   67

201  GATTGGACGTATCTCTGTAGTGGTGGGCCACCAACTACAACCCGTCC  250
     |||||| ||| :|||||||||::||||||||:||||||||
 67  pIleGlyTyrIleTyrGlySerGlyGlyThrAsnTyrAsnProSerL   84

251  TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC  300
     ||:::::|||||  ||||| ||||||||||||  |||||
 84  euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer  100

301  CTGAACCTGAACTCTGTGACCGCCGGACACGGCCGTGTATTACTGTGC  350
     |||:::||:::|||||||||||||||||||||||||||
101  LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl  117

351  CAGAGAT...............TGGGGCCAAATAGCTGGAACAACGC  382
     ::||                          ||
117  aSerAsnIleLeuLysTyrLeuHisTrp.................L  127

383  TAGGCTTCTGGGGCCAGGAGTCCTGGTCACCGTCCTCCTCA  423
     ||  :::||||||||||||||||||||||||||||||
127  euLeuTyrTrpGlyGlnGlyValLeuValThrValSerSer  140

seq_name: /cgn2_6/ptodata/2/paa/US096_COMB.pep:US-09-612-914A-12

seq_documentation_block:
; Sequence 12, Application US/09612914A
; GENERAL INFORMATION:
    APPLICANT: Hanna, Nabil
               Newman, Roland A.
               Reff, Mitchell E.
    TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
    NUMBER OF SEQUENCES: 59
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
      STREET: 699 Prince Street
      CITY: Alexandria
      STATE: VA
      COUNTRY: USA
      ZIP: 22314-3187
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/612,914A
      FILING DATE: 10-Jul-2000
      CLASSIFICATION: <Unknown>
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/523,894
      FILING DATE: 06-SEP-1995
    ATTORNEY/AGENT INFORMATION:
      NAME: Teskin, Robin L.
      REGISTRATION NUMBER: 35,030
      REFERENCE/DOCKET NUMBER: 012712-165
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 703-836-6620
      TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 467 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: protein
  SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-612-914A-12

alignment_scores:
    Quality:    555.50              Length:      147
    Ratio:        4.480              Gaps:          2
Percent Similarity:  84.354    Percent Identity: 74.830

alignment_block:
US-09-019-441-2 x US-09-612-914A-12

Align seg 1/1  to: US-09-612-914A-12  from: 1  to: 467     .

  1  ATGAAACACCTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGT   50
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  1  MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa   17

 51  CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
     |||||||:::||||::||||||:::||:||:||:||||||||
 17  lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS   34

101  CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT  150
     |||||||||||||||||||||||||:||||::::||:::::
 34  erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly   50

151  AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG  200
     :::  :||||||||||||||  ||||||||||||||||||||
 51  AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr   67

201  GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCCGTCCC  250
     |||||| ||  |||||||||||::||||||||||:||||||||
 67  pIleGlyTyrIleTyrGlySerGlyGlyThrAsnTyrAsnProSerL   84

251  TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC  300
     ||:::||||| ||||| |||||||||||||||  ||||||
 84  euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer  100

301  CTGAACCTGTCTGACCGCCCGGACACGGCCGTGTATTACTGTGC  350
     |||:::||:::|||||||||||||||||||||||||||||||
101  LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl  117

351  CAGAGAT..........TGGGGCCAAATAGCTGGAACAACGC  382
     :::                         |||
117  aSerAsnIleLeuLysTyrLeuHisTrp..........L  127

383  TAGGCTTCTGGGGCCAGGAGTCCTGGTCACCGTCTCCTCA  423

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        ||   :::||||||||||||||||||||||||||
    127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSerSer 140
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seq_name: /cgn2_6/ptodata/2/paa/US093_COMB.pep:US-09-383-916-12

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seq_documentation_block:
; Sequence 12. Application US/09383916
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION:   TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION:   PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION:   IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES:  12
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;     STREET:  699 Prince Street
;     CITY:  Alexandria
;     STATE:  VA
;     COUNTRY:  USA
;     ZIP:  22314
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0,  Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/383,916
;     FILING DATE:  26-AUG-1999
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/487,550
;     FILING DATE:  07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Teskin, Robin L.
;     REGISTRATION NUMBER:  35,030
;     REFERENCE/DOCKET NUMBER:  012712-131
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  703-836-6620
;     TELEFAX:   703-836-2021
;   INFORMATION FOR SEQ ID NO:  12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  476 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-383-916-12
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alignment_scores:
        Quality:  550.50              Length:       153
        Ratio:    4.476               Gaps:          2
Percent Similarity:  80.392      Percent Identity: 71.242

alignment_block:
US-09-019-441-2 x US-09-383-916-12

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    1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

   51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
      ||||||||::||||||||||::|||||||||||||::::|||||||||||
   17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS  34

  101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT  150
      |||||||||||||||||||||||:::|||||||::|||:|||||||||||
   34 erGluThrLeuSerLeuThrCysAlaValSerGlyGlySerIleSerGly  50

  151 AGTAACTGGTGGACTGGATCCGCCAGCCCCCAGGAGAGGACTGGAGTG  200
      ::: ||||||||||||||||||||||||||||||||||||||||||||
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    51 GlyTyrGlyTrpGlyTrpIleArgGlnProProGlyLysGlyLeuGluTr  67

   201 GATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACAACCGTCCC  250
       |||||||  :::  ::::|||||:::|||  ||| |||||||||||||||
    67 pIleGlySerPheTyrSerSerSerGlyAsnThrTyrTyrAsnProSerL  84

   251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC  300
       |||||||||:|||  |||||| |||||| ||||||||||||||||||||
    84 euLysSerGlnValThrIleSerThrAspThrSerLysAsnGlnPheSer  100

   301 CTGAACCTGAACTCTGTGACCGCCGGACACGGCCGTGTATTACTGTGC  350
       ||::||||||||||||||::|||||||||||::|||||||||:::|||||
   101 LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyrTyrCysVa  117

   351 CAGAGAT.............TGGGCCC  364
       :||||||                ||| :
   117 lArgAspArgLeuPheSerValValGlyMetValTyrAsnAsnTrpPheA  134

   365 AAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGAGTCCTGGTCACC  414
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   134 spVal..............TrpGlyProGlyValLeuValThr  143

   415 GTCTCCTCA  423
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   144 ValSerSer  146
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seq_name: /cgn2_6/ptodata/2/paa/US095_COMB.pep:US-09-576-424-12

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seq_documentation_block:
; Sequence 12. Application US/09576424
; GENERAL INFORMATION:
;   APPLICANT: ANDERSON, DARRELL R.
;   APPLICANT: HANNA, NABIL
;   APPLICANT: BRAMS, PETER
;   APPLICANT: HEARD, CHERYL
;   TITLE OF INVENTION:  INDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN
;   TITLE OF INVENTION:  CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
;   TITLE OF INVENTION:  CO-STIMULATORY ANTIGENS
;   FILE REFERENCE: 37003-275681
;   CURRENT APPLICATION NUMBER: US/09/576,424
;   CURRENT FILING DATE:  2000-05-22
;   PRIOR APPLICATION NUMBER: PCT/US97/19906
;   PRIOR FILING DATE: 1997-10-29
;   PRIOR APPLICATION NUMBER: 08/746,361
;   PRIOR FILING DATE: 1996-11-08
;   PRIOR APPLICATION NUMBER: 08/487,550
;   PRIOR FILING DATE: 1995-06-07
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 476
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-576-424-12
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alignment_scores:
        Quality:  550.50              Length:       153
        Ratio:    4.476               Gaps:          2
Percent Similarity:  80.392      Percent Identity: 71.242

alignment_block:
US-09-019-441-2 x US-09-576-424-12

Align seg 1/1  to: US-09-576-424-12  from: 1  to: 476        ..

    1 ATGAAACACCTGTTCTTCCTCCTCCTCGTGGTGGCAGCTCCCAGATGGGT  50
      ||||||||||||||::|||||||||||||||||||||||::||||||||||
    1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

   51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
      ||||||||::||||||||||::|||||||||||||::::|||||||||||
   17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS  34
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                          TYPE: amino acid
                          TOPOLOGY: linear
                          MOLECULE TYPE: protein
                    US-09-612-914-2

                    alignment_scores:
                              Quality:  548.50              Length:    146
                                Ratio:    4.459               Gaps:       2
                    Percent Similarity:  84.247    Percent Identity: 73.973

                    alignment_block:
                    US-09-019-441-2 x US-09-612-914-2

                    Align seg 1/1  to: US-09-612-914-2  from: 1  to: 139

                      1 ATGAAACACCTGGTTCTTCCTCCTCCGTGGCCAGCTCCAGATGGGT  50
                        |||||||||||||||||||||||||||||::|||||||||||||||
                      1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa  17

                     51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
                        ||||||||||:|||||||:||||||::::||::::|::|||||||||
                     17 lLeuSerGlnValGlnLeuGlnGluAlaGlyProGlyLeuValLysProS  34

                    101 CGGAGACCCTGTCCCTCACCTGCGTGTCTCTGGTGGCTGTTGTCAGCAGT  150
                        ||||||||||||||||||::||||:||||||||||||||::|||||||
                     34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly  50

                    151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG  200
                        ||||||||||||:||||::|||||||||||||||||||||||||||||
                     51 AspTyrTyrTrpIleTyrTrpIleArgGlnSerProGlyLysGlyLeuGluTr  67

                    201 GATTGGACGTATCTCTGGTAGTGGTGGCCACCAACTACAACCCGTCCC  250
                        |||||||||||::|||||||||::|||||::||||||||||||||||
                     67 pIleGlyTyrIleTyrGlySerGlyGlyGlyThrAsnTyrAsnProSerL  84

                    251 TCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTCTCC  300
                        ||::|||:|||||::|||||||||||||||||||||||||| |||||
                     84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer  100

                    301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC  350
                        ||:::||:|||||||||||||||||||||||||||::|||||||||||
                    101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl  117

                    351 CAGAGAT..........TGGGCCCAAATAGCTGGAACAACGC  382
                        :|||||          |||
                    117 aSerAsnIleLeuLysTyrLeuHisTrp.............L  127

                    383 TAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC  420
                        || :|||||||||||:|||||||||||||||||||||
                    127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSer  139

seq_name: /cgn2_6/ptodata/2/paa/US096_COMB.pep:US-09-612-914A-2

seq_documentation_block:
;  Sequence 2, Application US/09612914A
;  GENERAL INFORMATION:
;      APPLICANT: Hanna, Nabil
;             Newman, Roland A.
;             Reff, Mitchell E.
;      TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
;                         Therapy
;      NUMBER OF SEQUENCES: 59
;      CORRESPONDENCE ADDRESS:
;          ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;          STREET: 699 Prince Street
;          CITY: Alexandria
;          STATE: VA
;          COUNTRY: USA
;          ZIP: 22314-3187
;      COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
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                    101 CGGAGACCCTGTCCCTCACCTGCGTGTCTCTGGTGGCTCTGTCAGCAGT  150
                        |||||||||||||||||||||||||||||||||::|||||||||:::
                     34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly  50

                    151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG  200
                        ::|  |||  ||||||||||||||||||||||||||||||||||||
                     51 GlyTyrTyrGlyTyrIleGlyTrpIleArgGlnProGlyLysGlyLeuGluTr  67

                    201 GATTGGACGTATCTCTGGTAGTGGTGGCCACCAACTACAACCCGTCCC  250
                        |||||| ::|::|||::|||||||||||||||||||||||||||||
                     67 pIleGlySerPheTyrSerSerGlyAsnThrTyrTyrAsnProSerL  84

                    251 TCAAGAGTCGAGTCATCATTTCACAGACGTCCAAGAACCAGTTCTCC  300
                        ||||||||::|||||| |||| |:|||||||||||||||||:|||
                     84 euLysSerGlnValThrIleSerThrAspThrSerLysAsnGlnPheSer  100

                    301 CTGAACCTGAACTCTGTGACCGCCGGACACGGCCGTGTATTACTGTGC  350
                        ||:::||||||||:::|||||::|||||||||||||||||||||:::
                    101 LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyrTyrCysVa  117

                    351 CAGAGAT.................TGGGCCC  364
                        :||||||                 |||
                    117 lArgAspArgLeuPheSerValValGlyMetValTyrAsnAsnTrpPheA  134

                    365 AAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACC  414
                        ::::                |||||||||||||||||||||||||
                    134 spVal.................TrpGlyProGlyValLeuValThr  143

                    415 GTCTCCTCA  423
                        |||||||||
                    144 ValSerSer  146

seq_name: /cgn2_6/ptodata/2/paa/US096_COMB.pep:US-09-612-914-2

seq_documentation_block:
;  Sequence 2, Application US/09612914
;  GENERAL INFORMATION:
;      APPLICANT: Hanna, Nabil
;             Newman, Roland A.
;             Reff, Mitchell E.
;      TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
;                         Therapy
;      NUMBER OF SEQUENCES: 59
;      CORRESPONDENCE ADDRESS:
;          ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;          STREET: 699 Prince Street
;          CITY: Alexandria
;          STATE: VA
;          COUNTRY: USA
;          ZIP: 22314-3187
;      COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/612,914
;          FILING DATE: 10-JUL-2000
;          CLASSIFICATION:
;      PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US/08/523,894
;          FILING DATE: 06-SEP-1995
;      ATTORNEY/AGENT INFORMATION:
;          NAME: Teskin, Robin L.
;          REGISTRATION NUMBER: 35,030
;          REFERENCE/DOCKET NUMBER: 012712-165
;      TELECOMMUNICATION INFORMATION:
;          TELEPHONE: 703-836-6620
;          TELEFAX: 703-836-2021
;  INFORMATION FOR SEQ ID NO:  2:
;      SEQUENCE CHARACTERISTICS:
;          LENGTH: 139 amino acids
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        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/612,914A
        FILING DATE: 10-Jul-2000
        CLASSIFICATION: <Unknown>
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 08/523,894
        FILING DATE: 06-SEP-1995
    ATTORNEY/AGENT INFORMATION:
        NAME: Teskin, Robin L.
        REGISTRATION NUMBER: 35,030
        REFERENCE/DOCKET NUMBER: 012712-165
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: 703-836-6620
        TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 2:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 139 amino acids
        TYPE: amino acid
        TOPOLOGY: linear
    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-612-914A-2
```

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alignment_scores:
        Quality:  548.50              Length:   146
        Ratio:    4.459               Gaps:     2
Percent Similarity: 84.247    Percent Identity: 73.973

alignment_block:
US-09-019-441-2 x US-09-612-914A-2  ..

Align seg 1/1  to: US-09-612-914A-2  from: 1  to: 139

  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGT 50
    |||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaLeuAlaProArgTrpVa 17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGCTCGGGCCCAGGAGTGGTGAAGCCTT 100
    |||||||||::::||||||||||||||||||||||||||||||::||||||
 17 lLeuSerGlnValGlnLeuGlnGluAlaGlyProGlyLeuValLysProS 34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    ||||||||||||||||||||::|||:||::|||:||||||||||
 34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly 50

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
    :: ::|||   |||||||||||||||||||||||||||||||
 51 AspTyrTyrTrpThrTrpIleArgGlnSerProGlyLysGlyLeuGluTr 67

201 GATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTACAACCCGTCCC 250
    ||||| ||| ||  |||||||||:::||||||||||||||||||||||||
 67 pIleGlyTyrIleTyrTyrGlySerGlyGlyGlyThrAsnTyrAsnProSerL 84

251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    |::||:|||||| |||||||||||||   |||||||
 84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100

301 CTGAACCTGAACTCTGACCGCGCGGACACGGCCGTGTATTACTGTGC 350
    |||||||||||||||||||||||||||||||||||||||
101 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 117

351 CAGAGAT.........TGGGCCCAAATAGCTGGAACAACGC 382
    |  ::|               |||
117 aSerAsnIleLeuLysTyrLeuHisTrp...........L 127

383 TAGGCTTCTGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
    |||||||||||||||||||||||||||||||
127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSer 139
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seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCTUS01-18569-4331

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seq_documentation_block:
; Sequence 4331, Application PC/TUS0118569
; GENERAL INFORMATION:
;   APPLICANT: Human Genome Sciences, Inc.
;   TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;   FILE REFERENCE: PA133PCT
;   CURRENT APPLICATION NUMBER: PCT/US01/18569
;   CURRENT FILING DATE: 2001-06-07
;   PRIOR APPLICATION NUMBER: 60/209,467
;   PRIOR FILING DATE: 2000-06-07
;   NUMBER OF SEQ ID NOS: 4360
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4331
;   LENGTH: 193
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (5)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (188)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-18569-4331
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alignment_scores:
        Quality:  546.00              Length:   146
        Ratio:    4.368               Gaps:     4
Percent Similarity: 85.616    Percent Identity: 77.397

alignment_block:
US-09-019-441-2 x PCT-US01-18569-4331

Align seg 1/1  to: PCT-US01-18569-4331  from: 1  to: 193

  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGT 50
    |||||||||||||||||||||||||||||||||||||||||||||||||
  6 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaLeuAlaProArgTrpVa 22

 51 CCTGTCCCAGCTGCAGCTGCAGGAGCTCGGGCCCAGGAGTGGTGAAGCCTT 100
    |||||||||::::||||||||||||||||||||||||||||||::||||||
 22 lLeuSerGlnValGlnLeuGlnGluAlaGlyProGlyLeuValLysProS 39

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    ||||||||||||||||||||::|||:||::|||:||||||       |||
 39 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIle...Ser 54

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
    ::    ::|||   |||||||||||||||||||||||||||||||
 55 SerTyrTyrTrpSerTrpIleArgGlnSerProGlyLysGlyLeuGluTr 71

201 GATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTACAACCCGTCCC 250
    ||||| |||   || |||||    ::GlySerThrAsnTyrAsnProSerL 87
 71 pIleGlyTyrIleTyrTyrSer...GlySerThrAsnTyrAsnProSerL 87

251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    |::||:|||||| |||||||||||||   |||||||
 87 euLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 103

301 CTGAACCTGAACTCTGACCGCGCGGACACGGCCGTGTATTACTGTGC 350
    |||:|||||||:||||||||||||||||||||||||||||
104 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 120

351 CAGA...........GATTGGGCCCAAATAGCTGGAACAACGCTAG 385
    ||||              ::||       ||
120 aArgGlyProTyrSerSerTrpTyrProArgAla...GluTyrPheG 136

386 GCTTCTGGGCCAGGGAGTCCTGGTCACCGTCCTCTCA 423
    ::||||||||||::|||||||||||||||||
136 lnHisTrpGlyGlnGlyThrLeuValThrValSerSer 148
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seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-11988-2194

seq_documentation_block:
; Sequence 2194, Application PC/TUS0111988
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: PCT/US01/11988
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2194
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-11988-2194

alignment_scores:
        Quality:       544.00              Length:    148
        Ratio:         4.283               Gaps:        3
Percent Similarity:    85.811   Percent Identity: 74.324

alignment_block:
US-09-019-441-2 x PCT-US01-11988-2194

Align seg 1/1 to: PCT-US01-11988-2194  from: 1 to: 487

  1 ATGAAACACCTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGT  50
    |||||||||||||||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa 17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTGCGGGCCCAGGAGTGTGAAGCCTT 100
    ||||||||||||||||||||::||||||||||::||||||||:::||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34

101 CGGAGACCCTGCGTCCCTCACCTGCGCTGTCTCGGTGGCTCTGTCAGCAGT 150
    ||||||||||||:::||||||||:::||||||||:::||||||||
 34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIleSerSer 50

151 ...AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGA 197
       :::::|||::|||||||||||||||   ||||||||||||||
 51 GlyGlyHisTyrTrpSerTrpIleArgGlnHisProGlyLysGlyLeuGl 67

198 GTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACAACCCGT 247
    ||||||||    :::||||||   ::::||||    |||||||||||
 67 uTrpIleGlyTyrIleSer...TyrAsnGlyValThrTyrTyrAsnProS 83

248 CCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC 297
    |||||||||   ||||||   |||||||||||||||||||||||
 83 erLeuLysSerArgValThrIleSerValAspThrSerGlnAsnGlnPhe 99

298 TCCCTGAACCTGAACTCTGTGACCGCCGGACACGGCCGTGTATTACTG 347
    ||||||||::::|||||||  |||||||||||||||||||||||
100 SerLeuAsnLeuAsnSerValThrAlaAlaAspThrAlaValTyrTyrCy 116

348 TGCC...........AGAGATTGGGCCCAAATAGCTGGAACAA 379
    ||||           |||:::
116 sAlaLysAspHisArgAlaThrArgAspGlyTyrGlnLeuGluTyrArgG 133

380 CGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 423
    :::  :::|||||||||:::||||||||||||||||||||||
133 lyPheAspTyrTrpGlyGlnGlyIleLeuValThrValSerSer 147

seq_name: /cgn2_6/ptodata/2/paa/US098_COMB.pep:US-09-800-729-145
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seq_documentation_block:
; Sequence 145, Application US/09800729
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-145

alignment_scores:
        Quality:       544.00              Length:    148
        Ratio:         4.283               Gaps:        3
Percent Similarity:    85.811   Percent Identity: 74.324

alignment_block:
US-09-019-441-2 x US-09-800-729-145

Align seg 1/1 to: US-09-800-729-145  from: 1 to: 487

  1 ATGAAACACCTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGT  50
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  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa 17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTGCGGGCCCAGGAGTGTGAAGCCTT 100
    ||||||||||||||||||||::||||||||||::||||||||:::||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34

101 CGGAGACCCTGCGTCCCTCACCTGCGCTGTCTCGGTGGCTCTGTCAGCAGT 150
    ||||||||||||:::||||||||:::||||||||:::||||||||
 34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIleSerSer 50

151 ...AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGA 197
       :::::|||::|||||||||||||||   ||||||||||||||
 51 GlyGlyHisTyrTrpSerTrpIleArgGlnHisProGlyLysGlyLeuGl 67

198 GTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACAACCCGT 247
    ||||||||    :::||||||   ::::||||    |||||||||||
 67 uTrpIleGlyTyrIleSer...TyrAsnGlyValThrTyrTyrAsnProS 83

248 CCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC 297
    |||||||||   ||||||   |||||||||||||||||||||||
 83 erLeuLysSerArgValThrIleSerValAspThrSerGlnAsnGlnPhe 99

298 TCCCTGAACCTGAACTCTGTGACCGCCGGACACGGCCGTGTATTACTG 347
    ||||||||::::|||||||  |||||||||||||||||||||||
100 SerLeuAsnLeuAsnSerValThrAlaAlaAspThrAlaValTyrTyrCy 116

348 TGCC...........AGAGATTGGGCCCAAATAGCTGGAACAA 379
    ||||           |||:::
116 sAlaLysAspHisArgAlaThrArgAspGlyTyrGlnLeuGluTyrArgG 133

380 CGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 423
    :::  :::|||||||||:::||||||||||||||||||||||
133 lyPheAspTyrTrpGlyGlnGlyIleLeuValThrValSerSer 147

seq_name: /cgn2_6/ptodata/2/paa/US098_COMB.pep:US-09-833-245-2194

seq_documentation_block:
; Sequence 2194, Application US/09833245
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
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;   TITLE OF INVENTION: Albumin Fusion Proteins
;   FILE REFERENCE: PF546PCT
;   CURRENT APPLICATION NUMBER: US/09/833,245
;   CURRENT FILING DATE:     2001-04-12
;   PRIOR APPLICATION NUMBER: 60/229, 358
;   PRIOR FILING DATE: 2000-04-12
;   PRIOR APPLICATION NUMBER: 60/256, 931
;   PRIOR FILING DATE: 2000-12-21
;   PRIOR APPLICATION NUMBER: 60/199, 384
;   PRIOR FILING DATE: 2000-04-25
;   NUMBER OF SEQ ID NOS: 2267
;   SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 2194
;       LENGTH: 487
;       TYPE: PRT
;       ORGANISM: Homo sapiens
US-09-833-245-2194
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alignment_scores:
          Quality:    544.00              Length:        148
          Ratio:       4.283              Gaps:            3
Percent Similarity:   85.811     Percent Identity:   74.324

alignment_block:
US-09-019-441-2 x US-09-833-245-2194

Align seq 1/1  to: US-09-833-245-2194   from: 1   to: 487


   1 ATGAAACACCTGTGTTCCTCCCTCCTGTGGCAGCTCCCAGATGGGT   50
     ||||||||||||||||||||||||||||||||||||||||||||||
   1 MetLysHisLeuTrpPhePheLeuLeuLeuLeuValAlaAlaProArgTrpVa   17

  51 CCTGTCCCAGCTGCAGCTGCCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTT   100
     ||||||||::|||||||||||||||||||::||||||||
  17 lLeuSerGlnValGlnLeuGlnLeuGluSerGlyProGlyLeuValLysProS   34

 101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT   150
     ||:||||||||||||||||||||||::|||||||:::||||
  34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIleSerSer   50

 151 ...AGTAACTGGTGACCTGGATCCGCCAGCCCCAGGGAAGGGACTGGA   197
     :::::|||||||||||||| ||||||||||||||
  51 GlyGlyHisTyrTrpSerTrpIleArgGlnHisProGlyLysGlyLeuGl   67

 198 GTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACAACCCGT   247
     ||||||||| ::|||||||::|||
  67 uTrpIleGlyTyrIleSer...TyrAsnGlyValThrTyrTyrAsnProS   83

 248 CCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC   297
     ||||||||||| ||||||||::||||||
  83 erLeuLysSerArgValThrIleSerValAspThrSerGlnAsnGlnPhe   99

 298 TCCCTGAACCTGAACTCTGTGACCGCCGGACACGGCCGTGTATTACTG   347
     |||||::|||::||||||||||||||||||||||||
 100 SerLeuArgLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCy   116

 348 TGCC..............AGAGATTGGGCCCAAATAGCTGGAACAA   379
     ||||                 |||:::
 116 sAlaLysAspHisArgAlaThrArgAspGlyTyrGlnLeuGluTyrArgG   133

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 133 lyPheAspTyrTrpGlyGlnGlyIleLeuValThrValSerSer   147
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OM of: US-09-019-441-2 to: Pending_Patents_AA_New:*    out_format : pfs

Date: Sep 23, 2002  9:59 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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Search information block:
Query: US-09-019-441-2
Query length: 423
Database: Pending_Patents_AA_New:*
Database sequences: 949130
Database length: 267991220
Search time (sec): 353.570000
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score_list:

| Sequence | Std | Orig | ZScore | EScore | Len | ! | Documentation |
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seq_documentation_block:
; Sequence 39900, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 15305
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39900
;   LENGTH: 144
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-39900

alignment_scores:
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        Ratio:           4.587              Gaps:           3
Percent Similarity:     87.586       Percent Identity:   78.621

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251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC  300
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; Sequence 14676, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14676
;   LENGTH: 137
;   TYPE: PRT
;   ORGANISM: Macaca mulatta
US-09-791-537-14676

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seq_documentation_block:
; Sequence 88397, Application US/09791537

GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88397
;   LENGTH: 142
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-88397

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Percent Similarity:   88.889       Percent Identity: 78.472

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; Sequence 24944, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24944
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-24944

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    Ratio:    4.366        Gaps:    3
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  336 CGTGTATTACTGTGCCAGAGATTGGCCCAAATAGCTGAACAACGCCTAG 385
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  386 GCTTCTGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 423
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seq_documentation_block:
; Sequence 14698, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055

---

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14698
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-791-537-14698

alignment_scores:
    Quality:    570.50        Length:    141
    Ratio:    4.492        Gaps:    2
Percent Similarity:  90.071   Percent Identity: 80.142

alignment_block:
US-09-019-441-2 x US-09-791-537-14698   ..

Align seg 1/1  to: US-09-791-537-14698  from: 1  to: 138

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    1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT  50
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    1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

   51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGCGCCCAGGAGTGTGAAGCCTT 100
      |||||||||||::||||||||||||||||||||||||||::||||||||
   17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS  34

  101 CGGAGACCCTGCCTGTCTCTGGTGGCTCTGTCAGCAGT 150
      ||||||||||||||||||||||||||||||| |||::||
   34 erGluThrLeuSerLeuThrCysThrValSerGlyTyrSerIle...Ser  49

  151 AGTAACTGGTGGACCTGGATCCGCCAGGCCCCAGGAAGGGACTGGAGTG 200
      ::::::::|||::|||||||||||||||||||||||||||||||||||||
   50 SerAsnTyrTrpSerTrpIleArgGlnAlaProGlyLysGlyLeuGluTr  66

  201 GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCCGTCCC 250
      ||||||  |||  ||||||:::|||::||||:       |||||||||||
   66 pIleGlyTyrIleTyrGlySerSerGlySerAlaTyrTyrAsnProSerL  83

  251 TCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
      ||||||||||||  ||||||  ||||||||||||||||||||||||||||
   83 euLysSerArgValThrIleSerIleAspThrSerLysAsnGlnPheSer  99

  301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
      |||::|||::|||||||||||||||||||||||||||||||||||||||
  100 LeuLysLeuSerValThrAlaAlaAspThrAlaValTyrTyrCysAl  116

  351 CAGAGATTGGGCCCAAATAGCTGGACAACCTAGGCTTCTGGGGCCAGG 400
      |||||| :::  |||    :::|||||||||||||:::||||||||||
  116 aArgAsp......ProTyrGlyProThrTyrPheAspTyrTrpGlyGlnG  131

  401 GAGTCCTGGTCACCGTCTCCTCA 423
      |||||||||||||||||||||||
  131 lyValLeuValThrValSerSer  138
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-14679

seq_documentation_block:
; Sequence 14679, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14679
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Macaca mulatta

US-09-791-537-14679

alignment_scores:
         Quality:   570.50              Length:       146
         Ratio:     4.528               Gaps:           3
Percent Similarity: 86.301    Percent Identity: 77.397

alignment_block:
US-09-019-441-2 x US-09-791-537-14679

Align seg 1/1 to: US-09-791-537-14679  from: 1  to: 140

    1 ATGAAACACCTGGTTCTTCCTCCTCCTGGTGGCAGCTCCAGATGGGT  50
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    1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa 17

   51 CCTGTCCCAGCTGCAGCTGCAGGAGTGCGGGCCCAGGAGTGTGAAGCCTT 100
      |||||||||||::|||||||||||||||||||||::|||||||||||
   17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34

  101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTCAGCAGT 150
      ||||||||||||||:::||||||||||||:::|||||||||||||||
   34 erGluThrLeuSerLeuThrCysAlaValSerGlyGlySerIleSerP 49

  151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
      |||  :::|||  ||||||||||||||||||||||||||||||||||
   50 SerTyrTrpTrpGlyTrpIleArgGlnGlnProGlyLysGlyLeuGluTr 66

  201 GATTGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCCGTCCC 250
      |||  |||||  |||  ||||||||  :::||||  ||||||||||||
   66 pIleGlySerIleTyrTyrSerGlySerThrGluTyrAsnProSerL 83

  251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
      ||||||||||::|||||||||||||||||||||||||||||||||||
   83 euLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 99

  301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
      |||||:::|::|||||||||||||||||||||||||||||||||||||
  100 LeuLysValSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 116

  351 CAGA...........GATTGGGCCCAAATAGCTGGAACAACGCTAG 385
      |||            :::||        ::
  116 aArgGlyAspTyrSerSerAsnTrpTrpTyrPheGlu........... 128

  386 GCTTCTGGGGCCAGGAGTCCTGTTCACCGTCTCCTCA 423
      ||||||||||||||||||||||||||||||||||
  129 ..PheTrpGlyGlnGlyAlaLeuValThrValSerSer 140

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-104990

seq_documentation_block:
; Sequence 104990, Application US/09791537
; GENERAL INFORMATION:
;    APPLICANT: Bionomix, Inc.
;    APPLICANT: Debe, Derek
;    APPLICANT: Danzer, Joseph
;    TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;    TITLE OF INVENTION: METHODS OF USE THEREOF
;    FILE REFERENCE: 261/210
;    CURRENT APPLICATION NUMBER: US/09/791,537
;    CURRENT FILING DATE: 2001-02-22
;    NUMBER OF SEQ ID NOS: 153055
;    SOFTWARE: PatentIn version 3.0
;    SEQ ID NO 104990
;    LENGTH: 140
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-791-537-104990

alignment_scores:
         Quality:   568.50
         Ratio:     4.512
Percent Similarity: 88.112

Length:       141

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US-09-791-537-104990

alignment_scores:
         Quality:   570.50              Ratio:     4.548
Percent Similarity: 88.652    Percent Identity: 80.142

Length:       146              Gaps:       1

alignment_block:
US-09-019-441-2 x US-09-791-537-104990

Align seg 1/1 to: US-09-791-537-104990  from: 1  to: 140

    1 ATGAAACACCTGGTTCTTCCTCCTCCTGGTGGCAGCTCCAGATGGGT  50
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    1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa 17

   51 CCTGTCCCAGCTGCAGCTGCAGGAGTGCGGGCCCAGGAGTGTGAAGCCTT 100
      |||||||||||:||||||||||||||||||::|||||||||||||||
   17 lLeuSerGlnLeuGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34

  101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTCAGCAGT 150
      ||||||||||||||:::||||||||||||:::|||||||||||||||
   34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIleSerSer 50

  151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
      |||  :::||  ||||||||||||||||||||||||||||||||||
   51 SerPheTyrTrpGlyTrpIleArgGlnGlnProGlyLysGlyLeuGluTr 67

  201 GATTGACGTATCTCGGTAGTGGTGGGGCCACCAACTACAACCCGTCCC 250
      ||||||  |||  :||  :||::|||  |||  ||||||||||||||
   67 pIleGlySerIleTyrTyrSer...GlySerThrTyrTyrAsnProSerL 83

  251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
      ||||||||||:::||||||||||||||||||||||||||||||||||
   83 euLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 99

  301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
      |||::|||::|||||||||||||||||||||||||||||||||||||
  100 LeuLysLeuSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 116

  351 CAGAGATTGGGCCCAAATAGCTGGAACAACGCTAGCCTTCTGGGGCCAGG 400
      |||           :::||||        ::::||
  116 aArgArgSerProArgIleValGlyAlaAsnLysAspValTrpGlyGlnG 133

  401 GAGTCCTGGTCACCGTCTCCTCA 423
      |::::|||||||||||||||||
  133 lyThrThrValThrValSerSer 140

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-89302

seq_documentation_block:
; Sequence 89302, Application US/09791537
; GENERAL INFORMATION:
;    APPLICANT: Bionomix, Inc.
;    APPLICANT: Debe, Derek
;    APPLICANT: Danzer, Joseph
;    TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;    TITLE OF INVENTION: METHODS OF USE THEREOF
;    FILE REFERENCE: 261/210
;    CURRENT APPLICATION NUMBER: US/09/791,537
;    CURRENT FILING DATE: 2001-02-22
;    NUMBER OF SEQ ID NOS: 153055
;    SOFTWARE: PatentIn version 3.0
;    SEQ ID NO 89302
;    LENGTH: 143
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-791-537-89302

alignment_scores:
         Quality:   568.50              Length:       143
         Ratio:     4.512               Gaps:           2
Percent Similarity: 88.112    Percent Identity: 78.322

alignment_block:
US-09-019-441-2 x US-09-791-537-89302

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Align seg 1/1  to: US-09-791-537-89302   from: 1  to: 143

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   1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaProArgTrpVa      17

  51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT     100
     ||||||||:::||||||||||||||||||||||||||||||||||||||
  17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS      34

 101 CGGAGACCCTGTCCTCACCTGCACTGTCTCTGGTGGCTCTGTCAGCAGT     150
     ||||||||||:::||||||||||||||||||||:||:::||||||
  34 erGlyThrLeuSerLeuThrCysAlaValSerGlyGlySerIleSerSer      50

 151 AGTAACTGGTGGACCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTG     200
     || ||||||||||||||||||||||||||||:||||
  51 erGlyThrLeuSerLeuThrCysAlaValSerGlySerIleSerSer      50

 201 AGTAACTGGTGGACCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTG     200
     ||||||||  ||:||||||||||||||:||||
  51 SerAsnTrpTrpSerTrpValArgGlnProProGlyLysGlyLeuGluTr      67

 251 GATTGGAGTCATCATTCACAAGACACGTCCAACTACAACCCGTCC     250
     ||||||  ||:||||||||||||||||||:||||||
  67 pIleGlySerIleIleTyrHisSer...GlySerThrAsnTyrAsnProSerL      83

 301 TCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC     300
     |||||||||||||||  ||:||||||||||||||||
  83 euLysSerArgValThrIleSerValAspLysSerLysAsnGlnPheSer      99

 351 CTGAACCTGAACTCTGTGACCGCCGCGACACGCCGTGTATTACTGTGC     350
     ||:::||||||||||||||||||||||||||:||||||
 100 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAl      116

 401 CAGAGATTGGGCCCAAATAGCTGGAACACACGCTAGGCTTC......TGGG     394
     ||||   ::||||||||:||||
 116 aTrpAspSerGlyLeuPheMetProGlnInGlyAlaPheAspIleTrpPG      133

 395 GCCAGGGAGTCCTGGTCACCGTCTCCTCA     423
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 133 lyGlnGlyThrMetValThrValSerSer     142
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-14665

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; seq_documentation_block:
; Sequence 14665, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE:  2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14665
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-791-537-14665
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alignment_scores:
        Quality:   566.50        Length:   141
        Ratio:       4.461        Gaps:       1
Percent Similarity:  90.071   Percent Identity: 78.723
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alignment_block:
US-09-019-441-2 x US-09-791-537-14665

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   1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaAlaProArgTrpVa      17

  51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT     100
     ||||||||:::||||||||||||||||||||||||||::||||||||
  17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS      34

 101 CGGAGACCCTGTCCTCACCTGCGTCTCTGGTGGCTCTGTCAGCAGT     150
     ||||||:::||||||||||||||||||| |||:::||||||||
  34 erGluThrLeuSerLeuThrCysAlaValSerGlyTyrSerIleSerSer      50

 151 AGTAACTGGTGGACCTGGATCCGGCAGCCCCAGGGAAGGGACTGGAGTG     200
       ::: ||||||||||||||||||||||||||||:::||||||
  51 GlyTyrGlyTrpAsnTrpIleArgGlnProProGlyLysGlyLeuGluTr      67

 201 GATTGGAGTATCTCTGGTAGTGGTGGGGGCCACCAACTACACCCCGTCC     250
     |||||  ||::||||||||||  ||  ||||||:::|||||||
  67 pIleGlySerIleGlyGlySerArgGlyAsnThrAsnHisAsnProSerL      84

 251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCAAGAACCAGTTCTCC     300
     |||||||||:::|||||||||||||||||||:::||||||
  84 euLysSerArgValThrIleSerIleAspThrSerLysAsnGlnPheSer     100

 301 CTGAACCTGTGACCGCGGACACGCCGTGTATTACTGTGC     350
     ||:::|| :||||||||||:::||||||||
 101 LeuLysLeuArgSerLeuThrAlaAlaAspThrAlaValPheTyrCysAl     117

 351 CAGAGATTGGGCCCAAATAGCTGGAACAACCCTAGGCTTCTGGGCCAGG     400
     |||||  :::  ::  :::||||||||||
 117 aArgAsp...GlyGlyTyrSerSerArgPhePheAspTyrTrpGlyGlnG     133

 401 GAGTCCTGGTCACCGTCTCCTCA     423
     ||||||||||||||||||||||
 133 lyValLeuValThrValSerSer     140
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; seq_documentation_block:
; Sequence 5239, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE:  2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5239
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-5239
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alignment_scores:
        Quality:   564.00        Length:   150
        Ratio:       4.476        Gaps:       3
Percent Similarity:  84.000   Percent Identity: 74.000
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alignment_block:
US-09-019-441-2 x US-09-791-537-5239

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   1 HisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpValLeuSe      17

  57 CCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGA     106
     ||||||:::||||||||||||||||||||||||||||||||
  17 rGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGlyT      34
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## Left column

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107 CCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTCGTCAGCAGTAGTAAC 156
    ||||||||||||||||||||||||||||||:::||||||||
 34 hrLeuSerLeuThrCysAlaValSerGlyGlySerIleSerSerSerAsn 50

157 TGGTGGACCTGGATCCCCAGCCCCCAGGGAAGGGACTGGAGTGGATTGG 206
    |||::||||||| ||||||||||||||||||||||||||||||
 51 TrpTrpSerTrpValArgGlnProProGlyLysGlyLeuGluTrpIleGl 67

207 ACGTATCTCTGTAGTGGTGGGCCACCAACTACAACCCGTCCCTCCCTCAAGA 256
    |:::|||   |||  ||||||||||||||||||||||||||||
 67 yGlyIleTyrHisSer...GlySerThrAsnTyrAsnProSerLeuLysS 83

257 GTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCCCTGAAC 306
    ||  ||||   ||||| ||| ||||||||||||||:::||||||||||
 83 erAlaValThrIleSerValAspLysSerGlnPheSerLeuLys 99

307 CTGAACTCTGTGACCCGCCGGACACGGCCGTGTATTACTGTGCCCAGAGA 356
    ||:::||||||||    :|||||||||||||||||||||||||
100 LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArg.. 115

357 TTGGGCCCAAATAGCTGGAACAACG.................... 381
    :::|||||||::||
116 .........ValThrGlySerThrPhePheTrpSerGlyTyrTyrThrArgG 129

382 .......CTAGGCTTCTGGGCCCAGGAGTCCTGCTGTCACCGTCTCCTCA 423
    ::    :||||||||||||||||||||||||||||||||||||
129 lyTyrTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 145
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seq_documentation_block:
; Sequence 87942, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 87942
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-87942

alignment_scores:
    Quality:    560.00          Length:    146
    Ratio:      4.341           Gaps:      4
Percent Similarity: 88.356      Percent Identity: 76.712

alignment_block:
US-09-019-441-2 x US-09-791-537-87942
Align seg 1/1  to: US-09-791-537-87942  from: 1  to: 142

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  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT 50
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  1 MetLysHisLeuTrpPhePheLeuLeuLeuLeuValAlaAlaProArgTrpVa 17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    |||||||||||||||||:::|||||||||||||||||:::||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGCTCTGTCAGCAGT 150
    ||||||||||||||||||||||||||||||||||:::||||||||
 34 erGluThrLeuSerLeuThrCysSerValSerGlyLysGlySerIle...Ser 50
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-87942

## Right column

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151 AGTAACTGGTGACCTGATCCGCCACGCCCCAGGGAAGGGACTGGAGTG 200
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 50 ThrTyrTrpTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTr 66

201 GATTGGACGTATCTCTGTAGTGGTGGGCCACCAACTACAACCCGTCCC 250
    |||||| ||||| ||  :: ||:::||||||||||||||||||||
 66 pIleGlyTyrIleSerTyrSer...GlySerThrAsnTyrAsnProSerL 82

251 TCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    |||||||||||||   |||||:::||||||||||||||||||||||
 82 euLysSerArgValThrIleSerGluAspThrSerLysAsnGlnPheSer 98

301 CTGAACTGAACTCTGTGACCCGCCGGACACGGCCGTGTATTACTGTGC 350
    |||::|||::|||||||||||||||:::||||||||||||||||
 99 LeuArgLeuSerSerValThrAlaAlaAspThrAlaLeuTyrTyrCysAl 115

351 CAGAGATTGGGCCCAAATAGCTGGAACAACGCTAGGC............. 387
    ||||::|       :::        :||
115 aArgGluArgArgAsp........ThrThrMetGlyLeuTyrTyrPheA 129

388 ..TTCTGGGCCCAGGAGTCCTGGTCACCGTCTCCTCA 423
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129 spTyrTrpGlyGlnGlyThrArgValThrValSerSer 141
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-105316

seq_documentation_block:
; Sequence 105316, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 105316
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-105316

alignment_scores:
    Quality:    559.00          Length:    141
    Ratio:      4.333           Gaps:      3
Percent Similarity: 91.489      Percent Identity: 78.723

alignment_block:
US-09-019-441-2 x US-09-791-537-105316
Align seg 1/1  to: US-09-791-537-105316  from: 1  to: 138

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  2 MetLysHisLeuTrpPhePheLeuLeuLeuLeuValAlaAlaProArgTrpVa 18

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
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 18 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysPros 35

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGCTCTGTCTCAGCAGT 150
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 35 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIle...Ser 50

151 AGTAACTGGTGACCTGATCCGCCACGCCCCAGGGAAGGGACTGGAGTG 200
    ||| :::|||::||||||||||||||||||||||||||||||||
 51 SerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTr 67

201 GATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACAACCCGTCCC 250
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 67 pIleGlyTyrIleTyrTyrSer...GlySerThrAsnTyrAsnProSerL 83

251 TCAAGAGTCGAGTCATCATTCACAGAACACGTCCAAGAACCAGTTCTCC 300
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301 CTGAACCTGTGACCGCCGACACGGCCGTGTATTACTGTGC 350
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116 aArg.......ValSerLeuThrGlyAspAlaPheAspIleTrpGlyGlnG 131

401 GAGTCCTGTCACCGTCCCTCA 423
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131 lyThrMetValThrValSerSer 138
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-24120

seq_documentation_block:
; Sequence 24120, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24120
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-24120

alignment_scores:
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  Ratio:  4.437     Gaps:    2
Percent Similarity: 81.290  Percent Identity: 69.032

alignment_block:
US-09-019-441-2 x US-09-791-537-24120

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 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProP 34

101 CGGAGACCCGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
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 34 roGlyThrLeuSerLeuThrCysAlaIleSerGlyGlySerIleSerSer 50

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
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201 GATTGGACGTATCTCTGGTAGT.................G 223
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 67 pIleGlyGluLeuSerHisThrAlaSerThrArgAspLysLeuTyrGlnS 84

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101 ValAspLysSerArgAsnGlnPheSerLeuArgLeuSerValThrAl 117

324 CGCGGACACGGCCGTGTATTACTGTGCCAGAGAT............T 358
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359 GGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGCCCAGGAGTCCTG 408
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-89384

seq_documentation_block:
; Sequence 89384, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89384
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; TYPE: PRT
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US-09-791-537-89384

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  Ratio:  4.433     Gaps:    3
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 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysPros 34

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251 TCAAGAGTCGAGTCATCATTCACAGAACACGTCCAAGAACCAGTTCTCC 300
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seq_documentation_block:
; Sequence 16932, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16932
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-16932

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       Ratio:       4.359       Gaps:          3
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alignment_block:
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Date: Sep 23, 2002 10:00 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

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Search information block:
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; Patent No. 6135941
; GENERAL INFORMATION:
;   APPLICANT:  Hillman, Jennifer L.
;   APPLICANT:  Lal, Preeti
;   APPLICANT:  Tang, Y. Tom
;   APPLICANT:  Yue, Henry
;   APPLICANT:  Au-Young, Janice
;   APPLICANT:  Corley, Neil C.
;   APPLICANT:  Guegler, Karl J.
;   APPLICANT:  Baughn, Mariah R.
;   TITLE OF INVENTION:  HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;   NUMBER OF SEQUENCES:  28
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;     STREET:  3174 Porter Drive
;     CITY:  Palo Alto
;     STATE:  CA
;     COUNTRY:  USA
;     ZIP:  94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  DOS
;     SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/049,672A
;     FILING DATE:  HEREWITH
;     CLASSIFICATION:  536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Cerrone, Michael C
;     REGISTRATION NUMBER:  39,132
;     REFERENCE/DOCKET NUMBER:  PF-0497 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  650-855-0555
;     TELEFAX:  650-845-4166
;     TELEX:
;   INFORMATION FOR SEQ ID NO:  4:
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;       TYPE:  amino acid
;       STRANDEDNESS:  single
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;       CLONE:  1513264
US-09-049-672A-4

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        Ratio:  4.333                        Gaps:  3
Percent Similarity:  89.583    Percent Identity:  78.472

alignment_block:
US-09-019-441-2 x US-09-049-672A-4     .

Align seg 1/1  to: US-09-049-672A-4  from: 1  to: 473

    1 ATGAAACACCTGGTTCTTCCTCCTCCTCCTGGTGGCAGCTCCAGATGGGT 50
      ||||||||||||||||||||||||||||||||||||||||||||||||||

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                              TOPOLOGY: linear
                        ;  MOLECULE TYPE: protein
                        ;  US-08-523-894-8

                        alignment_scores:
                                 Quality:  555.50         Length:   147
                                   Ratio:    4.480           Gaps:     2
                        Percent Similarity: 84.354    Percent Identity: 74.830

                        alignment_block:
                        US-09-019-441-2 x US-08-523-894-8

                        Align seg 1/1  to: US-08-523-894-8  from: 1  to: 467

                           1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGTGGCAGCTCCCAGATGGGT  50
                             ||||||||||||||::|||||||||||||||||||||||||||||||||
                           1 MetLysHisLeuTrpPhePheLeuLeuLeuLeuTrpGlnLeuProAspGlyVa  17

                          51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
                             |||||||||||||||||||||||||||||||||||||||||||||||||||
                          17 lLeuSerGlnLeuGlnLeuGlnGluSerGlyProGlyValValLysPro  34

                         101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT  150
                             |||||||||||||:|||||||||||||::|||
                          34 erGluThrLeuSerLeuThrCysAlaValSerGlyGlySerIleThrSer  50

                         151 AGTAAC...TGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGA  197
                             :::::|  ::||||||||||||||||||||||||||||||||||||||||||
                          51 GlyGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGl  67

                         198 GTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACAACCCGT  247
                             |||||||||| ||| ||:::|||  |||:::|||  ||||||||||||||
                          67 uTrpIleGlyTyrIleTyrTyrSer...GlySerThrLeuTyrAsnProS  83

                         248 CCCTCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTC  297
                             ||||||||||||  |:|||  ||||||||||||||||||
                          83 erLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPhe  99

                         298 TCCCTGAACCTGAACTCTGTGACCGCCCGGGACACGGCCGTGTATTACTG  347
                             |||||||::|||:::|||||||||||||||||||||||||||||||||
                         100 SerLeuLysSerSerValThrAlaAlaAspThrAlaValTyrTyrCy  116

                         348 TGCCAGAGATTGGGCCAAATAGCTGGAACAACGCTAGGCTTC.....T  391
                             |||||||||  :::  :::  |||  ||:::|||
                         116 sAlaArgAspAspValGlyLeuArgGlyGlyAsnTyrGlyMetAspValT  133

                         392 GGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA  423
                             ||||||||||||::|||||||||||||||||
                         133 rpGlyGlnGlyThrLeuValThrValSerSer  143

                        seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-523-894-8

                        seq_documentation_block:
                        ;  Sequence 8, Application US/08523894
                        ;  Patent No. 6136310
                        ;  GENERAL INFORMATION:
                        ;     APPLICANT:  Hanna, Nabil
                        ;     APPLICANT:  Newman, Roland A.
                        ;     APPLICANT:  Reff, Mitchell E.
                        ;     TITLE OF INVENTION:  Recombinant Anti-CD4 Antibodies for Human
                        ;     TITLE OF INVENTION:  Therapy
                        ;     NUMBER OF SEQUENCES:  59
                        ;     CORRESPONDENCE ADDRESS:
                        ;        ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
                        ;        STREET:  699 Prince Street
                        ;        CITY:  Alexandria
                        ;        STATE:  VA
                        ;        COUNTRY:  USA
                        ;        ZIP:  22314-3187
                        ;     COMPUTER READABLE FORM:
                        ;        MEDIUM TYPE:  Floppy disk
                        ;        COMPUTER:  IBM PC compatible
                        ;        OPERATING SYSTEM:  PC-DOS/MS-DOS
                        ;        SOFTWARE:  PatentIn Release #1.0, Version #1.30
                        ;     CURRENT APPLICATION DATA:
                        ;        APPLICATION NUMBER:  US/08/523,894
                        ;        FILING DATE:  06-SEP-1995
                        ;        CLASSIFICATION:  424
                        ;     ATTORNEY/AGENT INFORMATION:
                        ;        NAME:  Teskin, Robin L.
                        ;        REGISTRATION NUMBER:  35,030
                        ;        REFERENCE/DOCKET NUMBER:  012712-165
                        ;     TELECOMMUNICATION INFORMATION:
                        ;        TELEPHONE:  703-836-6620
                        ;        TELEFAX:  703-836-2021
                        ;  INFORMATION FOR SEQ ID NO:  8:
                        ;     SEQUENCE CHARACTERISTICS:
                        ;        LENGTH:  467 amino acids
                        ;        TYPE:  amino acid
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/523,894
;       FILING DATE:  06-SEP-1995
;       CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;       NAME:  Teskin, Robin L.
;       REGISTRATION NUMBER:  35,030
;       REFERENCE/DOCKET NUMBER:  012712-165
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  703-836-6620
;       TELEFAX:   703-836-2021
; INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  467 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;       MOLECULE TYPE:  protein
US-08-523-894-10

alignment_scores:
          Quality:  555.50                   Length:   147
          Ratio:    4.480                     Gaps:      2
Percent Similarity:  84.354     Percent Identity:  74.830

alignment_block:
US-09-019-441-2 x US-08-523-894-10          ..

Align seg 1/1  to: US-08-523-894-10  from: 1  to: 467

    1 ATGAAACACCTGGTTCTTCCTCCTCCTCGTGGCAGCTCCCAGATGGGT  50
      |||||||||||||||||||||||||||||||||||||||||||||||||
    1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

   51 CCTGTCCCAGCTGCAGCTGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
      ||||||||||||||::||||||||||||||||||||:||||||||||
   17 lLeuSerGlnValGlnLeuGluSerGlyProGlyLeuValLysProS  34

  101 CGGAGACCCGTCCCTCACCTGCCTGTCTCGGTGGCTCGTGTCAGCAGT  150
      |||||||||||||||||||||::||||||||||::|||::|||||||
   34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly  50

  151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG  200
      :::  ::||||  |||||  ||||||||||||||||||||||||||||
   51 AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr  67

  201 GATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACAAACCCGTCCC  250
      |||||||    ||::||||||||||||||||||||||||||||||||
   67 pIleGlyTyrIleTyrGlySerGlyGlyGlyThrAsnTyrAsnProSerL  84

  251 TCAAGAGTCGAGTCATCATTTCACAGAGACACGTCCAAGAACCAGTTCTCC  300
      ||::||::||||  |||||  |||||||||||||||||||||
   84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer  140

  301 CTGAACCTGAACTCTGTGACCCGCCGCGGACACGGCCGTGTATTACTGTGC  350
      ||::|::||::||||||||||||||||||||||||||||||||
  101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl  117

  351 CAGAGAT............TGGGGCCCAAATAGCTGGAACAACGC  382
      |  ::|              ||
  117 aSerAsnIleLeuLysTyrLeuHisTrp.............L  127

  383 TAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA  423
      ||  ::||||||||||||||||||||||||
  127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSerSer  140

seq_name:  /cgn2_6/ptodata/2/iaa/6B_COMB pep:US-08-523-894-12

seq_documentation_block:
; Sequence 12, Application US/08523894
; Patent No. 6136310

;    GENERAL INFORMATION:
;       APPLICANT:  Hanna, Nabil
;       APPLICANT:  Newman, Roland A.
;       APPLICANT:  Reff, Mitchell E.
;       TITLE OF INVENTION:  Recombinant Anti-CD4 Antibodies for Human
;       TITLE OF INVENTION:  Therapy
;       NUMBER OF SEQUENCES:  59
;       CORRESPONDENCE ADDRESS:
;          ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;          STREET:  699 Prince Street
;          CITY:  Alexandria
;          STATE:  VA
;          COUNTRY:  USA
;          ZIP:  22314-3187
;       COMPUTER READABLE FORM:
;          MEDIUM TYPE:  Floppy disk
;          COMPUTER:  IBM PC compatible
;          OPERATING SYSTEM:  PC-DOS/MS-DOS
;          SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;          APPLICATION NUMBER:  US/08/523,894
;          FILING DATE:  06-SEP-1995
;          CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;          NAME:  Teskin, Robin L.
;          REGISTRATION NUMBER:  35,030
;          REFERENCE/DOCKET NUMBER:  012712-165
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE:  703-836-6620
;          TELEFAX:   703-836-2021
; INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  467 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;       MOLECULE TYPE:  protein
US-08-523-894-12

alignment_scores:
          Quality:  555.50                   Length:   147
          Ratio:    4.480                     Gaps:      2
Percent Similarity:  84.354     Percent Identity:  74.830

alignment_block:
US-09-019-441-2 x US-08-523-894-12          ..

Align seg 1/1  to: US-08-523-894-12  from: 1  to: 467

    1 ATGAAACACCTGGTTCTTCCTCCTCCTCGTGGCAGCTCCCAGATGGT  50
      |||||||||||||||||||||||||||||||||||||||||||||||
    1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

   51 CCTGTCCCAGCTGCAGCTGGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
      ||||||||||||||::||||||||||||||||||||:||||||||||
   17 lLeuSerGlnValGlnLeuGluSerGlyProGlyLeuValLysProS  34

  101 CGGAGACCCGTCCCTCACCTGCCTGTCTCGGTGGCTCGTGTCAGCAGT  150
      |||||||||||||||||||||::||||||||||::|||::|||||||
   34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly  50

  151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG  200
      :::  ::||||  |||||  ||||||||||||||||||||||||||||
   51 AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr  67

  201 GATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACAACCCGTCCC  250
      ||||||    |||::||||||||::||||||||||||||||||
   67 pIleGlyTyrIleTyrGlySerGlyGlyGlyThrAsnTyrAsnProSerL  84

  251 TCAAGAGTCGAGTCATCATTCACAGAGACACGTCCAAGAACCAGTTCTCC  300
      ||::||::||||||||  ||||||||||||||||||||||
   84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer  100

301 CTGAACCTGAACTCTGTGACCGCCGCGGGACACGGCCGTGTATTACTGTGC 350
    ||||::::||:::||||||||||||||||||||||||||||||||||
101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 117

351 CAGAGAT..............TGGGGCCAAATAGCTGGAACAACGC 382
    |                    |||
117 aSerAsnIleLeuLysTyrLeuHisTrp.............L 127

383 TAGGCTTCTGGGGCCAGGGAGTCCTGTCACCGTCCTCA 423
    ||  ::||||||||||||||||||||||||||||||
127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSerSer 140

seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-487-550-12

alignment_scores:
       Quality:  550.50          Length:         153
         Ratio:    4.476            Gaps:           2
Percent Similarity:  80.392   Percent Identity:  71.242

alignment_block:
US-09-019-441-2 x US-08-487-550-12   ..

Align seg 1/1  to: US-08-487-550-12  from: 1  to: 476

  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT 50
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  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa 17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    ||||||||||:::||||||||||||||||||:::||||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34

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101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTCTGTCAGAGT 150
    |||||||||||||||||||||||||||||||||::::||:::||||||||
 34 erGluThrLeuSerLeuThrCysAlaValSerGlyGlySerIleSerGly 50

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
    :::||||||||||||||||||||||||||||||||||||||
 51 GlyTyrTrpGlyTrpIleArgGlnProProGlyLysGlyLeuGluTr 67

201 GATTGGACGTATCTCTGGTAGTGTGGGGCCACCAACTACAACCCGTCCC 250
    ||||||  :::|||||::||   ||||||||||||||
 67 pIleGlySerPheTyrSerSerGlyAsnThrTyrTyrAsnProSerL 84

251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    ||||||||:::|||  |||||  ||||||||||||||||||||
 84 euLysSerGlnValThrIleSerThrArgAspThrSerLysAsnGlnPheSer 100

301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
    |||:::||||||||:::|||||||||||||||||||||||||
101 LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyrTyrCysVa 117

351 CAGAGAT..............................TGGGCCC 364
    :||||||                               |||
117 lArgAspArgLeuPheSerValValGlyMetValTyrAsnAsnTrpPheA 134

365 AAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACC 414
    :::||                 |||||||||||||||||||||
134 spVal..................TrpGlyProGlyValLeuValThr 143

415 GTCTCCTCA 423
    |||||||||
144 ValSerSer 146

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-478-039-108

;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince St.
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22313-1404
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/476,349A
;     FILING DATE: 07-JUN-1995
;     CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/379,072
;     FILING DATE: 25-JAN-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/912,292
;     FILING DATE: 10-JUL-1992
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/856,281
;     FILING DATE: 23-MAR-1992
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/735,064
;     FILING DATE: 25-JUL-1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Teskin Esq., Robin L.
;     REGISTRATION NUMBER: 35,030
;     REFERENCE/DOCKET NUMBER: 012712-161
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 703-836-6620
;     TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 108:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 139 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-476-349A-108

alignment_scores:
        Quality: 548.50           Length: 146
        Ratio: 4.459              Gaps: 2
Percent Similarity: 84.247     Percent Identity: 73.973

alignment_block:
US-09-019-441-2 x US-08-476-349A-108      ..

Align seg 1/1 to: US-08-476-349A-108 from: 1 to: 139

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  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa 17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    |||||||||:::||||||||:::||||||||:::||||||||||||||||
 17 lLeuSerGlnValGlnLeuGlnSerProGlyLysLysGlyLeuValLysProS 34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    ||||||||||||||||||||||||::::||||:::||::||:::::||||
 34 erGluThrLeuSerLeuThrCysSerValSerGlySerIleSerGly 50

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
    ::: ::||||   ||||||||||||||||||  ||||||||||||||||
 51 AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr 67

201 GATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTACAACCCGTCC 250
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 67 pIleGlyTyrIleTyrGlyGlyGlyGlyThrAsnTyrAsnProSerL 84

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-476-349A-108

;   NAME: Teskin Esq., Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-160
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 703-836-6620
;     TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 108:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 139 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-478-039-108

alignment_scores:
        Quality: 548.50           Length: 146
        Ratio: 4.459              Gaps: 2
Percent Similarity: 84.247     Percent Identity: 73.973

alignment_block:
US-09-019-441-2 x US-08-478-039-108       ..

Align seg 1/1 to: US-08-478-039-108 from: 1 to: 139

  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT 50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa 17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    |||||||||:::||||||||:::||||||||:::||||||||||||||||
 17 lLeuSerGlnValGlnLeuGlnGluAlaGlyProGlyLeuValLysProS 34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGT 150
    ||||||||||||||||||||||||||||||||:::||:::||:::::||
 34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly 50

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
    |||::::|||   |||||||||||||||||  |||||||||||||||||
 51 AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr 67

201 GATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTACAACCCGTCC 250
    ||||||  ||   |||  :::|||||||||:::::||||||||||||||
 67 pIleGlyTyrIleTyrGlySerGlyGlyGlyThrAsnTyrAsnProSerL 84

251 TCAAGAGTCCAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    ||:::::|||||  |||||  ||||||| |||||||  |||||||||||
 84 euAsnAsnArgValSerIleSerIleSerLysAspThrSerLysAsnPheSer 100

301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
    |||:::||:::||||||||||||||||||||||||||||||||||||||
101 LeuLysLeuArgServalThrAlaAlaAspThrAlaValTyrTyrCysAl 117

351 CAGAGAT...........TGGGCCCAAATAGCTGGAACAACGC 382
    |||        ::|        ||
117 aSerAsnIleLeuLysTyrLeuHisTrp............L 127

383 TAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
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127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSer 139

seq_documentation_block:
; Sequence 108, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
;   APPLICANT: Newman, Roland A.
;   APPLICANT: Hanna, Nabil
;   APPLICANT: Raab, Ronald W.
;   TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
;   NUMBER OF SEQUENCES: 114
;   CORRESPONDENCE ADDRESS:

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251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    |!:::::!!!!!  !!!!!  !!!!!!!!!!!!  !!!!!
 84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100

301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
    !!!:::!!:::!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 117

351 CAGAGAT...............TGGGCCCAAATAGCTGGAACAACGC 382
    |  ::                              ||
117 aSerAsnIleLeuLysTyrLeuHisTrp...............L 127

383 TAGGCTTCTGGGGCCAGGAGTCCTGGTCACCGTCTCC 420
    ||  ::!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSer 139

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-523-894-2

seq_documentation_block:
; Sequence 2, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
;.  APPLICANT: Hanna, Nabil
;.  APPLICANT: Newman, Roland A.
;.  APPLICANT: Reff, Mitchell E.
;.  TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human.
;.  TITLE OF INVENTION: Therapy
;.  NUMBER OF SEQUENCES: 59
;.  CORRESPONDENCE ADDRESS:
;.   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;.   STREET: 699 Prince Street
;.   CITY: Alexandria
;.   STATE: VA
;.   COUNTRY: USA
;.   ZIP: 22314-3187
;.  COMPUTER READABLE FORM:
;.   MEDIUM TYPE: Floppy disk
;.   COMPUTER: IBM PC compatible
;.   OPERATING SYSTEM: PC-DOS/MS-DOS
;.   SOFTWARE: PatentIn Release #1.0, Version #1.30
;.  CURRENT APPLICATION DATA:
;.   APPLICATION NUMBER: US/08/523,894
;.   FILING DATE: 06-SEP-1995
;.   CLASSIFICATION: 424
;.  ATTORNEY/AGENT INFORMATION:
;.   NAME: Teskin, Robin L.
;.   REGISTRATION NUMBER: 35,030
;.   REFERENCE/DOCKET NUMBER: 012712-165
;.  TELECOMMUNICATION INFORMATION:
;.   TELEPHONE: 703-836-6620
;.   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 2:
;.  SEQUENCE CHARACTERISTICS:
;.   LENGTH: 139 amino acids
;.   TYPE: amino acid
;.   TOPOLOGY: linear
;.  MOLECULE TYPE: protein
US-08-523-894-2

alignment_scores:
    Quality:  548.50              Length:  146
    Ratio:   4.459                Gaps:    2
Percent Similarity: 84.247    Percent Identity: 73.973

alignment_block:
US-09-019-441-2 x US-08-523-894-2

Align seg 1/1 to: US-08-523-894-2  from: 1 to: 139

  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT 50
    |   |||||||||||||||!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
  1 MetLysHisLeuTrpPhePheLeuLeuLeuLeuValAlaAlaProArgTrpVa 17
```

```
 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCGCAGGAGTGGTGAAGCCTT 100
    |||||||||||||||||||||||||||||||||||||::!!!!!!!!!!!!
 17 lLeuSerGlnValGlnLeuGlnGluGluSerGlyAlaGlyProGlyLeuValLysPros 34

101 CGGAGACCCCTGCCCTCACCTGCGCTGTCTGTGGTGGTGCCTCTGTCAGCAGT 150
    |||||||!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!::!!!::!!!:::
 34 erGluThrLeuSerLeuThrCysSerValSerGlySerIleSerGly 50

151 AGTAACTGGTGACCTGGACCCAGCCCCAGGGAAGGGACTGGAGTG 200
    :::  ::!!! |||||||||||   |||||||||||||||||||||
 51 AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr 67

201 GATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTACACCCGTCCC 250
    |||||| |||| ::|||||||!!!!!!!!!!!!!!!!!!!!!!!!!!!!
 67 pIleGlyTyrIleTyrGlySerGlyGlyThrAsnTyrAsnProSerL 84

251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC 300
    !!:::::!!!!! |||||  !!!!!!!!!!!!!  !!!!!
 84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100

301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCCGTGTATTACTGTGC 350
    !!!:::!!:::!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 117

351 CAGAGAT...............TGGGCCCAAATAGCTGGAACAACGC 382
    |   ::                              |||
117 aSerAsnIleLeuLysTyrLeuHisTrp...............L 127

383 TAGGCTTCTGGGGCCAGGAGTCCTGGTCACCGTCTCC 420
    ||  ::!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSer 139

seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-487-550-4

seq_documentation_block:
; Sequence 4, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
;.  APPLICANT: Anderson, Darrell R.
;.  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;.  TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;.  TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;.  TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;.  NUMBER OF SEQUENCES: 12
;.  CORRESPONDENCE ADDRESS:
;.   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;.   STREET: 699 Prince Street
;.   CITY: Alexandria
;.   STATE: VA
;.   COUNTRY: USA
;.   ZIP: 22314
;.  COMPUTER READABLE FORM:
;.   MEDIUM TYPE: Floppy disk
;.   COMPUTER: IBM PC compatible
;.   OPERATING SYSTEM: PC-DOS/MS-DOS
;.   SOFTWARE: PatentIn Release #1.0, Version #1.30
;.  CURRENT APPLICATION DATA:
;.   APPLICATION NUMBER: US/08/487,550
;.   FILING DATE: 07-JUN-1995
;.   CLASSIFICATION: 435
;.  ATTORNEY/AGENT INFORMATION:
;.   NAME: Teskin, Robin L.
;.   REGISTRATION NUMBER: 35,030
;.   REFERENCE/DOCKET NUMBER: 012712-131
;.  TELECOMMUNICATION INFORMATION:
;.   TELEPHONE: 703-836-6620
;.   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 4:
;.  SEQUENCE CHARACTERISTICS:
;.   LENGTH: 476 amino acids
;.   TYPE: amino acid
;.   TOPOLOGY: linear
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;  MOLECULE TYPE: protein
US-08-487-550-4

alignment_scores:
        Quality:     524.50              Length:     146
        Ratio:       4.264               Gaps:       2
Percent Similarity: 84.247    Percent Identity: 71.233

alignment_block:
US-09-019-441-2 x US-08-487-550-4       .

Align seg 1/1  to: US-08-487-550-4   from: 1  to: 476

   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGTGGCAGCTCCCAGATGGGT    50
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa    17

  51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT   100
     ||||||||||||:::||||||  ||| ||:::||||||||||||||||||
  17 lLeuSerGlnValLysLeuGlnLeuGlnTrpGlyGluGlyLeuLeuGlnProS    34

 101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCTGTCAGCAGT   150
     |||||||||||  |||||:|||||||:::|||||||||||::::|||:::
  34 erGluThrLeuSerArgThrCysValSerGlyGlySerIleSerGly    50

 151 AGTAACTGGTGACCTGGATCCGCCAGCCCCCAGGGAAGGACTGGAGTG    200
     :::||||||||||||||||  ||||||::||||||||||||||||||||
  51 TyrTyrTyrTrpThrTrpIleArgGlnThrProGlyArgGlyLeuGluTr    67

 201 GATTGGACGTATCTTCTGGTAGTGTTGGGGCCACCAACTACAACCCGTCC   250
     ||||||||||||  ||:||||||||||||||||||||||||||||||||||
  67 pIleGlyHisIleTyrGlyAlaAsnGlyAlaThrThrAsnTyrAsnProSerL    84

 251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC   300
     ||||||||||||||||||||||:::||||||||||||||||||||||||
  84 euLysSerArgValThrIleSerLysAspThrSerLysAsnGlnPhePhe   100

 301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC   350
     |||||||||||||||||||||  ||||||||||||||||||||||||||||
 101 LeuAsnLeuAsnSerValThrAspAlaAspThrAlaValTyrTyrCysAl    117

 351 CAGA........GATTGGGCCAAATAGCT...GGAACAACGCTAG   385
     ||||          ||| ::: |||||     |:|
 117 aArgGlyProArgProAspCysThrThrIleCysTyrGlyGlyTrpValA   134

 386 GCTTCTGGGGCCAGGGAGCTCCTGTCACCGTCTCCTCA   423
     |||||   ||| ||||||||||||||||||||||
 134 spValTrpGlyProGlyAlaAspLeuValThrValSerSer    146
```

```
;  MOLECULE TYPE: protein
US-08-480-774A-2

alignment_scores:
        Quality:     519.50              Length:     150
        Ratio:       4.190               Gaps:       4
Percent Similarity: 82.667    Percent Identity: 71.333

alignment_block:
US-09-019-441-2 x US-08-480-774A-2

Align seg 1/1  to: US-08-480-774A-2   from: 1  to: 142

   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGTGGCAGCTCCCAGATGGGT    50
     ||:::||||||||||||||||||||||||||||||||||||||||||||
   1 MetGluHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa    17

  51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT   100
     |||||| |||||||||||  ||| |||:::||||||||||||||||||||
  17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS    34

 101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCTGTCAGCAGT   150
     ||||||||||||||:::||||||||||:::||||||||||:::|||:::||
  34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIle...Ser    49

 151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGACTGGAGTG   200
     ||:::||||||||||||||||||||:::||||||||||||||||||:||
  50 SerHisTyrTrpSerTrpIleArgGlnSerProGlyLysGlyLeuGlnTr    66

 201 GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCCGTCCC   250
     ||||||| ||||:|| ||:::||||||||:||||||:::|||||||||||
  66 pIleGlyTyrIleTyrTyrSer...GlySerThrAsnTyrSerProSerL    82

 251 TCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC   300
     |||||||||| ||||  ::|||||||||||||||||||||||||||||||
  82 euLysSerArgValThrIleSerValGluThrSerLysAsnGlnPheSer    98

 301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC   350
     |||::|||:::||||||||||||||||||||||||||||||||||||||
  99 LeuLysLeuThrSerMetThrAlaAlaAspThrAlaValTyrTyrCysAl    115

 351 CAGA...................GATTGGGCCCAAATAGCTG   373
     ||||                    ||:::
 115 aArgGlyProValProAlaValPheTyrGlyAspTyr...............   127
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seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-480-774A-2

seq_documentation_block:
;  Sequence 2, Application US/08480774A
;  Patent No. 5852186
;  GENERAL INFORMATION:
;  APPLICANT:    MARASCO, Wayne A.
;  APPLICANT:    SODROSKI, Joseph G.
;  APPLICANT:    HASELTINE, William A.
;  APPLICANT:    POSNER, Marshall R.
;  TITLE OF INVENTION:    REACTIVE NEUTRALIZING HUMAN
;  TITLE OF INVENTION:    ANTI-gp 120 RECOMBINANT ANTIBODY, DNA CODING THE SAME
;  TITLE OF INVENTION:    AND USE THEREOF
;  NUMBER OF SEQUENCES:   16
;  CORRESPONDENCE ADDRESS:
;     ADDRESSEE:   DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
;     STREET:  130 Water Street
;     CITY:    Boston
;     STATE:   MA
;     COUNTRY: USA
;     ZIP:     02109
;  COMPUTER READABLE FORM:
;     MEDIUM TYPE:   Diskette
```

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;     COMPUTER:       IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE:  FastSEQ for Windows Version 2.0
;  CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/480,774A
;     FILING DATE:   07-JUN-1995
;     CLASSIFICATION: 435
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/400,674
;     FILING DATE:   08-MAR-1995
;     APPLICATION NUMBER:  07/804,652
;     FILING DATE:   10-DEC-1991
;  ATTORNEY/AGENT INFORMATION:
;     NAME:  Resnick, David S
;     REGISTRATION NUMBER:  34,235
;     REFERENCE/DOCKET NUMBER:  41450-FWC-DIV
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  617-523-3400
;     TELEFAX:   617-523-6440
;     TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;     LENGTH:  142 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;  MOLECULE TYPE:  protein
;  FRAGMENT TYPE:  internal
US-08-480-774A-2
```

374 GAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACGGTCCTCCTCA 423
　　　||| 　　||||||||||||::::|||||||||||||||
128 .....ArgLeuAspProTrpGlyGlnGlyThrLeuValThrValSerSer 142

seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-545-809A-114

seq_documentation_block:
; Sequence 114, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
;　APPLICANT: Honjo, Tasuku
;　APPLICANT: Matsuda, Fumihiko
;　TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
;　TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;　NUMBER OF SEQUENCES: 145
;　CORRESPONDENCE ADDRESS:
;　　ADDRESSEE: Fish & Richardson, P.C.
;　　STREET: 225 Franklin Street
;　　CITY: Boston
;　　STATE: MA
;　　COUNTRY: US
;　　ZIP: 02110-2804
;　COMPUTER READABLE FORM:
;　　MEDIUM TYPE: Diskette
;　　COMPUTER: IBM Compatible
;　　OPERATING SYSTEM: Windows95
;　　SOFTWARE: FastSEQ for Windows Version 2.0
;　CURRENT APPLICATION DATA:
;　　APPLICATION NUMBER: US/08/545,809A
;　　FILING DATE: 27-MAR-1996
;　PRIOR APPLICATION DATA:
;　　APPLICATION NUMBER: PCT/JP93/00603
;　　FILING DATE: 10-MAY-1993
;　ATTORNEY/AGENT INFORMATION:
;　　NAME: Freeman, John W.
;　　REGISTRATION NUMBER: 29,066
;　　REFERENCE/DOCKET NUMBER: 06501/004001
;　TELECOMMUNICATION INFORMATION:
;　　TELEPHONE: 617-542-5070
;　　TELEFAX: 617-542-8906
;　　TELEX: 200154
; INFORMATION FOR SEQ ID NO: 114:
;　SEQUENCE CHARACTERISTICS:
;　　LENGTH: 117 amino acids
;　　TYPE: amino acid
;　　TOPOLOGY: linear
;　MOLECULE TYPE: protein
US-08-545-809A-114

alignment_scores:
　　Quality: 518.50　　　　　Length: 118
　　Ratio: 4.757　　　　　　 Gaps: 1
Percent Similarity: 92.373　　Percent Identity: 84.746

alignment_block:
US-09-019-441-2 x US-08-545-809A-114

Align seq 1/1　to: US-08-545-809A-114　from: 1　to: 117

1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT 50
　||||||||||||||||||||||||||||||||||||||||||||||||||
1 MetLysHisLeuTrpPhePheLeuLeuLeuLeuValAlaAlaProArgTrpVa 17

51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyValLysProS 34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTGTGGCTCTGTCAGCAGT 150
34 erAspThrLeuSerLeuThrCysAlaValSerGlyTyrSerIleSerSer 50

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200

51 SerAsnTrpTrpThrTrpIleArgGlnProProGlyLysGlyLeuGluTr 67

201 GATTGGACGTATCTCGGTAGTGGTGGGGCCACCAACTACACACCCGTCCC 250
　||||||||　|||　　|||　　　|||::||| 　|||||||||||
67 pIleGlyTyrIleTyrTyrSer...GlySerThrTyrTyrAsnProSerL 83

251 TCAAGAGTCCAGTCATCATTCACAAGACACGTCCAAGAACCAGTCTCC 300
　||||||||||　||| 　　::||| 　　||| 　||||||||||||||
83 euLysSerArgValThrMetSerValAspThrSerLysAsnGlnPheSer 99

301 CTGAACCTGAACTCTGTGACCGCCCGGACACGGCCGTGTATTACTGTGC 350
　|||::||:||:::||||||||||||::|||||::||||||||||||||||
100 LeuLysLeuSerValThrAlaValAspThrAlaValThrTyrTyrCysAl 116

351 CAGA 354
　||||
116 aArg 117

seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-545-809A-142

seq_documentation_block:
; Sequence 142, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
;　APPLICANT: Honjo, Tasuku
;　APPLICANT: Matsuda, Fumihiko
;　TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
;　TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;　NUMBER OF SEQUENCES: 145
;　CORRESPONDENCE ADDRESS:
;　　ADDRESSEE: Fish & Richardson, P.C.
;　　STREET: 225 Franklin Street
;　　CITY: Boston
;　　STATE: MA
;　　COUNTRY: US
;　　ZIP: 02110-2804
;　COMPUTER READABLE FORM:
;　　MEDIUM TYPE: Diskette
;　　COMPUTER: IBM Compatible
;　　OPERATING SYSTEM: Windows95
;　　SOFTWARE: FastSEQ for Windows Version 2.0
;　CURRENT APPLICATION DATA:
;　　APPLICATION NUMBER: US/08/545,809A
;　　FILING DATE: 27-MAR-1996
;　PRIOR APPLICATION DATA:
;　　APPLICATION NUMBER: PCT/JP93/00603
;　　FILING DATE: 10-MAY-1993
;　ATTORNEY/AGENT INFORMATION:
;　　NAME: Freeman, John W.
;　　REGISTRATION NUMBER: 29,066
;　　REFERENCE/DOCKET NUMBER: 06501/004001
;　TELECOMMUNICATION INFORMATION:
;　　TELEPHONE: 617-542-5070
;　　TELEFAX: 617-542-8906
;　　TELEX: 200154
; INFORMATION FOR SEQ ID NO: 142:
;　SEQUENCE CHARACTERISTICS:
;　　LENGTH: 118 amino acids
;　　TYPE: amino acid
;　　TOPOLOGY: linear
;　MOLECULE TYPE: protein
US-08-545-809A-142

alignment_scores:
　　Quality: 518.00　　　　　Length: 119
　　Ratio: 4.667　　　　　　 Gaps: 2
Percent Similarity: 93.277　　Percent Identity: 86.555

alignment_block:
US-09-019-441-2 x US-08-545-809A-142

Align seg 1/1  to: US-08-545-809A-142  from: 1  to: 118

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  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT  50
    ||||||||||||||||||||||:::|||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    ||||||||||::::|||||||||||||||||||:::||||||||||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS  34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTCTCTGCTCTCAGCAGT 150
    |||||||||||||||||||||||:::||||||||||||||||||||||||
 34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerValSerSer  50

151 ...AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGA 197
    ||   ::|||:::||||||||||||||||||||||||||||||||||||
 51 GlySerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGl  67

198 GTGGATTGGACGTATCCTGGTAGTGGTGGGCCACCAACTACAACCCGT   247
    ||||||||| ||   |||   |||||:::||||||||||||||||||||
 67 uTrpIleGlyTyrIleTyrTyrSer...GlySerThrAsnTyrAsnProS  83

248 CCCTCAAGAGTGGAGTCACATTCACAAGACACGTCCAAGAACCAGTTC   297
    ||||||||||||||| ||||| ||||||||||||||||||||||||||||
 83 erLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPhe  99

298 TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTG 347
    |||:::|||:::|||:::|||||||||||||||||||||||||||||||
100 SerLeuSerLeuSerValThrAlaAlaAspThrAlaValTyrTyrCy    116

348 TGCCAGA  354
    |||||||
116 sAlaArg 118
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INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:

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LENGTH: 116 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
    MOLECULE TYPE: protein
US-08-545-809A-140

alignment_scores:
    Quality: 514.00          Length: 118
    Ratio:  4.673             Gaps:   2
Percent Similarity: 93.220   Percent Identity: 86.441

alignment_block:
US-09-019-441-2 x US-08-545-809A-140

Align seg 1/1  to: US-08-545-809A-140  from: 1  to: 116

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  1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT  50
    ||||||||||||||||||||||:::|||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    ||||||||||::::|||||||||||||||||||:::||||||||||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS  34

101 CGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTCTCTGCTCTCAGCAGT 150
    |||||||||||||||||||||||:::||||||||||||:::||
 34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerVal...Ser  49

151 AGTAACTGGTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTG 200
    |||   ::|||:::||||||||||||||||||||||||||||||||||
 50 SerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTr  66

201 GATTGGACGTATCCTGGTAGTGGTGGGCCACCAACTACAACCCGTCCC   250
    ||| ||| |||   |||   |||||:::.GlySerThrAsnProSerL   82
 66 pIleGlyTyrIleTyrTyrSer...GlySerThrAsnProSerL       82

251 TCAAGAGTGGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTCTCC  300
    |||||||||||| ||||| ||||||||||||||||||||||||||||||
 82 euLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer  98

301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
    |||:::|||:::|||:::|||||||||||||||||||||||||||||||
 99 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 115

351 CAGA 354
    ||||
115 aArg 116
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seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-545-809A-140

seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-545-809A-123

seq_documentation_block:
; Sequence 123, Application US/0854809A
; Patent No. 6096878
; GENERAL INFORMATION:
;   APPLICANT: Honjo, Tasuku
;   APPLICANT: Matsuda, Fumihiko
;   TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
;   TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;   NUMBER OF SEQUENCES: 145
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Fish & Richardson, P.C.
;     STREET: 225 Franklin Street
;     CITY: Boston
;     STATE: MA
;     COUNTRY: US
;     ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: Windows95
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-123

alignment_scores:
         Quality:    513.00              Length:    119
           Ratio:      4.664              Gaps:        2
Percent Similarity:   92.437    Percent Identity:  85.714

alignment_block:
US-09-019-441-2 x US-08-545-809A-123        ..

Align seg 1/1  to: US-08-545-809A-123   from: 1  to: 118

  1 ATGAAACACCTGTGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT  50
    |||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    |||||||||||||||||||||||||||||||||||||||||||:|||||||
 17 lLeuSerGlnLeuGlnLeuGlnGluSerGlyProGlyLeuValLysProS  34

101 CGGAGACCCTGTCCCTCACCTGCGTCTCTGGTGGCTCTGTCAGCAGT 150
    |||||||||||||||||||||||||||||:||| ||||||||||||
 34 erGluThrLeuSerLeuThrCysValSerGlyGlySerIleSerSer  50

151 AGTAAC...TGGTGGACCTGGATCGGCCAGCCCCCAGGGAAGGGACTGGA 197
    ||||::   :::|||| |||||||||||||||||||||||||||||||||
 51 SerSerTyrTyrTrpGlyThrTrpIleArgGlnProProGlyLysGlyLeuGl  67

198 GTGGATTGGACGTATCTCGGTAGTGGTGGGGGCCACCAACCCGT 247
    ||||||||  |||||  || :||||||||||||||||||||||||
 67 uTrpIleGlySerIleTyrTyrSer...GlySerThrTyrTyrAsnProS  83

248 CCCTCAAGAGTCGAGTCATCATTTCACAGACACGTCCAAGAACCAGTTC 297
    ||||||||||| |||||||||||||||||||||||||||||||||||||
 83 erLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPhe  99

298 TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTG 347
    ||||||:||:|||||||||||||||||||||||||||||||||||||||
100 SerLeuLysLeuAsnSerValThrAlaAlaAspThrAlaValTyrTyrCy 116

348 TGCCAGA 354
    |||||||
116 sAlaArg 118

seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-545-809A-92

seq_documentation_block:
; Sequence 92, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

TITLE OF INVENTION:  SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Fish & Richardson, P.C.
  STREET: 225 Franklin Street
  CITY: Boston
  STATE: MA
  COUNTRY: US
  ZIP: 02110-2804
COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette
  COMPUTER: IBM Compatible
  OPERATING SYSTEM: Windows95
  SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/545,809A
  FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/JP93/00603
  FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
  NAME: Freeman, John W.
  REGISTRATION NUMBER: 29,066
  REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 617-542-5070
  TELEFAX: 617-542-8906
  TELEX: 200154
INFORMATION FOR SEQ ID NO:    92:
SEQUENCE CHARACTERISTICS:
  LENGTH: 116 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: protein
US-08-545-809A-92

alignment_scores:
         Quality:    510.00              Length:    118
           Ratio:      4.636              Gaps:        2
Percent Similarity:   93.220    Percent Identity:  84.746

alignment_block:
US-09-019-441-2 x US-08-545-809A-92         ..

Align seg 1/1  to: US-08-545-809A-92   from: 1  to: 116

  1 ATGAAACACCTGTGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT  50
    |||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpVa  17

 51 CCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTT 100
    |||||||||:|||||||||||||||||||||||||::|||||||||
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS  34

101 CGGAGACCCTGTCCCTCACCTGCGTCTCTGGTGGCTCTGTCAGCAGT 150
    |||||||||||||||||||||||||||||||||||::|||||||||
 34 erGluThrLeuSerLeuThrCysValSerGlyGlySerIle...Ser  49

151 AGTAACTGGTGGACCTGGATCGGCCAGCCCCCAGGAAGGGACTGGAGTG 200
    ||| :::|||::|||:|||||||||||||||||||||||||||||
 50 SerTyrTyrTrpSerTrpIleArgGlnProAlaGlyLysGlyLeuGluTr  66

201 GATTGGACGTATCTCGGTAGTGGTGGGGGCCACCAACACCCGTCCC 250
    |||||||||||  ||| |||:|||||||||||||||||||||||||
 66 pIleGlyArgIleTyrThrSer...GlySerThrAsnTyrAsnProSerL  82

251 TCAAGAGTCGAGTCATCATTTCACAGACACGTCCAAGAACCAGTTCTCC 300
    |||||||||||| :::||| |||||||||||||||||||||||||||||
 82 euLysSerArgValThrMetSerValAspThrSerLysAsnGlnPheSer  98

301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGC 350
    |||:::||:||||||||||||||||||||||||||||||||||||||||

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OM of: US-09-019-441-3 to: PIR_71:*     out_format : pfs

Date: Sep 23, 2002 10:02 AM
About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09019441/runat_23092002_095258_6306/app_query.fasta_1.1860
-DB=PIR_71 -QFMT=fastan -SUFFIX=rpr -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -USER=US09019441_@CGN1_1_227
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-019-441-3
Query length: 387
Database: PIR_71:*
Database sequences: 283138
Database length: 96089334
Search time (sec): 132.110000
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score_list:

| sequence | Strd | Orig | ZScore | EScore | Len | ! Documentation |
|---|---|---|---|---|---|---|
| pir2:S52793 | + | 588.00 | 934.06 | 4.8e-44 | 129 | ! Ig kappa chain V region - human |
| pir2:S40331 | + | 586.00 | 931.19 | 7.2e-44 | 123 | ! Ig kappa chain - human |
| pir2:S40317 | + | 586.00 | 930.90 | 7.2e-44 | 129 | ! Ig kappa chain - human |
| pir2:S40367 | + | 578.00 | 918.34 | 3.6e-43 | 127 | ! Ig kappa chain V-J-C region - h |
| pir1:K1HUWK | + | 578.00 | 918.24 | 3.6e-43 | 129 | ! Ig kappa chain precursor V-I re |
| pir1:S38646 | + | 571.00 | 907.02 | 1.5e-42 | 132 | ! Ig kappa chain V region - human |
| pir2:S40334 | + | 571.00 | 907.02 | 1.5e-42 | 132 | ! Ig kappa chain V region - human |
| pir2:S52792 | + | 569.00 | 904.00 | 2.3e-42 | 129 | ! Ig kappa chain - human |
| pir2:S46372 | + | 565.00 | 897.72 | 5.1e-42 | 128 | ! IG light chain variable region |
| pir2:S52789 | + | 564.00 | 896.09 | 6.2e-42 | 129 | ! Ig kappa chain V region - human |
| pir2:S40333 | + | 559.00 | 888.38 | 1.7e-41 | 125 | ! Ig kappa chain V-J region - human |
| pir2:S24206 | + | 557.00 | 885.62 | 2.6e-41 | 117 | ! Ig kappa chain V region (Vx O12 |
| pir2:A49134 | + | 554.00 | 879.72 | 4.6e-41 | 141 | ! Ig kappa chain V-I region (ISE) |
| pir2:S40352 | + | 553.00 | 878.59 | 5.8e-41 | 131 | ! Ig kappa chain V-J-C region - h |
| pir2:S11240 | + | 548.00 | 870.88 | 1.6e-40 | 127 | ! Ig kappa chain V region - human |
| pir2:S40313 | + | 545.00 | 866.33 | 3.0e-40 | 123 | ! Ig kappa chain V-J region - hum |
| pir2:A27594 | + | 542.00 | 861.94 | 5.5e-40 | 116 | ! Ig kappa chain precursor V-I re |
| pir2:S42264 | + | 542.00 | 861.89 | 5.5e-40 | 117 | ! Ig kappa chain V region (L1l) - |
| pir2:S40314 | + | 541.00 | 860.05 | 6.7e-40 | 122 | ! Ig kappa chain precursor V-I re |
| pir2:S40335 | + | 538.00 | 855.10 | 1.5e-39 | 126 | ! Ig kappa chain V-J-C region - h |
| pir2:S41809 | + | 537.00 | 853.98 | 1.5e-39 | 117 | ! Ig kappa chain V region A30 - h |
| pir2:S40336 | + | 535.50 | 851.25 | 2.0e-39 | 124 | ! Ig kappa chain V-J region - hum |
| pir2:S40349 | + | 535.00 | 850.41 | 2.0e-39 | 125 | ! Ig kappa chain V-J region - hum |
| pir2:S40369 | + | 535.00 | 850.21 | 2.2e-39 | 129 | ! Ig kappa chain - human |
| pir2:S40370 | . + | 534.00 | 848.97 | 2.8e-39 | 122 | ! Ig kappa chain - human |
| pir2:S40318 | + | 532.00 | 845.71 | 4.1e-39 | 124 | ! Ig kappa chain V region - human |
| pir2:S24320 | + | 530.00 | 842.02 | 6.1e-39 | 135 | ! Ig kappa chain precursor - huma |
| pir2:S21527 | + | 528.00 | 839.74 | 9.4e-39 | 117 | ! Ig kappa chain V region - human |
| pir2:S40368 | + | 527.00 | 837.51 | 1.2e-38 | 130 | ! Ig kappa chain V-J region - hum |
| pir2:S40353 | + | 525.00 | 834.59 | 1.7e-38 | 125 | ! Ig kappa chain V-J-C region - h |
| pir1:K1HUDI | + | 524.00 | 832.81 | 2.1e-38 | 129 | ! Ig kappa chain precursor V-I re |
| pir1:K1HU12 | + | 521.00 | 828.67 | 3.9e-38 | 117 | ! Ig kappa chain precursor V-I re |
| pir2:S42263 | + | 520.00 | 827.08 | 4.8e-38 | 117 | ! Ig kappa chain V region (OB) - |
| pir2:S40315 | + | 518.50 | 824.30 | 6.4e-38 | 125 | ! Ig kappa chain - human |
| pir2:S10227 | + | 518.00 | 823.92 | 7.2e-38 | 117 | ! Ig kappa chain precursor V regi |
| pir2:S41810 | + | 515.00 | 819.17 | 1.3e-37 | 117 | ! Ig kappa chain V region L14 - h |
| pir2:S43528 | + | 514.00 | 817.59 | 1.6e-37 | 117 | ! Ig kappa chain V region (O18) - |
| pir2:S11700 | + | 513.00 | 816.01 | 2.0e-37 | 117 | ! Ig kappa chain precursor V-I re |
| pir2:S24207 | + | 513.00 | 816.01 | 2.0e-37 | 117 | ! Ig kappa chain V region (Vx O14 |
| pir2:S40348 | + | 513.00 | 815.65 | 2.0e-37 | 124 | ! Ig kappa chain V-J region - hum |
| pir2:S40316 | + | 513.00 | 815.60 | 2.0e-37 | 125 | ! Ig kappa chain - human |
| pir2:S40350 | + | 513.00 | 815.60 | 2.0e-37 | 125 | ! Ig kappa chain - human |
| pir2:S46376 | + | 510.00 | 811.26 | 3.6e-37 | 117 | ! Ig kappa chain V-J region (T |
| pir2:S41814 | + | 508.00 | 808.10 | 5.5e-37 | 117 | ! Ig kappa chain V region (L23 |
| pir2:S21668 | + | 507.00 | 806.52 | 6.7e-37 | 117 | ! Ig kappa chain V region (Z4) |

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seq_name: pir2:S52793

seq_documentation_block:
Ig kappa chain v region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
R:Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Der
  submitted to the EMBL Data Library, March 1995
A:Description: Light chain V region gene usage restriction and peculiarities in myelo
A:Reference number: S52789
A:Accession: S52793
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <ROC>
A:Cross-references: EMBL:X85997; NID:g758600; PIDN:CAA59989.1; PID:g758601
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

alignment_scores:
     Quality:       588.00              Length:     129
     Ratio:           4.580             Gaps:         0
Percent Similarity:  94.574     Percent Identity:  88.372

alignment_block:
US-09-019-441-3 x S52793

Align seg 1/1  to: S52793   from: 1  to: 129

  1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCT 50
    |||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17

 51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
    |||||||||||||||||||||||||||||||||||||||||||||||||||
 17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34

101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
    ||||||||||||||||||||||||||||||||||||:|||||||||||
 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnAsn 50

151 ATTAGGTATTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    ||| |||||||||||||:||::|||||||||||||||||||||||||:|||
 51 IleIleSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67

201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT 250
    |||||:::|||::||||::|||||||||||||||||||||||::::||
 67 sLeuLeuMetTyrAlaAlaSerSerLeuGlnSerGlyValProAlaArgP 84

251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
    |||||||||||||||||||||||||||||:||||||||||||||||||
 84 heValGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGTTTATAGTACCCC 350
    ||||||||||||||:|||||||||||||||| |||::||||||:::|||
101 GlnProGluAspPheAlaThrTyrTyrCysLeuGlnThrTyrSerAlaPr 117

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    |||||||| |||||||||||||||||||||||||||
117 oLeuThrPheGlyGlyGlyThrLysValGluIleLys 129

seq_name: pir2:S40331

seq_documentation_block:
Ig kappa chain - human
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C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40331
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891
A;Accession: S40331
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-123 <KLE>
A;Cross-references: EMBL:X72441: NID:g441350; PIDN:CAA51109.1; PID:g441351
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-106/Domain: immunoglobulin homology <IMM>

alignment_scores:
                Quality:    586.00           Length:       123
                  Ratio:     4.966             Gaps:          0
Percent Similarity:  95.935     Percent Identity:  92.683

alignment_block:
US-09-019-441-3 x S40331

Align seg 1/1    to: S40331    from: 1   to: 123

  19 GCTCAGCTCCTCGGGCTCCTTCGCTCGCTGGCTCCCAGGTGCCAGATCTGA  68
     |||||||||||||||||||||||||||||  |||||||||||||||||
   1 AlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuArgGlyAlaArgCysAs  17

  69 CATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACA  118
     |||||||||||||||||||||||||||||||||||||||||||||||||
  17 pIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspA  34

 119 GAGTCACCATCACTTGCCAGGGCAAGTCAGGACATTAGGTATTATTTAAAT  168
     ||||||||||||||||||||||||||||::::|||   ||||||||
  34 rgValThrIleThrCysGlnGlyLysSerArgAlaSerGlnSerIleSerSerTyrLeuAsn  50

 169 TGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGC  218
     |||||||||||||||||||||||||||||||||||||||||::::|||
  51 TrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrAlaAl  67

 219 ATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTG  268
     |||||||||||||||||||||||||||||||||||||||||||||||||
  67 aSerSerLeuGlnSerGlyValProSerArgPheSerGlySerGlySerG  84

 269 GGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTTTGCG  318
     |||::|||||||||||||::::|||||||||||||||||||||||||
  84 lyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheAla  100

 319 ACTTATTACTGTCTACAGGTTTATAGTAGTACCCCTCGGACGTTCGGCCAAGG  368
     |||||||||   |||  |||||||||||||||||||||||||||||||
 101 ThrTyrTyrCysLeuGlnSerTyrSerSerThrProArgThrPheGlyGlnGl  117

 369 GACCAAGGTGGAAATCAAA  387
     |||||||||||||||||
 117 yThrLysValGluIleLys  123

seq_name: pir2:S40317

seq_documentation_block:
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40317
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891
A;Accession: S40317
A;Status: preliminary; translation not shown
A;Molecule type: mRNA

A;Residues: 1-129 <KLE>
A;Cross-references: EMBL:X72427; NID:g441322; PIDN:CAA51095.1; PID:g441323
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>

alignment_scores:
                Quality:    586.00           Length:       128
                  Ratio:     4.843             Gaps:          0
Percent Similarity:  94.531     Percent Identity:  89.062

alignment_block:
US-09-019-441-3 x S40317

Align seg 1/1    to: S40317    from: 1   to: 129

   4 GACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCC  53
     |||||||||||||||||||||||||||||||||||||||||||||||
   1 AspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuAr  17

  54 AGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTG  103
     ||||||||||||||||||||||||||||||||||||||||:::||
  17 gGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerT  34

 104 CATCTGTAGGGGACAGAGTCACCATCACTTGCCAGGGCAAGTCAGGACATT  153
     ::||:::||||||||||||||||||||||||||||||||::::||
  34 hrSerLeuGlyAspArgValThrIleThrCysArgAlaSerGlnSerIle  50

 154 AGGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCT  203
     |||||||||||||||||||||||||||||||||||||||||||||||
  51 GlyThrTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLysPh  67

 204 CCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA  253
     :||||||||  ||||||||||||||||||||||||||||||||||||
  67 eLeuIleTyrGlyAlaSerSerLeuGlnSerGlyValProSerArgPheS  84

 254 GCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAG  303
     |||||||||||||:::||||||||||||||||||||||||||||||
  84 erGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGln  100

 304 CCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTAGTACCCCTG  353
     ||||||||||||||   |||  ::|||||||||||||||||||||||
 101 ProGluAspPheAlaThrTyrTyrCysLeuGlnValTyrSerThrProPr  117

 354 GACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA  387
     ||||||||||||||||||||||||||||||
 117 oThrPheGlyGlyGlyThrLysValGluIleLys  128

seq_name: pir2:S40367

seq_documentation_block:
Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40367
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891
A;Accession: S40367
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-127 <KLE>
A;Cross-references: EMBL:X72477
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

alignment_scores:
                Quality:    578.00           Length:       124
                  Ratio:     4.898             Gaps:          0

Percent Similarity: 95.161    Percent Identity: 90.323

alignment_block:
US-09-019-441-3 x S40367

Align seg 1/1    to: S40367    from: 1    to: 127

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  16 CCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCCAGATG   65
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   1 ProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuArgGlyAlaArgCy   17

  66 TGACATCCAGATGACCCAGTCTCCATCTTCCTGTCTGCATCTGTAGGGG   115
     |||||||||||||||||||||||||||||||||||||||||||||||
  17 sAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyA   34

 116 ACAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTA  165
     ||||||||||||||||||||||||||||||:::|||     |||||||
  34 spArgValThrIleThrCysArgGlnSerIleSerSerAsnTyrLeu     50

 166 AATTGGTATCAGCAGAAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGT  215
     ||||||||:::||||||||||||||||||||||||||||:||||
  51 AsnTrpTyrGlnArgLysProGlyLysAlaProLysLeuLeuIleTyrAl   67

 216 TGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT  265
     :||||||||||||||||||||||||||||||||||||||||||
  67 aAlaSerLeuGlnSerGlyValProSerArgPheSerGlySerGlyS     84

 266 CTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTTT  315
     ||||||:::||||||||||||||::|||||||||||||||||||
  84 erGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPhe  100

 316 GCGACTTATTACTGTGCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCA  365
     |||||||||||| |||   |||:::||||    ||||||||||||||
 101 AlaThrTyrTyrCysGlnSerTyrAsnThrProTrpPheThrPheGlyGl  117

 366 AGGGACCAAGGTGGAAATCAAA  387
     ||||||||||||||||||||
 117 nGlyThrLysValGluIleLys  124
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seq_name: pir1:K1HUWK

seq_documentation_block:
Ig kappa chain precursor V-I region (Walker) - human
C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 21-Jan-2000
C;Accession: A01883
R;Klobeck, H.G.; Combriato, G.; Zachau, H.G.
Nucleic Acids Res. 12, 6995-7006, 1984
A;Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cell
A;Reference number: A93534; MUID:85014148
A;Accession: A01883
A;Molecule type: DNA
A;Residues: 1-129 <KLO>
A;Note: the sequence was determined from the differentiated gene
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-129/Product: Ig kappa chain V-I region (Walker) #status predicted <MAT>
F;23-45/Region: framework 1
F;38-112/Domain: immunoglobulin homology <IMM>
F;46-56/Region: complementarity-determining 1
F;57-71/Region: framework 2
F;72-78/Region: complementarity-determining 2
F;79-110/Region: framework 3
F;111-119/Region: complementarity-determining 3
F;120-129/Region: framework 4
F;45-110/Disulfide bonds: #status predicted

alignment_scores:
    Quality:   578.00    Length:    129
    Ratio:       4.817    Gaps:        0
Percent Similarity:  93.023    Percent Identity:  88.372

alignment_block:
US-09-019-441-3 x K1HUWK

Align seg 1/1    to: K1HUWK    from: 1    to: 129

```
   1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCT   50
     |||||||||||||||||||||||||||||||||||||||||||||||
   1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe   17

  51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCTGT  100
     | |||||||||||||||||||||||||||||||||||||||||||||
  17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS   34

 101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC  150
     |||||||||||||||||||||||||||||||||||||||||||:::|
  34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer   50

 151 ATTAGGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA  200
     ||||     |||||||||||||||||||||||||||||||||||||
  51 IleSerArgTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy   67

 201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGT  250
     |||||||||:::|||||||||||||||||||||||||||  |||||
  67 sLeuLeuIleTyrAlaAlaSerLeuGlnSerGlyValThrSerArgP   84

 251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG  300
     ||||||||||||||||||:::|||||||||||||::|||||||||
  84 heSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu  100

 301 CAGCCTGAAGATTTTGCGACTTATTACTGTGCTACAGGTTTATAGTACCCC  350
     ||||||||||||||| |||:||||||||||||||||||||||||
 101 GlnProGluAspSerAlaThrTyrTyrCysGlnSerTyrSerThrLe  117

 351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA  387
     ||||||||||||||||||:::|||||||||||
 117 uIleThrPheGlyGlnGlyThrArgLeuGluIleLys  129
```

seq_name: pir2:S38646

seq_documentation_block:
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38646
R;Bensimon, C.; Chastagner, P.; Zouali, M.
A;Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
submitted to the EMBL Data Library, November 1993
A;Reference number: S38643
A;Accession: S38646
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <BEN>
A;Cross-references: EMBL:Z27173; NID:g415961; PIDN:CAA81697.1; PID:g415962
A;Cross-references: EMBL:Z27173; NID:g415961; PIDN:CAA81697.1; PID:g415962
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;40-114/Domain: immunoglobulin homology <IMM>

alignment_scores:
    Quality:   571.00    Length:    129
    Ratio:       4.798    Gaps:        0
Percent Similarity:  92.248    Percent Identity:  86.047

alignment_block:
US-09-019-441-3 x S38646

Align seg 1/1    to: S38646    from: 1    to: 132

```
  1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCT  50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe  19

 51 CCCAGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT  100
    ||||||||||||||||||||:::||||:||||||||||||||||||||||
 19 uProGlyAlaArgCysAlaIleArgIleAlaGlnSerProSerSerLeuS  36

101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC  150
    |||||||||||||||||||||||::||||||||||||||||||||||
 36 erAlaSerThrGlyAspArgValThrIleThrCysArgAlaSerGlnGly  52

151 ATTAGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAAGCTCCTAA  200
    |||   ||||||    ||||||||||||||||||||||||||||||||
 53 IleSerSerTyrLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLy  69

201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT  250
    |||||:::||||::|||||||||||||||:||||||||||||||||||
 69 sLeuLeuIleTyrValAlaSerThrLeuGlnSerGlyValProSerArgP  86

251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG  300
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 86 heSerGlySerGlyThrGlyAspPheThrLeuThrIleSerCysLeu  102

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC  350
    |||    ||||||||:|||||||||||||    |||||||  ||||||
103 GlnSerGluAspPheAlaThrTyrTyrCysLeuGlnGlnTyrTyrSerTyrPr  119

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA  387
    ||||||||||||||||||||||||||||||||||
119 oArgThrPheGlyGlnGlyThrLysValGluIleLys  131
```

seq_name: pir2:S40334

seq_documentation_block:
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40334
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891
A;Accession: S40334
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-132 <KLE>
A;Cross-references: EMBL:X72244
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>

alignment_scores:
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           Quality:   571.00           Length:    128
             Ratio:     4.839             Gaps:      0
Percent Similarity:    92.188   Percent Identity:  86.719
```

alignment_block:
US-09-019-441-3 x S40334

Align seg 1/1    to: S40334    from: 1    to: 132

```
  4 GACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCC  53
    ||||||||||||||||||||||||||||||||||||||||||||||
  1 AspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuPr  17

 54 AGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTG  103
    ||||||||||||||||||||||||||||||||||||::::||||:::
 17 oGlyAlaArgCysAlaAspIleGlnLeuThrGlnSerProSerPheLeuSerA  34
```

seq_name: pir2:S52792

seq_documentation_block:
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C;Accession: S52792
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Der
submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myelo
A;Reference number: S52789
A;Accession: S52792
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85996; NID:g758598; PIDN:CAA59988.1; PID:g758599
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

alignment_scores:
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           Quality:   569.00           Length:    129
             Ratio:     4.702             Gaps:      0
Percent Similarity:    93.798   Percent Identity:  93.798
```

alignment_block:
US-09-019-441-3 x S52792

Align seg 1/1    to: S52792    from: 1    to: 129

```
  1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCT  50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe  17

 51 CCCAGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT  100
    ||||||||||||||||||||||||||||||||||||||||||||||||
 17 uArgGlyAlaArgCysAlaAspIleGlnMetThrGlnSerProSerLeuS  34

101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC  150
    ||||||||||||||||||||||||||||::|||||||||||||:::
 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer  50

151 ATTAGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGTCCTAA  200
    ||||||||||||    ||||||||||||||||||||||||||||||:
 51 IleAlaGlyTyrLeuAsnTrpTyrGlnGlnArgProGlyLysAlaProGl  67

201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT  250
    |||:::||||::||||||||||||||:||||||||||||||||||||||
```

```
 67  uLeuLeuIleTyrAlaAlaSerThrLeuArgSerGlyValProSerArgP  84
251  TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG  300
     |||||||||||||||||:::::||||||||||||:::||||||||||
 84  heSerGlySerGlyAlaAspPheThrLeuThrIleSerSerLeu        100
301  CAGCCTGAAGATTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC   350
     ||||||||||||  ||||||||||||||||||||  |||  :::|||||
101  GlnProGluAspSerAlaThrTyrTyrCysGlnSerTyrGlyThrPr     117
351  TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA               387
     |  ||||||  ||||||||||||:::||||||
117  oPheThrPheGlyProGlyThrLysValAspIleLys               129
```

seq_name: pir2:S46372

seq_documentation_block:
IG light chain variable region (VJ) - human
C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S46372
R;Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chl) gene rea
A;Reference number: S46369; MUID:94313975
A;Accession: S46372
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <BEN>
A;Cross-references: EMBL:Z27173
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

alignment_scores:
     Quality:      565.00        Length:      127
     Ratio:          4.829        Gaps:          0
Percent Similarity:  92.126    Percent Identity:  86.614

alignment_block:
US-09-019-441-3 x S46372

Align seg 1/1 to: S46372 from: 1 to: 128

  7  ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGG  56
     |||||||||||||||||||||||||||||||||||||||||||
  1  MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGl  17
 57  TGCCAGATGCGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT  106
     |||||||||||||:::|||||||||||||||||||||
 17  yAlaArgCysAlaIleArgIleThrGlnSerProSerSerLeuSerAlaS  34
107  CTGTAGGGACAGAGTCACCATCACTTGCAGGGCAGTCAGGACATTAGG    156
     |::||||||||||||||||||||||||||  ||
 34  erThrGlyAspArgValThrIleThrCysArgAlaSerGlnGlyIleSer  50
157  TATTATTTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCT  206
     |||||  |||||||||||||||||||||||||
 51  SerTyrLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLe  67
207  GATCTATGCTGCATCCAGTTGCAAAGTGGGTCCCATCAAGGTTCAGCG    256
     |||||:::||||:::|||||||||||||||||||
 67  uIleTyrAlaAlaSerThrLeuGlnSerGlyValProSerArgPheSerG  84
257  GCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT  306
     |||||||||||||||||||||||||:::|||     |||||
 84  lySerGlySerGlyThrAspPheThrLeuThrIleSerCysLeuGlnSer  100
307  GAAGATTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAC   356
     ||||||||||||  |||||||||||||||  |||||
101  GluAspPheAlaThrTyrTyrCysGlnSerTyrTyrSerTyrProArgTh  117
```

```
357  GTTCGGCCAAGGGACCAAGGTGGAAATCAAA  387
     |||||||||||||||||||||||:::|||||
117  rPheGlyGlnGlyThrLysValGluIleLys  127
```

seq_name: pir2:S52789

seq_documentation_block:
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Der
submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myelo
A;Reference number: S52789
A;Accession: S52789
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85595; NID:g758588; PIDN:CAA59987.1; PID:g758589
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

alignment_scores:
     Quality:      564.00        Length:      129
     Ratio:          4.700        Gaps:          0
Percent Similarity:  93.023    Percent Identity:  84.496

alignment_block:
US-09-019-441-3 x S52789

Align seg 1/1 to: S52789 from: 1 to: 129

  1  ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCT  50
     |||||||||||||||||||||||||||||||||||||||||||||||
  1  MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe  17
 51  CCCAGGTGCCAGATGACATGACCCAGTCTCCATCTTCCCTGT          100
     ||||||||||||||||||||||||||||||||||
 17  uSerGlyAlaArgCysAspAspIleGlnMetThrGlnSerProSerLeuS  34
101  CTGCATCTGTAGGGACAGAGTCACCATCACTTGCCAGGGCAAGTCAGGAC  150
     ||||||||||||||||||||||||||||:::||||||
 34  erAlaSerValGlyAspArgValThrIleThrCysGlnAlaSerGlnAsp  50
151  ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA   200
     |||  |||||||||||||||||||||||||||
 51  IleSerAsnTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy  67
201  GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGTCCCATCAAGGT    250
     |||||:::||||:::||||||||||||||::||||||
 67  sLeuLeuIleHisAlaAlaSerSerLeuGluThrGlyValProSerArgP  84
251  TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG  300
     |||||||||||||||||:::|||||||||||||:::||||||
 84  heSerGlySerGlyThrAspPheSerPheThrIleSerSerLeu        100
301  CAGCCTGAAGATTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC   350
     ||||||||||||  |||||||||||||||:::  |||  :::||
101  GlnProGluAspLeuAlaThrTyrTyrCysGlnGlnTyrAspAsnLeuPr  117
351  TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA               387
     |  ||||||  ||||||||||||:::||||||
117  oLeuThrPheGlyGlyGlyThrLysValGluIleLys               129
```

seq_name: pir2:S40333

seq_documentation_block:
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S40333
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Accession: S40333
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: EMBL:X72443; NID:g441354; PIDN:CAA51111.1; PID:g441355
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>

alignment_scores:
    Quality:    559.00              Length:    125
    Ratio:      4.819               Gaps:      0
Percent Similarity:  92.800    Percent Identity: 87.200

alignment_block:
US-09-019-441-3 x S40333        ..

Align seg 1/1  to: S40333  from: 1  to: 125

13  GTCCCCGCTCAGCTCCTGGGCTCCTTCTGCTCTGGCTCCCAGGTGCCAG  62
    |||||||||||||||||||||||||||||||||||||||||||||::
 1  ValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAlaLy  17

63  ATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAG  112
    ||:||||||||||||||||||||||||::|||||||||||||||||||||
17  sCysAspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValG  34

113 GGACAGAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTAT  162
    ||||||||||||||||||||||||||||:::|||   : ::
34  lyAspArgValThrIleThrCysArgAlaSerGlnSerIleSerSerTrp  50

163 TTAAATTGGTATCAGCAGAAAACCAGGAAAGTCCTAAGCTCCTGATCTA  212
    |||  |||||||||||||||||||||||||||||||||
51  LeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuTy  67

213 TGTTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGTTCAGCGGCAGTG  262
    ||||||||:::|||||||||||||||||||||||||||||
67  rLysAlaSerSerLeuGluSerGlyValProSerArgPheSerGlySerG  84

263 GATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGAT  312
    |||||||||||||||||||||||||||||:::|||||:::|||
84  lySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnProAspAsp  100

313 TTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGGTTCGG  362
    ||||||||||||||||| ||| |||||||||
101 PheAlaThrTyrTyrCysLeuGlnValTyrAsnSerTyrProTrpThrPheGl  117

363 CCAAGGGACCAAGGTGGAAATCAAA  387
    |||||||||||||||||||||
117 yGlnGlyThrLysValGluIleLys  125

seq_name: pir2:S24206

seq_documentation_block:
Ig kappa chain V region (Vx O12 and Vx O2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: S24206; S24209
R;Pargent, W.; Meindl, A.; Thiebe, R.; Mitzel, S.; Zachau, H.G.
Eur. J. Immunol. 21, 1821-1827, 1991
A;Title: The human immunoglobulin kappa locus. Characterization of the duplicated O regi
A;Accession: S24206; MUID:91330953
A;Accession: S24206
A;Molecule type: DNA
A;Residues: 1-117 <PAR>
A;Cross-references: EMBL:X59315; NID:g33247; PIDN:CAA42002.1; PID:g33248
A;Experimental source: placenta

---

A;Genetics: G1
A;Accession: S24209
A;Molecule type: DNA
A;Residues: 1-117 <PAW>
A;Cross-references: EMBL:X59312; NID:g33252; PIDN:CAA41999.1; PID:g3253
A;Experimental source: placenta
A;Genetics: G2
C;Genetics: <G1>
A;Gene: Vx O12
A;Map position: 2
A;Introns: 19/1
C;Genetics: <G2>
A;Gene: Vx O2
A;Map position: 2
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

alignment_scores:
    Quality:    557.00              Length:    117
    Ratio:      4.973               Gaps:      0
Percent Similarity:  95.726    Percent Identity: 92.308

alignment_block:
US-09-019-441-3 x S24206        ..

Align seg 1/1  to: S24206  from: 1  to: 117

 1  ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCT  50
    |||||||||||||||||||||||||||||||||||||||||||||||||||
 1  MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe  17

51  CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT  100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
17  uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerLeuSer  34

101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCCAGTCAGGAC  150
    |||||||||||||||||||||||||||||||||||||||||||||::::
34  erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer  50

151 ATTAGGTATTATTAAATTGGTATCAGCAGAAAACCAGGAAAAGCTCCTAA  200
    |||   ||||||||||||||||||||||||||||||||||||||||
51  IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy  67

201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGT  250
    |||||||||::::|||||||||||||||||||||||||||||||||||
67  sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgP  84

251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG  300
    |||||||||||||||||||:::||||||||||||||||::|||||||
84  heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu  100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC  350
    |||||||||||||||||||||||||||||||||||||||||||||||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrPr  117

351 T 351
    |
117 o 117

seq_name: pir2:A49134

seq_documentation_block:
Ig kappa chain V-I region (ISE) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
A;Accession: A49134; S25515
C;Accession: A49134; S25515
R;Rocca, A.; Khamlichi, A.A.; Aucouturier, P.; Noel, L.H.; Denoroy, L.; Preud'homme,
Clin. Exp. Immunol. 91, 506-509, 1993
A;Title: Primary structure of a variable region of the V kappa I subgroup (ISE) in li
A;Reference number: A49134; MUID:93185310

A;Accession: A49134
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-141 <ROC>
A;Cross-references: EMBL:X67322; NID:g33268; PIDN:CAA47736.1; PID:g33269
A;Note: sequence extracted from NCBI backbone (NCBIP:127088)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

alignment_scores:
    Quality:     554.00              Length:    129
    Ratio:       4.655               Gaps:        0
Percent Similarity:  92.248     Percent Identity:  83.721

alignment_block:
US-09-019-441-3 x A49134    ..

Align seg 1/1 to: A49134  from: 1 to: 141

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   1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCT  50
     ||||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe  17

  51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
     ||||||||||||||||||||||||:::|||||||||:::|||||||
  17 uProGlyAlaLysCysAspIleGlnMetThrGlnSerProSerThrLeuS  34

 101 CTGGCATCGTGTAGGGACAGAGTCACCATCACTTGCCAGGCAAGTCAGGAC 150
     |||||||||||||||||||||||||||||||||||||||||||||||
  34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnLeuGly  50

 151 ATTAGGTATTATTTTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
     |||::: :||||||: |||||||||||||||||||||||::
  51 IleAsnIleTrpLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProAs  67

 201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGT 250
     :|||||||||||| ||::::|||||||||||||||||||||||
  67 nLeuLeuIleTyrValAlaThrAsnLeuGlnSerGlyValProSerArgP  84

 251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
     ||||||::::|||||||||||||||||||||||||:::::|||:||
  84 heSerAlaSerGlySerGlyThrGluPheThrLeuThrIleSerGlyLeu 100

 301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
     |||||::::|||||||||||||||||||::|||||  ||  ||
 101 GlnProAspAspPheAlaThrTyrTyrCysHisGlnTyrSerTyrPr 117

 351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
     | |||||||||||||||||||||||||||||
 117 oTrpThrPheGlyGlnGlyThrLysValGluIleLys 129
```

seq_name: pir2:S40352

seq_documentation_block:
Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40352
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891
A;Accession: S40352
A;Status: Preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-131 <KLE>
A;Cross-references: EMBL:X72462; NID:g441392; PIDN:CAA51130.1; PID:g441393
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

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alignment_scores:
    Quality:     553.00              Length:    127
    Ratio:       4.686               Gaps:        0
Percent Similarity:  92.913     Percent Identity:  84.252

alignment_block:
US-09-019-441-3 x S40352    ..

Align seg 1/1 to: S40352  from: 1 to: 131

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   7 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGG  56
     ||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProAs  17

  57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT 106
     :::::|||||||||||||||||||||||||||||||:::|||||||||
  17 pThrLysCysAspIleGlnMetThrGlnSerProSerLeuSerAlaS  34

 107 CTGTAGGGACAGAGTCACCATCACTTGCCAGGCAAGTCAGGACATTAGG 156
     |||||||:::|||||||||||||||||||||||||||||  |||
  34 erValGlyAsnArgValThrIleThrCysArgAlaSerGlnIleIleSer  50

 157 TATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCT 206
     ||||| ||||||||||||||||||||||:::||||||||||||
  51 AsnTyrLeuAlaTrpTyrGlnGlnLysProGlyLysValProLysLeuLe  67

 207 GATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCATCAAGGTTCAGCG 256
     ||||||||||| :|||||||:::||||||||||||||||||||||||
  67 uIleTyrAlaAlaSerThrLeuGlnSerGlyValProSerArgPheSerG  84

 257 GCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT 306
     ||||||||||||||||||::::|||||||||||||::::|||:|||||
  84 lySerGlySerGlyThrAspPheSerLeuThrIleSerLeuGlnPro 100

 307 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAC 356
     ||||| |||||||||||||   :::  ||::|||||||
 101 GluAspValAlaThrTyrTyrCysGlnLysTyrAsnSerValProArgTh 117

 357 GTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
     |||||||||||||||||||||||||||||
 117 rPheGlyGlnGlyThrLysValGluIleLys 127
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seq_name: pir2:S11240

seq_documentation_block:
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S11240
R;Feigenhauer, M.; Kohl, J.; Rueker, F.
Nucleic Acids Res. 18, 4927, 1990
A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains
A;Reference number: S11239; MUID:90370490
A;Accession: S11240
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-127 <FEL>
A;Cross-references: EMBL:X53612; NID:g23868; PIDN:CAA37674.1; PID:g762937
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

alignment_scores:
    Quality:     548.00              Length:    129
    Ratio:       4.644               Gaps:        1
Percent Similarity:  91.473     Percent Identity:  83.721

alignment_block:
US-09-019-441-3 x S11240    ..

Align seg 1/1 to: S11240  from: 1 to: 127

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  1 ATGGACATGAGGGTCCCGCCTCAGCTTCCTGGGCTCCTTCTTCTGCTCTGGCT  50
    |||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe    17

 51 CCCAGGTGCCAGTGCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
    |||||||||::||||||||||||||||||||||||||||||||||:::|||
 17 uProGlyAlaLysCysAspIleGlnMetThrGlnSerProSerThrLeuS    34

101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
    ||||||||||||||||||||||||||||||||||||||||||::::
 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer    50

151 ATTAGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    |||     |||||  |||||||||||||||||||:::::|||
 51 IleSerArgTrpLeuAlaTrpTyrGlnGlnLysProGlyLysValProLy    67

201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT 250
    |||||||||||||  ||||||||::::||||||||||||||||||
 67 sLeuLeuIleTyrLysAlaSerSerLeuGluSerGlyValProSerArgP    84

251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
    |||||||||||||||||||||||||||||||::::||||||||||||||
 84 heSerGlySerGlyThrGlyThrGluPheThrLeuThrIleSerSerLeu    100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
    ||||::::|||||||||||||||||     |||
101 GlnProAspAspPheAlaThrTyrTyrCysGlnGlnValTyrAsnSer.....  115

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    ::|||||| |||||||||::||||||
116 .TyrSerPheGlyProGlyThrLysValAspIleLys 127
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```
OM of: US-09-019-441-3 to: SwissProt_40:*     out_format : pfs
Date: Sep 23, 2002 10:24 AM
About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09019441/runat_23092002_095259_6394/app_query.fasta_1.1860
-DB=SwissProt_40 -QFMT=fastan -SUFFIX=rsp -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.000
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09019441_@CGN1_1_91 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-019-441-3
Query length: 387
Database: SwissProt_40:*
Database sequences: 105224
Database length: 38719950
Search time (sec): 62.410000
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score_list:

| Sequence | Strd | Orig | ZScore | EScore | Len | ! Documentation |
|---|---|---|---|---|---|---|
| SwissProt_40:KV1W_HUMAN | + | 578.00 | 1109.41 | 3.3e-54 | 129 | ! P04431 homo sapiens (human) |
| SwissProt_40:KV1X_HUMAN | + | 524.00 | 1005.33 | 2.1e-48 | 129 | ! P04432 homo sapiens (human) |
| SwissProt_40:KV1J_HUMAN | + | 521.00 | 1000.39 | 4.3e-48 | 117 | ! P01601 homo sapiens (human) |
| SwissProt_40:KV1I_HUMAN | + | 491.00 | 942.57 | 7.1e-45 | 117 | ! P01602 homo sapiens (human) |
| SwissProt_40:KV1H_HUMAN | + | 472.00 | 906.63 | 7.8e-43 | 108 | ! P01600 homo sapiens (human) |
| SwissProt_40:KV1G_HUMAN | + | 469.00 | 900.85 | 1.6e-42 | 108 | ! P01599 homo sapiens (human) |
| SwissProt_40:KV1R_HUMAN | + | 463.00 | 889.29 | 7.2e-42 | 108 | ! P01610 homo sapiens (human) |
| SwissProt_40:KV5E_MOUSE | + | 462.00 | 885.90 | 9.3e-42 | 128 | ! P01637 mus musculus (mouse) |
| SwissProt_40:KV1E_HUMAN | + | 456.00 | 875.80 | 4.0e-41 | 108 | ! P01597 homo sapiens (human) |
| SwissProt_40:KV1S_HUMAN | + | 456.00 | 875.80 | 4.0e-41 | 108 | ! P01611 homo sapiens (human) |
| SwissProt_40:KV1B_HUMAN | + | 452.00 | 868.09 | 1.1e-40 | 108 | ! P01594 homo sapiens (human) |
| SwissProt_40:KV1O_HUMAN | + | 452.00 | 868.09 | 1.1e-40 | 108 | ! P01607 homo sapiens (human) |
| SwissProt_40:KV1N_HUMAN | + | 450.00 | 864.23 | 1.8e-40 | 108 | ! P01606 homo sapiens (human) |
| SwissProt_40:KV1F_HUMAN | + | 449.00 | 862.30 | 2.3e-40 | 108 | ! P01598 homo sapiens (human) |
| SwissProt_40:KV1K_HUMAN | + | 448.00 | 860.38 | 2.9e-40 | 108 | ! P01603 homo sapiens (human) |
| SwissProt_40:KV1A_HUMAN | + | 447.00 | 858.45 | 3.7e-40 | 108 | ! P01593 homo sapiens (human) |
| SwissProt_40:KV3L_HUMAN | + | 444.50 | 852.10 | 7.1e-40 | 129 | ! P18135 homo sapiens (human) |
| SwissProt_40:KV1P_HUMAN | + | 444.00 | 852.67 | 7.9e-40 | 108 | ! P01608 homo sapiens (human) |
| SwissProt_40:KV5G_MOUSE | + | 444.00 | 851.07 | 8.0e-40 | 130 | ! P01639 mus musculus (mouse) |
| SwissProt_40:KV1M_HUMAN | + | 442.00 | 848.81 | 1.3e-39 | 108 | ! P01605 homo sapiens (human) |
| SwissProt_40:KV1Q_HUMAN | + | 440.00 | 844.96 | 2.1e-39 | 108 | ! P01609 homo sapiens (human) |
| SwissProt_40:KV1V_HUMAN | + | 439.00 | 843.03 | 2.7e-39 | 108 | ! P04430 homo sapiens (human) |
| SwissProt_40:KV1Y_HUMAN | + | 439.00 | 843.03 | 2.7e-39 | 108 | ! P80362 homo sapiens (human) |
| SwissProt_40:KV1C_HUMAN | + | 434.00 | 833.39 | 9.3e-39 | 108 | ! P01595 homo sapiens (human) |
| SwissProt_40:KV3M_HUMAN | + | 433.50 | 830.90 | 1.1e-38 | 129 | ! P18136 homo sapiens (human) |
| SwissProt_40:KV1D_HUMAN | + | 431.50 | 828.65 | 1.7e-38 | 107 | ! P01596 homo sapiens (human) |
| SwissProt_40:KV1L_HUMAN | + | 430.00 | 825.68 | 2.5e-38 | 108 | ! P01604 homo sapiens (human) |
| SwissProt_40:KV5H_MOUSE | + | 428.00 | 821.14 | 4.1e-38 | 117 | ! P01641 mus musculus (mouse) |
| SwissProt_40:KV1T_HUMAN | + | 425.50 | 816.93 | 7.6e-38 | 109 | ! P01612 homo sapiens (human) |
| SwissProt_40:KV4C_HUMAN | + | 424.00 | 812.26 | 1.1e-37 | 134 | ! P06314 homo sapiens (human) |
| SwissProt_40:KV5C_MOUSE | + | 423.00 | 811.65 | 1.4e-37 | 115 | ! P01635 mus musculus (mouse) |
| SwissProt_40:KV5F_MOUSE | + | 423.00 | 811.65 | 1.4e-37 | 115 | ! P01638 mus musculus (mouse) |
| SwissProt_40:KV3H_HUMAN | + | 419.50 | 803.91 | 3.4e-37 | 129 | ! P04207 homo sapiens (human) |
| SwissProt_40:KV5M_MOUSE | + | 406.00 | 779.42 | 9.4e-36 | 108 | ! P01646 mus musculus (mouse) |
| SwissProt_40:KV3K_HUMAN | + | 404.00 | 774.11 | 1.6e-35 | 128 | ! P06311 homo sapiens (human) |
| SwissProt_40:KV4B_HUMAN | + | 402.50 | 770.89 | 2.3e-35 | 133 | ! P06313 homo sapiens (human) |
| SwissProt_40:KV2F_HUMAN | + | 400.50 | 767.03 | 3.8e-35 | 133 | ! P06310 homo sapiens (human) |
| SwissProt_40:KV5K_MOUSE | + | 399.00 | 765.93 | 5.3e-35 | 108 | ! P01644 mus musculus (mouse) |
| SwissProt_40:KV5O_MOUSE | + | 398.00 | 764.00 | 6.8e-35 | 108 | ! P01648 mus musculus (mouse) |
| SwissProt_40:KV5N_MOUSE | + | 397.00 | 762.08 | 8.7e-35 | 108 | ! P01647 mus musculus (mouse) |

| SwissProt_40:KV5J_MOUSE | + | 395.00 | 758.22 | 1.4e-34 | 108 | ! P01643 mus musculus (mous |
| SwissProt_40:KV4A_HUMAN | + | 395.00 | 757.76 | 1.4e-34 | 114 | ! P01625 homo sapiens (huma |
| SwissProt_40:KV5L_MOUSE | + | 394.00 | 756.29 | 1.8e-34 | 108 | ! P01645 mus musculus (mous |
| SwissProt_40:KV3I_HUMAN | + | 394.00 | 755.75 | 1.8e-34 | 115 | ! P04433 homo sapiens (huma |
| SwissProt_40:KV3J_HUMAN | + | 392.50 | 752.79 | 2.7e-34 | 116 | ! P04434 homo sapiens (huma |

seq_name: SwissProt_40:KV1W_HUMAN

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seq_documentation_block:
ID   KV1W_HUMAN     STANDARD;      PRT;    129 AA.
AC   P04431;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Walker precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute.  There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; X00965; CAA25477.1; ALT_TERM.
DR   PIR; A01883; K1HUWK.
HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    129       IG KAPPA CHAIN V-I REGION WALKER.
FT   DOMAIN       23     45       FRAMEWORK-1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57     71       FRAMEWORK-2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       79    110       FRAMEWORK-3.
FT   DOMAIN      111    119       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      120    129       FRAMEWORK-4.
FT   DISULFID     45    110       BY SIMILARITY.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14069 MW;  F941FA07D4AFC2F9 CRC64;

alignment_scores:
                Quality:     578.00          Length:       129
                  Ratio:       4.817          Gaps:           0
  Percent Similarity:    93.023    Percent Identity:    88.372

alignment_block:
US-09-019-441-3 x KV1W_HUMAN        ..

Align seg 1/1  to: KV1W_HUMAN    from: 1  to: 129

     1 ATGGACGATGAGGGTCCCCGCTCAGCTCCTGGGCTCCTTCCTTCGCTCTGGCT  50
       ||||||||||||||||||||||||||||||||||||||||||||||||||
     1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe  17

    51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCAТCTTCCCTGT  100
       |  ||||||||||||||||||||||||||||||||||||||||||||||
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FT   NON_TER      129   129
SQ   SEQUENCE     129 AA;   14235 MW;   CAF076BC7E5574C8 CRC64;

alignment_scores:
                    Quality:   524.00          Length:     129
                      Ratio:   4.517            Gaps:        0
Percent Similarity: 89.922    Percent Identity: 79.845

alignment_block:
US-09-019-441-3 x KV1X_HUMAN

Align seg 1/1  to: KV1X_HUMAN   from: 1  to: 129

  1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGCTCCTCTGCTCTGGCT  50
    ||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe  17

 51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT  100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 17 uArgArgValArgCysAspIleGlnMetThrGlnSerProSerSerLeuS  34

101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC  150
    ||||||||||||||||||||||||||||||||||||||||||||||||
 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaGlyHisAsn  50

151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA  200
    ||   :: ||||||||||||||||||||||||||||||||||||||||
 51 IleThrAsnPheLeuSerTrpTyrGlnGlnLysProGlyLysAlaProTh  67

201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGT  250
    |||||||||||||||| :::::|||:|| |||||||||||||||||||||
 67 rLeuLeuIleTyrAlaValSerAsnLeuGlnValGlyValProSerArgP  84

251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG  300
    |||||||||||||| ||||||||:||||||||||||||||||||||||||
 84 heSerGlySerGlySerGlyAlaGluPheThrLeuThrIleSerSerLeu  100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC  350
    |||||||||||||||||||||||||||||||||||| ||| |||:||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnValTyrSerThrLe  117

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA  387
    |||||||||||||||||||||||||:||  |||
117 rPheThrPheGlyGlyGlyThrLysValAspAsnLys  129

seq_name: SwissProt_40:KV1J_HUMAN

seq_documentation_block:
ID   KV1J_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01602;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region HK102 precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81098966; PubMed=6779204;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Human immunoglobulin variable region genes -- DNA sequences of two v
RT   kappa genes and a pseudogene.";
RL   Nature 288:730-733(1980).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/

seq_name: SwissProt_40:KV1X_HUMAN

seq_documentation_block:
ID   KV1X_HUMAN     STANDARD;      PRT;   129 AA.
AC   P04433;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Daudi precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; X00966; CAA25478.1; ALT_TERM.
DR   PIR; A01884; KIHUDI.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; 1g; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    129       IG KAPPA CHAIN V-I REGION DAUDI.
FT   DOMAIN       23     45       FRAMEWORK-1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57     71       FRAMEWORK-2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       79    110       FRAMEWORK-3.
FT   DOMAIN      111    119       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      120    129       FRAMEWORK-4.
FT   DISULFID     45    110       BY SIMILARITY.

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CC   or send an email to license@isb-sib.ch).
CC   ----
DR   EMBL; J00245; AAA59087.1; -.
DR   EMBL; Z00001; CAA77292.1; -.
DR   PIR; A01882; KIHU12.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23   >117       IG KAPPA CHAIN V-I REGION HK102.
FT   DOMAIN       23    45        FRAMEWORK-1.
FT   DOMAIN       46    56        COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57    71        FRAMEWORK-2.
FT   DOMAIN       72    78        COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       79   110        FRAMEWORK-3.
FT   DOMAIN      111   >117       COMPLEMENTARITY-DETERMINING-3.
FT   DISULFID     45   110        BY SIMILARITY.
FT   NON_TER     117   117
SQ   SEQUENCE    117 AA;  12768 MW;  AD1DF3A40AF1A49B CRC64;

alignment_scores:
            Quality:   521.00                  Length:      115
              Ratio:     4.824                    Gaps:        0
Percent Similarity:    93.913       Percent Identity:   87.826

alignment_block:
US-09-019-441-3  x KV1J_HUMAN    ..

Align seg 1/1  to: KV1J_HUMAN  from: 1  to: 117

  1 ATGGACATGAGGGTCCCCGCTCAGCTCCTCGGGCTCCTTCTGCTCTGGCT 50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17

 51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
    |||||||||::::||||||||||||||||||||||||||||::::||||
 17 uProGlyAlaLysCysAspIleGlnMetThrGlnSerProSerThrLeuS 34

101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
    ||||||||||||||||||||||||||||||||||||||||:::::||||
 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50

151 ATTAGGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    ||  ::::||| |||||||||||||||||||||||||||||||||||||
 51 IleSerSerTrpLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLy 67

201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT 250
    :|||||||||||  ||||||:::|||||||||||||||||||||||||
 67 sLeuLeuIleTyrAspAlaSerLeuGluSerGlyValProSerArgP 84

251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
    ||||||||||||||||||||||||||||:::::||||||||||||||
 84 heSerGlySerGlyThrGlyThrGluPheThrLeuThrIleSerSerLeu 100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGT 345
    ||  ::::||||||||||||||||||||||||||| || |||
101 GlnProAspAspPheAlaThrTyrTyrCysGlnGlnThrTyrAsnSer 115

seq_name: SwissProt_40:KV1I_HUMAN

seq_documentation_block:
ID   KV1I_HUMAN    STANDARD;        PRT;    117 AA.
AC   P01601;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region HK101 precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81098966; PubMed=6779204;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Human immunoglobulin variable region genes -- DNA sequences of two v
RT   kappa genes and a pseudogene.";
RL   Nature 288:730-733(1980).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83129397; PubMed=6402305;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Evolution of immunoglobulin v genes: evidence indicating that
RT   recently duplicated human v kappa sequences have diverged by gene
RT   conversion.";
RL   Cell 32:181-189(1983).
CC   ----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----
DR   EMBL; K01322; AAA58930.1; -.
DR   EMBL; K01324; AAA58932.1; -.
DR   EMBL; V00558; CAA23824.1; -.
DR   PIR; A01881; KIHU11.
DR   PIR; A21056; A21056.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23   >117       IG KAPPA CHAIN V-I REGION HK101.
FT   DOMAIN       23    45        FRAMEWORK-1.
FT   DOMAIN       46    56        COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57    71        FRAMEWORK-2.
FT   DOMAIN       72    78        COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       79   110        FRAMEWORK-3.
FT   DOMAIN      111   >117       COMPLEMENTARITY-DETERMINING-3.
FT   DISULFID     45   110        BY SIMILARITY.
FT   NON_TER     117   117
SQ   SEQUENCE    117 AA;  12799 MW;  D7D0FF3718CEF587 CRC64;

alignment_scores:
            Quality:   491.00                  Length:      117
              Ratio:     4.721                    Gaps:        0
Percent Similarity:    88.889       Percent Identity:   84.615

alignment_block:
US-09-019-441-3  x KV1I_HUMAN    ..

Align seg 1/1  to: KV1I_HUMAN  from: 1  to: 117

  1 ATGGACATGAGGGTCCCCGCTCAGCTCCTCGGGCTCCTTCTGCTCTGGCT 50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetAspMetArgValLeuAlaGlnLeuLeuGlyLeuLeuLeuLeuCysPh 17

 51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
    :|||||||||||||||||||||||||||||||||||||||||||||||
 17 eProGlyAlaArgCysAspIleGlnMetThrGlnSerProSerLeuS 34

101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
    |||||||||||||||||||||||||||||||||||||||||| |||
 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaArgGlnGly 50

151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
```

```
  1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17
    |||                                |||||||||||||

117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGATATTATTAA 166
    ||||||||::::||||||||||||||||||||||||||||:::||| |||||
 17 pArgValThrIleThrCysArgAlaSerGlnSerIleSerSerTyrLeuS 34

167 ATTGGTATCAGCAGAAACCAGGAAAAGTCCTAAGCTCCTGATCTATGTT 216
    ::||||||||||||||||||||||||||:::||||::|||||||||:::
 34 erTrpTyrGlnGlnLysProGlyLysAlaProGlnValLeuIleTyrAla 50

217 GCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC 266
    |||||||| ||||||||||||||||||||||||||||||||||||||||
 51 AlaSerSerLeuProSerGlyValProSerArgPheSerGlySerGlySe 67

267 TGGGACAGAGTCACTCTCACCAGGTTTATAGTACCCCTGCAGCCTGAAGATTTTG 316
    |||||||::||||||||::::|||||||||||||||||||||||||||||
 67 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheA 84

317 CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
    ||||||||||| ||| |||||  ||||| ||||||||||||||||||||
 84 laThrTyrTyrCysGlnGlnAsnTyrIleThrProThrPheGlyGln 100

367 GGGACCAAGGTGGAAATCAAA 387
    |||||||||||||||||||||
101 GlyThrArgValGluIleLys 107
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seq_name: SwissProt_40:KV1G_HUMAN

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seq_documentation_block:
ID   KV1G_HUMAN      STANDARD;       PRT;    108 AA.
AC   P01599;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region GAL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75059122; PubMed=4215718;
RA   Laure C.J., Watanabe S., Hilschmann N.;
RT   "The primary structure of a monoclonal IgM-immunoglobulin
RT   (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT   kappa-type, subgroup I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC       MACROGLOBULIN.
DR   PIR; A01867; KIHUGL.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11814 MW;  C1AD3CB0F60DFF73 CRC64;

alignment_scores:
               Quality:    469.00        Length:      107
               Ratio:        4.737       Gaps:          0
Percent Similarity:  92.523   Percent Identity: 86.916
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 51 IleSerSerTrpLeuAlaTrpTyrGlnGlnLysProGluLysAlaProLy 67
    |||                    ||||||||||||||    ||||||||||

201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGT 250
    | |||||||||||:::|||||||||| ||||||||||||||||||||||||
 67 sSerLeuIleTyrAlaAlaSerGlnSerLeuGlnSerGlyValProSerArgP 84

251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
    |||||||||||||||||||:::|||||||||||::|||||||||
 84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
    ||||||||||||||||||||| |||  ||||||||||||||||  || ||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSerTyrPr 117

351 T 351
  !
117 o 117
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seq_name: SwissProt_40:KV1H_HUMAN

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seq_documentation_block:
ID   KV1H_HUMAN      STANDARD;       PRT;    108 AA.
AC   P01600;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Hau.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71032830; PubMed=4097974;
RA   Watanabe S., Hilschmann N.;
RT   "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT   chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT   subgroups.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01868; K1HUHU.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11671 MW;  08D3A6160D8D0618 CRC64;

alignment_scores:
               Quality:    472.00        Length:      107
               Ratio:        4.720       Gaps:          0
Percent Similarity:  93.458   Percent Identity: 85.047

alignment_block:
US-09-019-441-3 x KV1H_HUMAN

Align seg 1/1   to: KV1H_HUMAN   from: 1   to: 108

 67 GGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGA 116
    ||||||||||||||||||||||||||||||||||||||||||||||||||
```

alignment_block:
US-09-019-441-3 x KV1G_HUMAN

Align seg 1/1 to: KV1G_HUMAN from: 1 to: 108

```
 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGA 116
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAs    17

117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATATTTAA  166
    ||||||::::||||||||||||||||||||||||||||| ||    |||:
 17 pArgValThrIleIleThrCysArgAlaSerGlnGlyIleArgAsnAspLeuT 34

167 ATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTT 216
    ::||||||||||||||||||||||||| ||||||    ||||||||
 34 hrTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrAla  50

217 GCATCCAGTTTGCAAAGTGGGTCCCATCAAGGTTCAGCGGCAGTGGATC  266
    |||||::::|||||||||||::::|||||||||||||||||||||||||
 51 AlaSerAsnLeuGlnSerGlyValProSerArgPheSerGlySerGlyAl  67

267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTTG 316
    ::|||||||||||||||||::::||||||||||||||||||||||||||
 67 aGlyThrGluPheThrLeuThrIleSerSerLeuGlnProGluAspPheA  84

317 CGACTTATTACTGTCTACAGGTTTATGTACCCCTCGGACGTTCGGCCAA 366
    |||||||||||||||||   |||||::::||||||||||||||||||||
 84 laThrTyrTyrCysLeuGlnAsnSerTyrProArgSerPheGlyGln   100

367 GGGACCAAGGTGGAAATCAAA 387
    |||||||||||||||||||||
101 GlyThrLysValGluIleLys 107
```

seq_name: SwissProt_40:KV1R_HUMAN

seq_documentation_block:
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ID   KV1R_HUMAN    STANDARD;      PRT;     108 AA.
AC   P01610;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region WEA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83273707; PubMed=6410398;
RA   Goni F., Frangione B.;
RT   "Amino acid sequence of the Fv region of a human monoclonal IgM
RT   (protein WEA) with antibody activity against 3,4-pyruvylated
RT   galactose in Klebsiella polysaccharides K30 and K33.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC       AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC       WALDENSTROM'S MACROGLOBULINEMIA.
DR   PIR; A01876; K1HUWE.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Monoclonal antibody.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER       108  108
SQ   SEQUENCE   108 AA;  11840 MW;  9249B61F0945618C CRC64;
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alignment_scores:
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           Quality:  463.00      Length:      107
             Ratio:    4.773      Gaps:          0
Percent Similarity:   90.654      Percent Identity:  85.981
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alignment_block:
US-09-019-441-3 x KV1R_HUMAN

Align seg 1/1 to: KV1R_HUMAN from: 1 to: 108

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 67 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGGGA 116
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAs    17

117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATATTTAA  166
    |||||| ||||||||||||||||||||||||||||||   |||    |||:
 17 pArgValThrIleThrCysArgAlaSerGlnGlyIleArgAsnAspLeuT  34

167 ATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTT 216
    ::||||||||||||||||||||||||||  ||||||||    |||||||||
 34 hrTrpTyrGlnGlnLysProGlyThrAlaProLysArgLeuIleTyrGly  50

217 GCATCCAGTTTGCAAAGTGGGTCCCATCAAGGTTCAGCGGCAGTGGATC  266
    ||::||||||||||||||||||||||||||||||||||||||||||||||
 51 AlaThrSerLeuGlnSerGlyValProSerArgPheSerGlySerGlySe  67

267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTTG 316
    ||||||||||||||||||::::||||||||||||||||||||||||||||
 67 rGlyThrGluPheThrLeuThrIleAsnSerLeuGlnProGluAspPheA  84

317 CGACTTATTACTGTCTACAGGTTTATGTACCCCTCGGACGTTCGGCCAA 366
    ||||||||||||||||||  ||  ||||||||||||||||||||||||||
 84 laThrTyrTyrCysLeuGlnTyrSerSerPheProTrpThrPheGlyGln 100

367 GGGACCAAGGTGGAAATCAAA 387
    |||||||||||||||::::|||
101 GlyThrLysValGluValLys 107
```

seq_name: SwissProt_40:KV5E_MOUSE

seq_documentation_block:
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ID   KV5E_MOUSE    STANDARD;      PRT;     128 AA.
AC   P01637;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-V region T1 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81052342; PubMed=6776411;
RA   Altenburger W., Steinmetz M., Zachau H.G.;
RT   "Functional and non-functional joining in immunoglobulin light chain
RT   genes of a mouse myeloma.";
RL   Nature 287:603-607(1980).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; V00772; CAA24150.1; -.
DR   PIR; A01920; KVMST1.
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DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    128       IG KAPPA CHAIN V-V REGION T1.
FT   DOMAIN       21     43       FRAMEWORK-1.
FT   DOMAIN       44     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     69       FRAMEWORK-2.
FT   DOMAIN       70     76       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       77    108       FRAMEWORK-3.
FT   DOMAIN      109    117       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      118    127       FRAMEWORK-4.
FT   DISULFID     43    108       BY SIMILARITY.
FT   NON_TER     128    128
SQ   SEQUENCE    128 AA;   14385 MW;  AFA563D31BB7E05 CRC64;

alignment_scores:
          Quality:   462.00                  Length:     127
          Ratio:       4.125                  Gaps:         0
Percent Similarity:  88.189       Percent Identity:  66.929

alignment_block:
US-09-019-441-3 x KV5E_MOUSE

Align seg 1/1  to: KV5E_MOUSE   from: 1  to: 128

  7 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTCTGGCTCTCGGCTCCAGG  56
    |||||:|||:::||||||:|||||||||:::||||||||||||:::||||
  1 MetArgThrProAlaGlnPheLeuGlyIleLeuLeuLeuTrpPheProGl  17

 57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT 106
    | :::||||||||||||||||||||||||||||||||::: |||| ||||
 17 yIleLysCysAspIleLysMetThrGlnSerProSerMetTyrAlaS    34

107 CTGTAGGGGGACCAGAGTCACCATCACTTGCAGGGCAAGTCAGGACCATTAGG 156
    |||||||:::|||||||||||||||||||||||||:|||||||||::::|||
 34 erLeuGlyGluArgValThrIleSerCysArgAlaSerGlnAspIleAsn   50

157 TATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCT  206
    |||:|||||:::|:||||||||||||||||||||||:::|||| ||
 51 SerTyrLeuThrTrpPheGlnGlnLysProGlyLysSerProLysThrLe  67

207 GATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCG 256
    |:::||| ||| :::||||||||||||||||||||||||||||||
 67 uLeuTyrArgAlaAsnArgLeuValAspGlyValProSerArgPheSerG  84

257 GCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT 306
    |||||||||||||||||||||||:::|||||::::|||||||:::
 84 lySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGluTyr 100

307 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAC 356
    ||||||||:::||| ||||||:::::|||||| ||  :: ||
101 GluAspMetGlyIleTyrTyrCysLeuGlnTyrAspGluProLeuTh    117

357 GTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    ||||||| ||||||||:::||:::|||
117 rPheGlyAlaGlyThrLysLeuGluLeuLys 127

seq_name: SwissProt_40:KV1E_HUMAN

seq_documentation_block:
ID   KV1E_HUMAN     STANDARD;       PRT;    108 AA.
AC   P01597;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region DEE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72053133; PubMed=5124396;
RA   Milstein C.P., Deverson E.V.;
RT   "The amino acid sequence of a human kappa light chain.";
RL   Biochem. J. 123:945-958(1971).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR   PIR; A01865; K1HUDE.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE    108 AA;   11661 MW;  BDD6E350017F1E51 CRC64;

alignment_scores:
          Quality:   456.00                  Length:     106
          Ratio:       4.560                  Gaps:         0
Percent Similarity:  94.340       Percent Identity:  80.189

alignment_block:
US-09-019-441-3 x KV1E_HUMAN

Align seg 1/1  to: KV1E_HUMAN   from: 1  to: 108

 67 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGGGA 116
    ::|||||:|||||||||||||||||||||||||||||||||||:|||||
  1 ****IleMetThrGlnSerProSerLeuSerAlaSerValGlyAs     17

117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAA 166
    ||||||||||||||||:::|||||||:|||||||::||||||:|||||||
 17 pArgValThrIleThrCysArgAlaGlyGlnAsnValAsnLysTyrLeuA  34

167 ATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTT 216
    ||||||||||||||||||||||||||||||||||||:||:||||||||||
 34 snTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIlePheAla  50

217 GCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC 266
    ||||::||||||||||||||||||||||||||||||||||||||||||||
 51 AlaSerLeuLysSerGlyValProSerArgPheSerGlySerGlySe    67

267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTTTG 316
    |||||||||||||:::|||||::::|||||||:::||||||||||||||
 67 rGlyThrAspPheThrLeuThrIleSerGlyLeuProGluLeuAspPheA  84

317 CGACTTATTACTGTCTACAGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
    ||:::||||||:|| |||||||:||:::||||||| ||||||||||||
 84 laThrTyrTyrCysGlnGlnSerTyrThrProTyrThrPheGlyProGly 100

367 GGGACCAAGGTGGAAATC 384
    |||||||||||:::||
101 GlyThrLysValGluMet 106

seq_name: SwissProt_40:KV1S_HUMAN

seq_documentation_block:
ID   KV1S_HUMAN     STANDARD;       PRT;    108 AA.
AC   P01611;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
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seq_name: SwissProt_40:KV1B_HUMAN

seq_documentation_block:
ID   KV1B_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01594;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region AU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72189444; PubMed=5028201;
RA   Schiechl H., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT   protein Au).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=77022433; PubMed=1234024;
RA   Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA   Schwager P., Steigemann W., Schramm H.J.;
RT   "The structure determination of the variable portion of the
RT   Bence-Jones protein Au.";
RL   Biophys. Struct. Mech. 1:139-146(1975).
CC   -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC       MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC       REGION OF THE KAPPA CHAIN REI.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01862; K1HUAU.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11939 MW;  E8011187EE6F6FB9 CRC64;

alignment_scores:
        Quality:   452.00         Length:     107
        Ratio:       4.612           Gaps:       0
Percent Similarity:  91.589    Percent Identity:  83.178

alignment_block:
US-09-019-441-3  x KV1B_HUMAN      ..

Align seg 1/1  to: KV1B_HUMAN  from: 1  to: 108

 67 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGGGA 116
    |||||||||||||||||||||||||||||||||||||||||||||||||
  1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17

117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAA 166
    |||||||||||||||:::||||||::::||||||||||||
 17 pArgValThrIleThrCysGlnAlaSerGlnAspIleSerAspTyrLeuA 34

167 ATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTT 216
```

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DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Wes.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=81092279; PubMed=6778806;
RA   Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT   "Preparative separation of the tryptic hydrolysate of a protein by
RT   high-pressure liquid chromatography. The primary structure of a
RT   monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
RT   Wes).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01877; K1HUWS.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11608 MW;  782B14A649A60E45 CRC64;

alignment_scores:
        Quality:   456.00         Length:     107
        Ratio:       4.606           Gaps:       0
Percent Similarity:  92.523    Percent Identity:  82.243

alignment_block:
US-09-019-441-3  x KV1S_HUMAN      ..

Align seg 1/1  to: KV1S_HUMAN  from: 1  to: 108

 67 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGGGA 116
    |||||||||||||||||||||||||||||||||||::||||||||||
  1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17

117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAA 166
    |||||||||||||||||||||||||||||||||||  ::::::|||
 17 pArgValThrIleThrCysArgAlaSerGlnAspIleSerHisTrpLeuA 34

167 ATTGGTATCAGCAGAAACCAGAAAAGCTCCTAAGCTCCTGATCTATGTT 216
    ||||||||||||||  |||||||||||||||||||||||||||||||
 34 laTrpTyrGlnGlnLysSerGlyLysAlaProLysLeuLeuIleTyrSer 50

217 GCATCCAGTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC 266
    |||||||::||||||||||||||||||||||||:||||||||||||||
 51 AlaSerSerLeuGluAsnGlyValProSerArgPheSerGlySerGlySe 67

267 TGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTG 316
    |||||||||||||||||||||||::||||||||||||||||||||||
 67 rGlyThrGluPheThrLeuThrIleSerSerLeuGlnProGluAspPheA 84

317 CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
    ||||||||  :|||:::||||||||  ::|||  ::||||||||||||
 84 laThrTyrTyrCysLeuGlnGlnAsnProLeuThrPheGlyGlyGly 100

367 GGGACCAAGGTGGAAATCAAA 387
    |||||  ||||||||||
101 GlyThrLysValGluIleLys 107
```

```
FT   STRAND          33     38
FT   TURN            40     41
FT   STRAND          45     49
FT   TURN            50     52
FT   STRAND          53     54
FT   TURN            56     57
FT   TURN            60     61
FT   STRAND          62     67
FT   TURN            68     69
FT   STRAND          70     75
FT   HELIX           80     82
FT   STRAND          85     90
FT   STRAND          98     98
FT   STRAND         102    106
FT   NON_TER        108    108
SQ   SEQUENCE       108 AA;  11902 MW;  9E8143E1188BCE2A CRC64;
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alignment_scores:
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  Quality:  452.00                      Length:    106
  Ratio:      4.660                      Gaps:        0
  Percent Similarity: 91.509   Percent Identity: 82.075
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alignment_block:
US-09-019-441-3 x KV1O_HUMAN

Align seg 1/1  to: KV1O_HUMAN  from: 1  to: 108

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67  GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGA 116
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1   AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17

117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTAA  166
    |||||||||||||:::||||||||||||||||   |||||  ||||||||
17  pArgValThrIleThrCysGlnAlaSerGlnAspIleIleLysTyrLeuA 34

167 ATTGGTATCAGCAGAAAGCCAGGAAAAGCTCCTAAGCTCCTGATCTATGTT 216
    ||||||||| ||||||||   |||||||||||||||||||||:::|||||
34  snTrpTyrGlnGlnThrProGlyLysAlaProLysLeuLeuIleTyrGlu 50

217 GCATCCAGTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC  266
    ||||:::||||| |||||:::||||||||||||||||||||||||||||
51  AlaSerAsnLeuGlnSerGlyValProSerArgPheSerGlySerGlySe 67

267 TGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTG  316
    ||||:::|||| ||||:::|||||||||||||||||||||||||||::|
67  rGlyAlaHisPheThrPheThrIleSerSerLeuGlnProGluAspIleA 84

317 CGACTTATTACTGTCTACACAGTTTATAGTAGTACCCCTCGGACGTTCGGCCAA 366
    ||||||||||||||||   |||   |||||||||||||||
84  laThrTyrTyrCysGlnGlnTyrAspTyrLeuProTrpThrPheGlyGln 100

367 GGGACCAAGGTGGAAATCAAA 384
    ||||||||||:::::|||
101 GlyThrLysLeuGlnIle 106
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seq_name: SwissProt_40:KV1N_HUMAN

seq_documentation_block:
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ID   KV1N_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01606;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region OU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70201507; PubMed=5447531;
RA   Kohler H., Shimizu A., Paul C., Putnam F.W.;
```

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    ||||||||||||||||||||||||||||||||||||||
34  snTrpTyrGlnGlnLysProGlyGlnAlaProLysLeuLeuIleTyrAsp 50

217 TGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG 266
    ||||:::|||| ||||:::||||||||||||||||||||||||||||||
51  AlaSerAsnLeuGluSerGlyValProSerArgPheSerGlySerGlySe 67

267 GCATCCAGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTG 316
    |||||:::|||||   ||:::|||||||||||||||||||||||||||
67  rGlyAlaHisPheThrPheThrIleSerSerLeuGlnProGluAspIleA 84

317 CGACTTATTACTGTCTACACAGTTTATAGTAGTACCCCTCGGACGTTCGGCCAA 366
    ||||||||||||||||   |||   |||||||||||||||
84  laThrTyrTyrCysGlnGlnTyrAspTyrLeuProTrpThrPheGlyGln 100

367 GGGACCAAGGTGGAAATCAAA 387
    |||||||||||||||||
101 GlyThrLysValGluIleLys 107
```

seq_name: SwissProt_40:KV1O_HUMAN

seq_documentation_block:
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ID   KV1O_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Rel.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=1182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01873; KIHURE.
DR   PDB; 1REI; 17-FEB-84.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3d-structure.
FT   DOMAIN          1     23    FRAMEWORK-1.
FT   DOMAIN         24     34    COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN         35     49    FRAMEWORK-2.
FT   DOMAIN         50     56    COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN         57     88    FRAMEWORK-3.
FT   DOMAIN         89     97    COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN         98    107    FRAMEWORK-4.
FT   DISULFID       23     88
FT   STRAND          4      7
FT   STRAND         10     13
FT   TURN           15     16
FT   STRAND         19     25
FT   TURN           30     31
```

```
RT   "Macroglobulin structure: variable sequence of light and heavy
RT   chains.";
RL   Science 169:56-59(1970).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC       MACROGLOBULIN.
DR   PIR; A01872; K1HUOU.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE    108 AA;  11777 MW;  8283D4A24105827E CRC64;

alignment_scores:
       Quality:   450.00              Length:     107
         Ratio:     4.455               Gaps:       0
Percent Similarity:  94.393    Percent Identity:  73.832

alignment_block:
US-09-019-441-3  x  KVIN_HUMAN     ..

Align seg 1/1  to: KVIN_HUMAN     from: 1  to: 108

67  GACATCCAGATGACCCAGTCTCCATCTTCCTGTCTGCATCTGTAGGGGA 116
    ||||||||||||||||||::|||||||||||||||||||||||||||::
 1  AspIleGlnMetThr***SerProSerSerLeuSerAlaSerValGly** 17

117 CAGAGTCACCATCACTTGCCGAGGGCAAGTCAGGACATTAGGTATTATTAA 166
    ::||||||||||||||::|||||||    |||   ||  ||||||
17  *ArgValThrIleThrCysArgAlaSer***ThrIleSerSerTyrLeu* 34

167 ATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTT 216
    :::||||||::::|||||||||||||||||||||||||:::|||||||||
34  ***TrpTyr***LysProGlyLysAlaPro***LeuLeuIleTyrAla 50

217 GCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC 266
    ||||||:||||:||||||||||||||||||||||||||||||||||||||
51  AlaSer***LeuHisSerGlyValProSerArgPheSerGlySerGlySe 67

267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTTTG 316
    |||||:|||||||||||||||::|||||||||||||||||||||:|||||
67  rGlyThr***PheThrThrLeuThrIleSerSerLeu***Pro******PheA 84

317 CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
    |||||||||||||  |||     |||    |||    ||||||||||||||
84  laThrTyrTyrCys******SerTyrSerSerProThrThrPheGly*** 100

367 GGGGACCAAGGTGAAATCAAA 387
    ||||::::::::::||||||
101 GlyThrArgLeu***IleLys 107

seq_name: SwissProt_40:KV1F_HUMAN

seq_documentation_block:
ID   KV1F_HUMAN     STANDARD;      PRT;    108 AA.
AC   P01598;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region EU.
OS   Homo sapiens (Human).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71064023; PubMed=5489770;
RA   Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT   acid sequence of the light chain.";
RL   Biochemistry 9:3155-3161(1970).
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01866; K1HUEU.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE    108 AA;  11788 MW;  9CD294F2F4D88823 CRC64;

alignment_scores:
       Quality:   449.00              Length:     107
         Ratio:     4.629               Gaps:       0
Percent Similarity:  90.654    Percent Identity:  81.308

alignment_block:
US-09-019-441-3  x  KV1F_HUMAN     ..

Align seg 1/1  to: KV1F_HUMAN     from: 1  to: 108

67  GACATCCAGATGACCCAGTCTCCATCTTCCTGTCTGCATCTGTAGGGGA 116
    ||||||||||||||||||||::|||||||||||||||||||||||||:
 1  AspIleGlnMetThrSerProSerSerLeuSerAlaSerValGlyAs 17

117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTAA 166
    |||||||||||||||||||||||||||::|||||||||||:::||||
17  pArgValThrIleThrCysArgAlaSerGlnSerIleAsnThrTrpLeuA 34

167 ATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTT 216
    ||||||||||||||||||||||||||||||||||||||||||::||:|||
34  laTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuMetTyrLys 50

217 GCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC 266
    |||||||||||||||||||::|||||||||||||||||||||||||||||
51  AlaSerSerLeuGluSerGlyValProSerArgPheIleGlySerGlySe 67

267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTTTG 316
    |||||||||||||||||||||::|||||||||||||||||||||:|||||
67  rGlyThrGluPheThrLeuThrIleSerSerLeuGlnProAspAspPheA 84

317 CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
    |||||||||||||       |||    |||   |||||||||||||||||
84  laThrTyrTyrCysGlnGlnTyrAsnSerAspSerArgLysMetPheGlyGln 100

367 GGGGACCAAGGTGGAAATCAAA 387
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              101 GlyThrLysValGluValLys 107

seq_name: SwissProt_40:KV1K_HUMAN

seq_documentation_block:
ID   KV1K_HUMAN     STANDARD;        PRT;    108 AA.
AC   P01603;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Ka.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76189985; PubMed=818073;
RA   Shinoda T.;
RT   "Comparative structural studies on the light chains of human
RT   immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL   J. Biochem. 77:1277-1296(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01869; KIHUKA.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11900 MW;  768839FBED5A2F4B CRC64;

alignment_scores:
          Quality:   448.00               Length:    107
            Ratio:     4.480                 Gaps:      0
Percent Similarity:  93.458     Percent Identity:  75.701

alignment_block:
US-09-019-441-3 x KV1K_HUMAN       ..

Align seg 1/1  to: KV1K_HUMAN  from: 1  to: 108

   67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGA 116
      ||||||||||||||||||||||||||||::|||||:||::||||||||||
    1 AspIleGlnMetThrGlnSerProSerThrLeuSerValSerValGlyAs 17

  117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGTAGTTATTATTAA 166
      ||||||||||||||::||||||||     :::    ||||||
   17 pArgValThrIleThrCysGluAlaSerGlnThrValLeuSerTyrLeuA 34

  167 ATTGGTATCAGCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTT 216
      |||||||||||||||||||||||||||||||||||||||:||::
   34 snTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrAla 50

  217 GCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCCAGTGGATC 266
      ||||||||||||::::||||||||||||||||||||||||:||:||||
   51 AlaSerSerLeuGlnThrGlyValProSerArgPheSerGlyGlnGlySe 67

  267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTTTG 316
      |'|||||:::||||:::|||:::|||||||||||||::||:::||||||
   67 rGlyThr***PheThrPheIleSerSerVal***Pro******PheA 84
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      317 CGACTTATTACTGTCTACACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
          |||||||||||||     ::      :::      ||||||||||||||||||
       84 laThrTyrTyrCysGln***TyrLeuAspLeuProArgThrPheGlyGln 100

      367 GGGACCAAGTGGAAATCAAA 387
          ||||||||||::::::|||
      101 GlyThrLysValAspLeuLys 107

OM of: US-09-019-441-3 to: SPTREMBL_19:*    out_format : pfs
Date: Sep 23, 2002 10:23 AM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US0901944l/runat_23092002_095259_6361/app_query.fasta_1.1860
-DB=SPTREMBL_19 -QFMT=fastan -SUFFIX=rspt -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0901944l_@CGN1_1_409 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-019-441-3
Query length: 387
Database: SPTREMBL_19:*
Database sequences: 562222
Database length: 172994929
Search time (sec): 228.280000

score_list:

| sequence | Strd | Orig | zScore | EScore | Len | Documentation |
|---|---|---|---|---|---|---|
| sp_human:Q9UL77 | + | 486.00 | 1023.35 | 1.1e-48 | 108 | ! Q9ul77 homo sapiens (human). my |
| sp_human:Q96SA9 | + | 478.50 | 1007.53 | 8.4e-48 | 107 | ! Q96sa9 homo sapiens (human). ar |
| sp_human:Q9UL70 | + | 455.00 | 957.60 | 5.0e-45 | 108 | ! Q9ul70 homo sapiens (human). my |
| sp_human:Q9UL81 | + | 451.50 | 950.27 | 1.3e-44 | 107 | ! Q9ul81 homo sapiens (human). my |
| sp_human:Q9UL79 | + | 442.00 | 930.03 | 1.7e-43 | 108 | ! Q9ul79 homo sapiens (human). my |
| sp_rodent:Q925S9 | + | 439.00 | 922.16 | 4.0e-43 | 127 | ! Q925s9 mus musculus (mouse). in |
| sp_rodent:Q91WF8 | + | 435.00 | 907.98 | 1.3e-42 | 234 | ! Q91wf8 mus musculus (mouse). hy |
| sp_rodent:Q91WS9 | + | 417.00 | 869.85 | 1.8e-40 | 233 | ! Q91ws9 mus musculus (mouse). hy |
| sp_human:Q96PF6 | + | 414.00 | 869.99 | 3.5e-40 | 116 | ! Q96pf6 homo sapiens (human). ka |
| sp_rodent:Q920E6 | + | 397.00 | 834.51 | 3.6e-38 | 109 | ! Q920e6 mus musculus (mouse). pt |
| sp_rodent:Q9QYF0 | + | 392.00 | 814.53 | 1.7e-37 | 298 | ! Q9qyf0 mus musculus (mouse). cr |
| sp_rodent:Q9R1A5 | + | 385.00 | 802.78 | 1.1e-36 | 214 | ! Q9r1a5 mus musculus (mouse). ka |
| sp_rodent:Q99M37 | + | 371.00 | 772.09 | 4.9e-35 | 238 | ! Q99m37 mus musculus (mouse). hy |
| sp_human:Q9UL83 | + | 368.00 | 773.10 | 9.5e-35 | 108 | ! Q9ul83 homo sapiens (human). my |
| sp_rodent:Q91XL0 | + | 367.00 | 764.73 | 1.4e-34 | 211 | ! Q91xl0 mus musculus (mouse). ac |
| sp_human:Q9UL78 | + | 366.50 | 769.83 | 1.4e-34 | 109 | ! Q9ul78 homo sapiens (human). my |
| sp_human:Q9UL85 | + | 357.50 | 750.74 | 1.7e-33 | 109 | ! Q9ul85 homo sapiens (human). my |
| sp_rodent:Q9JL84 | + | 354.00 | 743.49 | 4.3e-33 | 107 | ! Q9jl84 mus musculus (mouse). an |
| sp_rodent:Q920E9 | + | 354.00 | 743.15 | 4.3e-33 | 111 | ! Q920e9 mus musculus (mouse). pt |
| sp_rodent:Q921A6 | + | 349.50 | 726.38 | 1.7e-32 | 241 | ! Q921a6 mus musculus (mouse). an |
| sp_rodent:Q9ERZ9 | + | 345.00 | 724.41 | 4.9e-32 | 107 | ! Q9erz9 mus musculus (mouse). an |
| sp_human:Q9UL86 | + | 343.50 | 721.05 | 7.5e-32 | 109 | ! Q9ul86 homo sapiens (human). my |
| sp_rodent:Q9JL74 | + | 335.00 | 703.92 | 7.4e-31 | 99 | ! Q9jl74 mus musculus (mouse). ant |
| sp_invertebrate:Q9U410 | + | 323.50 | 678.90 | 1.7e-29 | 106 | ! Q9u410 schistosoma japonicum an |
| sp_rodent:Q9JL80 | + | 319.00 | 669.62 | 5.8e-29 | 103 | ! Q9jl80 mus musculus (mouse). an |
| sp_rodent:Q91W12 | + | 316.50 | 656.63 | 1.3e-28 | 235 | ! Q91w12 mus musculus (mouse). un |
| sp_rodent:Q9JL78 | + | 315.00 | 661.32 | 1.7e-28 | 101 | ! Q9jl78 mus musculus (mouse). an |
| sp_human:Q9UL80 | + | 314.00 | 658.07 | 2.3e-28 | 114 | ! Q9ul80 homo sapiens (human). my |
| sp_mammal:Q9N0W5 | + | 301.00 | 630.92 | 7.8e-27 | 109 | ! Q9n0w5 oryctolagus cuniculus (I |
| sp_rodent:Q9JL76 | + | 298.00 | 625.65 | 1.7e-26 | 97 | ! Q9jl76 mus musculus (mouse). ant |
| sp_rodent:Q9JL82 | + | 297.50 | 623.94 | 2.0e-26 | 104 | ! Q9jl82 mus musculus (mouse). an |
| sp_human:Q9NP29 | + | 265.00 | 552.93 | 1.4e-22 | 130 | ! Q9np29 homo sapiens (human). mi |
| sp_human:Q9UL82 | + | 238.00 | 497.49 | 2.1e-19 | 107 | ! Q9ul82 homo sapiens (human). my |
| sp_human:Q9NSD6 | + | 230.50 | 481.58 | 1.7e-18 | 107 | ! Q9nsd6 homo sapiens (human). hy |
| sp_human:Q96E61 | + | 229.50 | 472.08 | 2.5e-18 | 236 | ! Q96e61 homo sapiens (human). un |
| sp_rodent:Q925S1 | + | 226.00 | 465.40 | 6.5e-18 | 218 | ! Q925s1 mus musculus (mouse). mr |
| sp_human:Q96SB0 | + | 214.50 | 447.56 | 1.3e-16 | 108 | ! Q96sb0 homo sapiens (human). an |
| sp_human:Q96JD1 | + | 202.50 | 421.77 | 3.4e-15 | 112 | ! Q96jd1 homo sapiens (human). am |
| sp_rodent:Q99M11 | + | 201.50 | 412.74 | 5.1e-15 | 235 | ! Q99m11 mus musculus (mouse). hy |
| sp_human:Q96JD0 | + | 197.00 | 409.78 | 1.5e-14 | 116 | ! Q96jd0 homo sapiens (human). am |
| sp_human:Q96JD2 | + | 191.00 | 397.38 | 7.8e-14 | 112 | ! Q96jd2 homo sapiens (human). |
| sp_human:Q96I69 | + | 182.00 | 371.47 | 1.0e-12 | 233 | ! Q96i69 homo sapiens (human). |
| sp_rodent:Q91V32 | + | 181.00 | 369.35 | 1.4e-12 | 233 | ! Q91v32 m adult male small in |
| sp_rodent:Q9ET13 | + | 166.50 | 345.68 | 6.0e-11 | 109 | ! Q9et13 mus musculus (mouse). |
| sp_human:Q9H5Z4 | + | 165.50 | 341.56 | 8.3e-11 | 135 | ! Q9h5z4 homo sapiens (human). |

seq_name: sp_human:Q9UL77

seq_documentation_block:
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ID   Q9UL77          PRELIMINARY;      PRT;     108 AA.
AC   Q9UL77;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035037; AAD56273.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1.
FT   NON_TER     108     108.
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alignment_scores:
Quality:       486.00        Length:     107
Ratio:           4.812       Gaps:         0
Percent Similarity:   94.393   Percent Identity:   88.785

alignment_block:
US-09-019-441-3 x Q9UL77

Align seg 1/1 to: Q9UL77    from: 1 to: 108

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 67 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCGCATCTGTAGGGGA 116
    ||||||||||||||||||||||||||||||||||||||||||  |||||
  1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17

117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTAA 166
    |||||||||||||||||||||||||||||||||||:::|||  ||||||
 17 pArgValThrIleThrCysArgAlaSerGlnSerIleSerSerTyrLeuA 34

167 ATTGGTATCAGCAGAAACCAGGAAAGCTCCTAAGCTCCTGATCTATGTT 216
    ||||||||||||||||||||||||||||||||||||||||||:|||:::
 34 snTrpTyrGlnGlnLysProGlyLysAlaProAsnLeuLeuIleTyrAla 50

217 GCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGGCGCAGTGGATC 266
    |||||||:::|||||||||||||||||||||||||||||||||||||||
 51 AlaSerSerLeuGlnSerGlyValProSerArgPheSerGlySerGlySe 67

267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTTG 316
    ||||||:::||||||||||:::||||||||||||||||||:||||||||
 67 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheA 84

317 CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
    |||||||||||||||::|||||||||||||||||||||||||:::::::
 84 laThrTyrTyrCysGlnGlnSerTyrSerThrSerTrpThrPheGlyGlu 100
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367 GGGACCAAGGTGGAAATCAAA 387
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101 GlyThrLysValGluIleLys 107

seq_name: sp_human:Q96SA9

seq_documentation_block:
ID   Q96SA9      PRELIMINARY;      PRT;   107 AA.
AC   Q96SA9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE   VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98375893; PubMed=9712075;
RA   Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT   "Molecular analysis of polyreactive monoclonal antibodies from
RT   rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT   antibody v region genes.";
RL   J. Immunol. 161:2020-2031(1998).
DR   EMBL; U96396; AAB68785.1; -.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE  107 AA;  11520 MW;  4BB43E9C5B577F16 CRC64;

alignment_scores:
           Quality:   478.50           Length:       107
           Ratio:       4.785          Gaps:           1
Percent Similarity:  93.458     Percent Identity:  89.720

alignment_block:
US-09-019-441-3 x Q96SA9       ..

Align seg 1/1  to: Q96SA9  from: 1  to to 107

 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGA 116
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17

117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAA 166
    ||||||||||||||||||||||||||||||||||||:::|||  ||||||
 17 pArgValThrIleThrCysArgAlaSerGlnSerIleSerSerTyrLeuA 34

167 ATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTT 216
    |||||||||||||||||||||||||||||||||||||||||||||:::||
 34 snTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrAla 50

217 GCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC 266
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 51 AlaSerThrLeuGlnSerGlyValProSerArgPheSerGlySerGlySe 67

267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTTTG 316
    |||||||:::||||||||||||||||||||||||||||||||||||||||
 67 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheA 84

317 CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
    |||||||||||||||  :::       |||:||||||||||||||||||
 84 laThrTyrTyrCysGlnLysTyrSerSerThr...LeuThrPheGlyGly 99

367 GGGACCAAGGTGGAAATCAAA 387
    |||||||||||||||||||||
100 GlyThrLysValGluIleLys 106

seq_name: sp_human:Q9UL70

seq_documentation_block:

---

ID   Q9UL70      PRELIMINARY;      PRT;   108 AA.
AC   Q9UL70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035044; AAD56280.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE  108 AA;  11633 MW;  B7BEDC3E41FCCA37 CRC64;

alignment_scores:
           Quality:   455.00           Length:       107
           Ratio:       4.691          Gaps:           0
Percent Similarity:  90.654     Percent Identity:  83.178

alignment_block:
US-09-019-441-3 x Q9UL70

Align seg 1/1  to: Q9UL70  from: 1  to to 108

 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGA 116
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17

117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAA 166
    |||||||||||||||||||||||||||||||||||||||  ||||||||
 17 pArgValThrIleThrCysArgAlaSerGlnGlyIleSerAsnTyrLeuA 34

167 ATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTT 216
    |||||||||||||||||||||||||||||||||:::|||  :::||||||
 34 laTrpTyrGlnGlnLysProGlyLysValProLysSerLeuIleTyrAla 50

217 GCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC 266
    ||||:::||||||||||||||||||||||||||||||||||||||||||||
 51 AlaSerThrLeuGlnSerGlyValProSerArgPheSerGlySerGlySe 67

267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTTTG 316
    |||||||:::||||||||||||||||||||||||||||||||||||||||
 67 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspValA 84

317 CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
    ||||||||||||||||:::         |||:::||||||||||||||||
 84 laThrTyrTyrCysGlnLysTyrAsnSerAlaProArgThrPheGlyPro 100

367 GGGACCAAGGTGGAAATCAAA 387
    |||||||||:::||||||||||
101 GlyThrLysLeuGluIleLys 107

seq_name: sp_human:Q9UL81

seq_documentation_block:
ID   Q9UL81      PRELIMINARY;      PRT;   107 AA.
AC   Q9UL81;

DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035033; AAD56269.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    107    107
SQ   SEQUENCE   107 AA;  11501 MW;  070549FDE0754748 CRC64;

alignment_scores:
      Quality:      451.50                Length:     107
      Ratio:          4.561                Gaps:        1
Percent Similarity:   92.523       Percent Identity:   84.112

alignment_block:
US-09-019-441-3 x Q9UL81

Align seg 1/1  to: Q9UL81  from: 1  to: 107

    67  GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCGTAGGGGA  116
        |||||||||||||||||||||||||||||||||||||||||||||||||
     1  AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs   17

   117  CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTAA  166
        |||||||||||||||||::||||||           ||||||
    17  pArgValThrIleThrCysArgAlaSerGlnSerIleSerAsnTyrLeuA   34

   167  ATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTT  216
        ||||||||||||||||||||||||||||:::|||||||||||:::
    34  snTrpTyrGlnGlnLysProGlyLysAlaProAsnLeuLeuIleTyrAla   50

   217  GCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC  266
        |||||||||||||||||||||||||||||||||||||||||||||||||
    51  AlaSerSerLeuGlnSerGlyValProSerArgPheSerGlySerGlySe   67

   267  TGGGACAGAGTTCACTCTCACCGTGCAGCCTGCAGCCTGAAGATTTTG  316
        ||||||::::||||||||||||::||||   |||||||  ||||||||
    67  rGlyThrAspPheThrLeuThrIleSerGlyLeuGlnAlaGluAspProA   84

   317  CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA  366
        |||||||||  ||||||  ||||||  ||||||||
    84  laThrTyrTyrCysGlnGlnSerTyrSerAla...LeuThrProPheGlyPro   99

   367  GGGACCAAGGTGGAAATCAAA  387
        |||||||||||::::||||:::
   100  GlyThrLysValAlaSerIleAarg  106

seq_name: sp_human:Q9UL79

seq_documentation_block:
ID   Q9UL79       PRELIMINARY;      PRT;    108 AA.
AC   Q9UL79;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035035; AAD56271.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    108    108
SQ   SEQUENCE   108 AA;  11787 MW;  DB5845F19724FB4E CRC64;

alignment_scores:
      Quality:      442.00                Length:     107
      Ratio:          4.702                Gaps:        0
Percent Similarity:   87.850       Percent Identity:   81.308

alignment_block:
US-09-019-441-3 x Q9UL79

Align seg 1/1  to: Q9UL79  from: 1  to: 108

    67  GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCGTAGGGGA  116
        |||||||  ||||||||||||||||||||||||||||||||:::||||
     1  AspIleValMetThrGlnSerProSerLeuLeuSerAlaSerThrGlyAs   17

   117  CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAA  166
        ||||||||||||::::||||||           |||||
    17  pArgValThrIleSerCysArgMetSerGlnGlyIleSerSerTyrLeuA   34

   167  ATTGGTATCAGCAGAAACCAGGAAAGCTCCTAAGCTCCTGATCTATGTT  216
        |||||||||||||||||||||  ::|||||||||:::|||||||:::
    34  laTrpTyrGlnGlnLysProGlyLysAlaProGluLeuLeuIleTyrAla   50

   217  GCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC  266
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    51  AlaSerThrLeuGlnSerGlyValProSerArgPheSerGlySerGlySe   67

   267  TGGGACAGAGTTCACTCTCACCGTGCAGCCTGCAGCCTGCAGCCTGAAGATTTTG  316
        ||||||::::||||||||||||||:::|||   |||||||  ||||||||
    67  rGlyThrAspPheThrLeuThrIleSerCysLeuGlnSerGluAspPheA   84

   317  CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA  366
        |||||||||  ||||||  |||  ||||||||||
    84  laThrTyrTyrCysGlnGlnTyrTyrSerPheProThrPheGlyGln   100

   367  GGGACCAAGGTGGAAATCAAA  387
        |||||||||||||||||||||
   101  GlyThrLysValGlyIleLys  107

seq_name: sp_rodent:Q92559

seq_documentation_block:
ID   Q92559       PRELIMINARY;      PRT;    127 AA.
AC   Q92559;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   IMUNOGLOBULIN LIGHT CHAIN (FRAGMENT).

```
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=99306687; PubMed=10380019;
RA   Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
RA   Foon K.A., Chatterjee S.K.;
RT   "Construction and characterization of a chimeric fusion protein
RT   consisting of an anti-idiotype antibody mimicking a breast cancer-
RT   associated antigen and the cytokine GM-CSF.";
RL   Hybridoma 18:193-202(1999).
DR   EMBL; AF124721; AAK55120.1; -.
FT   NON_TER       127    127
SQ   SEQUENCE   127 AA;  13794 MW;  13F61BEBBB981FA5 CRC64;

alignment_scores:
          Quality:   439.00                Length:    127
          Ratio:       3.955               Gaps:        0
Percent Similarity:  87.402   Percent Identity:  67.717

alignment_block:
US-09-019-441-3 x Q925S9

Align seg 1/1  to: Q925S9    from:  1   to: 127

    7 ATGAGGGTCCCCGCTCAGCTCCTTCTGCTCTGGCTCCCAGG        56
      |||||||||||||||||    :::|||||     :::|||||
    1 MetArgAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGl   17

   57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT 106
      |:::|||||||||||||||||||||||||||||||||     |||||
   17 yThrArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaS  34

  107 CTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGG 156
      ||:::|||:::|||||||||||||||||||||||||
   34 erLeuGlyGlnArgValSerLeuThrCysArgAlaSerGlnAspIleGly  50

  157 TATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCT  206
      ||:::|||    ||||||||||  ::  ||||
   51 IleAsnLeuHisTrpLeuGlnGlnLysProAspGlyThrIleLeuLysArgLe 67

  207 GATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGTTCAGCG  256
      |||||||||||||    ||||||||||||:::||||||
   67 uIleTyrArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer  84

  257 GCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCCTGCAGCCT     306
      |||||   ||||||||||:::||||||||||:::
   84 lySerArgSerGlySerAspTyrSerLeuGlnTyrAlaSerTyrProTyrTh 100

  307 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAC 356
      |||||||   |||||||||:::|||||
  101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrTh  117

  357 GTTCGGCCAAGGGACCAAGGTGGAAATCAAA                    387
      |||||||  ||||||||:::||||||
  117 rPheGlyGlyThrLysLeuGluIleLys                        127
```

seq_name: sp_rodent:Q91WF8

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seq_documentation_block:
ID   Q91WF8        PRELIMINARY;       PRT;   234 AA.
AC   Q91WF8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 25.9 KDA PROTEIN.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015292; AAH15292.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  25929 MW;  B0D0B0E6EB7812D2 CRC64;

alignment_scores:
          Quality:   435.00                Length:    127
          Ratio:       4.104               Gaps:        0
Percent Similarity:  83.465   Percent Identity:  67.717

alignment_block:
US-09-019-441-3 x Q91WF8

Align seg 1/1  to: Q91WF8    from:  1   to: 234

    7 ATGAGGGTCCCCGCTCAGCTCCTTCTGCTCTGGCTCCCAGG        56
      ||||||||||||||||||:::||||||        ::   ||
    1 MetMetSerSerAlaGlnPheLeuGlyLeuLeuLeuLeuCysPheGlnGl  17

   57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT 106
      |:::|||||||||||||||||||||||||||||||    ||||||||||
   17 yThrArgCysAspIleGlnMetThrGlnThrSerSerLeuSerAlaS     34

  107 CTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGG 156
      |:::||||||||:::||||||||||||||||||||||
   34 erLeuGlyAspArgValThrIleSerCysArgAlaSerGlnAspIleSer  50

  157 TATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCT  206
      ||:::|||||||||||||  ::  ||||
   51 AsnTyrLeuAsnTrpTyrGlnGlnLysProAspGlyThrValLysLeuIle  67

  207 GATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGTTCAGCG  256
      |||||||   |||  ||||||||||||||||||||:::
   67 uIleTyrTyrThrSerArgLeuTyrLeuGlyValProSerArgPheSerG  84

  257 GCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCGGCCTGCAGCCT 306
      ||||||||||||||||||||||:::||||||:::
   84 lySerGlySerGlyThrAspTyrSerLeuThrIleSerAsnLeuGluGln 100

  307 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAC 356
      |||||||   ||  ||||||||:::|||||
  101 GluAspIleAlaThrTyrPheCysGlnGlnGlyAsnThrProProPheTh  117

  357 GTTCGGCCAAGGGACCAAGGTGGAAATCAAA                    387
      ||||||:::|||||||:::||||||
  117 rPheGlySerGlyThrLysLeuGluValLys                     127
```

seq_name: sp_rodent:Q91WS9

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seq_documentation_block:
ID   Q91WS9        PRELIMINARY;       PRT;   233 AA.
AC   Q91WS9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 25.8 KDA PROTEIN (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013496; AAH13496.1; -.
KW   Hypothetical protein.
```

FT   NON_TER      1        1
SQ   SEQUENCE   233 AA;   25781 MW;  B1C184DA149A16EB CRC64;

alignment_scores:
        Quality:   417.00              Length:   117
        Ratio:     4.212               Gaps:       0
Percent Similarity:  84.615    Percent Identity:  70.085

alignment_block:
US-09-019-441-3 x Q91WS9      .

Align seg 1/1 to: Q91WS9  from: 1  to: 233

 37 CTTCTGCTCTGGCTCCCAGGTGCCAGATGTGACATCCAGATGACCCAGTC  86
    |||||||| ||| :::  ||::|||||||||||||||||||||||||::
 10 LeuLeuLeuCysPheGlnGlySerArgCysAspIleGlnMetThrGlnTh  26

 87 TCCATCTTCCCTGTCTGCATCTGTAGGGACAGAGTCACCATCACTTGCA  136
    :  |||||||||||||||||::|||||||||||:::::||||||||||||
 26 rThrSerLeuSerAlaSerLeuGlyAspValThrIleSerCysS   43

137 GGGCAAGTCAGGACATTAGGTATTATTAAATTGGTATCAGCAGAAACCA  186
    ::||||||  |||  ||||||||||||||||||||||||||||||||||
 43 erGlySerGlnGlyIleAlaAsnTrpLeuAsnTrpTyrGlnGlnLysPro  59

187 GGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGG  236
    ::::  ||||||||||||| ::||||||||||:||||
 60 AspGlyThrValLysLeuIleTyrTyrThrSerSerLeuHisSerGl  76

237 GGTCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCA  286
    |||||||||||||||||||||:::||||||||::::::|||||||
 76 yValProSerArgPheSerGlySerGlyTyrThrAspPhrSerLeuT  93

287 CCGTCAGCAGCCTGCAGCCTGAAGATTTTGCGACTTATTACTGTCTACAG  336
    ||:::|||:|||::||||||||||||||||| ||||||||||||||
 93 hrIleSerAsnLeuGluProGluAspPheAlaThrTyrTyrCysGlnGln 109

337 GTTTATAGTACCCCTCGGACGTTCCGCCAAGGACCAAGGTGGAAATCAA  386
    ||| ||||||  |||||||| |||||||||||||||||
110 TyrArgTyrTyrGlyTrpThrPheGlyGlyGlyThrLysGluIleLeuLy 126

387 A 387
126 s 126

seq_name: sp_human:Q96PF6

seq_documentation_block:
ID   Q96PF6        PRELIMINARY;        PRT;         116 AA.
AC   Q96PF6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
GN   SDNK1
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21361171; PubMed=11468171;
RA   Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT   "The tropism of organ involvement in primary systemic amyloidosis:
RT   contributions of Ig V(L) germ line gene use and clonal plasma cell
RT   burden.";
RL   Blood 98:714-720(2001).
DR   EMBL; AF361758; AAK51465.1; -.
FT   NON_TER       1        1
FT   NON_TER     116      116
SQ   SEQUENCE   116 AA;   12735 MW;  E796FC2217BFCF57 CRC64;

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alignment_scores:
        Quality:   414.00              Length:   107
        Ratio:     4.312               Gaps:       0
Percent Similarity:  89.720    Percent Identity:  73.832

alignment_block:
US-09-019-441-3 x Q96PF6      ..

Align seg 1/1 to: Q96PF6  from: 1  to: 116

 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGA 116
    |||||||||||||||||||||||||||||||||||||||||||||
  1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs  17

117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAA 166
    |||||||||||||  ||::::|||||||||||||     ::||||
 17 pArgValThrPheIleCysGlnAlaSerGlnAspIleAlaAsnHisLeuA  34

167 ATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTT 216
    ||||||||||| |||||::||||||:::|||||:::||||||  |||||
 34 snTrpTyrGlnLysProGlyGluAlaProLysPheLeuIleTyrAsp  50

217 GCATCCAGTTTGCAAAGTGGGTCCCATCAAGGTTCAGCGGCAGTGGATC  266
    :::|||  |||:::::||||||||||||||||||||::::|||||
 51 GlySerPheLeuLysThrGlyValProSerArgPheSerGlyGlyGlySe  67

267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTTTG 316
    |||||||||||||||:::||||||||||||||||||||||||||||
 67 rAlaThrAsnPheThrValThrIleSerSerLeuGlnProGluAspPheA  84

317 CGACTTATTACTGTCTACAGTTTATAGTACCCCTCGGACGTTCGGCCAA  366
    ||||||||||| ||  :::  ||||||| ||  ||||||
 84 laThrTyrTyrCysGlnGlnTyrHisHisLeuProPheThrPheGlyPro 100

367 GGGACCAAGGTGGAAATCAA 387
    ||||||||||||:::::|||
101 GlyThrLysValAspPheLys 107

seq_name: sp_rodent:Q920E6

seq_documentation_block:
ID   Q920E6        PRELIMINARY;        PRT;         109 AA.
AC   Q920E6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PTERIN-MIMICKING ANTI-IDIOTOPE KAPPA CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RA   Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT   "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
RT   in Mammalian Cells.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF307938; AAL09422.1; -.
FT   NON_TER       1        1
FT   NON_TER     109      109
SQ   SEQUENCE   109 AA;   11943 MW;  DAD3F98E05DD1501 CRC64;

alignment_scores:
        Quality:   397.00              Length:   107
        Ratio:     4.179               Gaps:       0
Percent Similarity:  88.785    Percent Identity:  70.093

alignment_block:
US-09-019-441-3 x Q920E6      ..

Align seg 1/1 to: Q920E6 from: 1 to: 109

```
 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGA 116
    ||||||||||||||| |||||| :: |||||||||||||::|||||||::
  1 AspIleGlnMetThrGlnSerProAlaSerLeuSerAlaSerValGlyGl 17

117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTAA 166
    : ||||||||||||||||||| :::|||::: |||||
 17 uThrValThrIleThrCysArgAlaSerGlnAsnIleHisAsnTyrLeuA 34

167 ATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTT 216
    ||||||||||| |||||:::||:|||:::||||
 34 laTrpTyrGlnGlnLysProGlyLysSerProGlnLeuLeuValTyrAsn 50

217 GCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC 266
    ||:::||| ::||||||||||||||||||||||||||||||
 51 AlaLysThrLeuAlaAspGlyValProSerArgPheSerGlySerGlySe 67

267 TGGGACAGAGTTCACTCTCACCGTCAGCCTGCAGCCTGAAGATTTTG 316
    |||:::||||||||||||||||||||||
 67 rGlyThrGlnTyrSerLeuLysIleAsnSerLeuGlnProGluAspPheG 84

317 CGACTTATTACTGTCTACAGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
    ::::||||||| ::: ::||||||||| ||||||||
 84 lySerTyrTyrCysGlnHisPheTrpSerThrProTrpThrPheGlyGly 100

367 GGGACCAAGGTGGAAATCAAA 387
    |||||||||||:::|||||||
101 GlyThrLysLeuGluIleLys 107
```

seq_name: sp_rodent:Q9QYF0

alignment_scores:
          Quality:     392.00           Length:    111
          Ratio:       4.041            Gaps:        0
Percent Similarity:   87.387      Percent Identity: 65.766

alignment_block:
US-09-019-441-3 x Q9QYF0

Align seg 1/1 to: Q9QYF0 from: 1 to: 298

```
 55 GGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGC 104
    ||||::::||||||||||||||||||||||||||||||||||||||||||
 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGC 104
```

---

```
169 GlyGlyGlySerAspIleGluLeuThrGlnSerProAlaSerLeuSerAl 185
    |||||:  :::||||||||::||||||||||||:::||||||||||||||

105 ATCTTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGACACATTA 154
    ||||||||||||||||||||||||||||||| ::||:
185 aSerValGlyGluThrValThrIleThrCysArgAlaSerGlyAsnIleH 202

155 GGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTC 204
    :: |||||  |||||:::|||:|||:::|||||:::||:::||||
202 isAsnTyrLeuAlaTrpTyrGlnGlnLysGlnLysSerProGlnLeu 218

205 CTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAG 254
    ||:::||| ||:::|||  :::||||||||||||||||||||||||||||
219 LeuValTyrAsnAlaLysThrLeuAlaAspGlyValProSerArgPheSe 235

255 CGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGC 304
    |||||||||||||:::|||  :::|||||||||||||||||||||||||
235 rGlySerGlySerGlyThrGlnTyrSerLeuLysIleAsnSerLeuGlnP 252

305 CTGAAGATTTGCGACTTATTACTGTCTACAGTTTATAGTACCCCTCGG 354
    ||||||||||:::|||||| :::||||||| ::: ::||||||||| |||
252 roGluAspPheGlySerTyrTyrCysGlnHisPheTrpThrThrProTyr 268

355 ACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    |||||||||||||||||||||||||:::|||||||
269 ThrPheGlyGlyGlyThrLysLeuGluIleLys 279
```

seq_name: sp_rodent:Q9R1A5

alignment_scores:
          Quality:     385.00           Length:    107
          Ratio:       4.096            Gaps:        0
Percent Similarity:   87.850      Percent Identity: 68.224

alignment_block:
US-09-019-441-3 x Q9R1A5

Align seg 1/1 to: Q9R1A5 from: 1 to: 214

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 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGA 116
    |||||||||||||||||||||:::: |||||:::|||::
```

```
                           1 AspIleGlnLeuThrGlnSerProSerMetTyrAlaSerLeuGlyGl 17

117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAA 166
    ::||||||||||||||||:::||||||||||::: ||||||
 17 uArgValThrIleThrCysLysAlaSerGlnAspIleAsnSerTyrLeuS 34

167 ATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTT 216
    ||||:||||||||||||||||||||| ||||||||
 34 erTrpPheGlnGlnLysProGlyLysSerProLysThrLeuIleTyrArg 50

217 GCATCCAGTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC 266
    ||:: |||  ::||||||||||||||||||||
 51 AlaAsnArgLeuValAspGlyValProSerArgPheSerGlySerGlySe 67

267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTTG 316
    |||   ::::||:||||:::||||||||| ::||||||
 67 rGlyGlnAspTyrSerLeuThrIleSerSerLeuGluTyrGluAspMetG 84

317 CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
    :: |||||||||||| ::: ||| ||||||||
 84 lyIleTyrTyrCysLeuGlnTyrAspGluPheProPheThrPheGlySer 100

367 GGGACCAAGGTGGAAATCAAA 387
    |||||||:::||||||
101 GlyThrLysLeuGluIleLys 107
```

seq_name: sp_rodent:Q99M37

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seq_documentation_block:
ID  Q99M37      PRELIMINARY;    PRT;    238 AA.
AC  Q99M37;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  HYPOTHETICAL 26.3 KDA PROTEIN.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC  TISSUE.;
RA  Strausberg R.;
RL  Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; BC002035; AAH02035.1; -.
DR  HSSP; P01679; 2FBJ.
DR  InterPro; IPR003599; Ig.
DR  InterPro; IPR003597; Ig_cl.
DR  InterPro; IPR003600; Ig_like.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; ig; 2.
DR  SMART; SM00409; IG; 2.
DR  SMART; SM00407; IGc1; 1.
DR  SMART; SM00406; IGv; 1.
DR  SMART; SM00410; IG_like; 1.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW  Hypothetical protein.
SQ  SEQUENCE  238 AA;  26344 MW;  FB2B06A0B801330A CRC64;
```

alignment_scores:
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        Quality:  371.00         Length:   132
        Ratio:    3.404          Gaps:       2
Percent Similarity: 82.576   Percent Identity: 53.788
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alignment_block:
US-09-019-441-3 x Q99M37

Align seq 1/1  to: Q99M37  from: 1  to: 238

```
  7 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGG 56
```

---

```
    |||:::|||||| :::||||||||:||||::
  1 MetLysLeuProValArgLeuLeu..ValLeuMetPheTrpIleProAl 16

 57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCAT 106
    :::: ||||||||||||:|||||||||::||
 16 aSerSerAspValAlaMetThrGlnThrProLeuSerLeuProValS 33

107 CTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGG 156
    |||:||||||||||:||:||||||::|||||||||:||||
 33 erLeuGlyAspGlnAlaSerIleSerCysArgSerSerGlnSerIleVal 49

157 TAT..........TATTTAAATTGGTATCACGAGAAACCAGGAAA 191
    :::  |||||||||::|||||
 50 HisSerAsnGlyAsnThrTyrLeuGlnTrpTyrLeuGlnLysProGlyGl 66

192 AGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCC 241
    :::||||||||||:||:::|||::||||||||:||||
 66 nSerProLysLeuLeuIleTyrLysValSerAsnArgPheSerGlyValP 83

242 CATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTC 291
    ||:||||||||||||||||||::|||||
 83 roAspArgPheSerGlySerGlyThrAspPheThrLeuIle 99

292 AGCAGCCTGCAGCCTGAAGATTTGCGACTTATTACTGTCTACAGGTTTA 341
    |||  :::::: ||||| ||||||||:::||||||
100 SerArgValGluAlaGluAspLeuGlyValThrTyrCysPheGlnGlySe 116

342 TAGTACCCCTCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    :::||| |||||||||||||::::||||||
116 rHisValProTyrThrPheGlySerGlyThrLysLeuGluIleLys 131
```

seq_name: sp_human:Q9UL83

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seq_documentation_block:
ID  Q9UL83      PRELIMINARY;    PRT;    108 AA.
AC  Q9UL83;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE  (FRAGMENT).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=98277139; PubMed=9614934;
RA  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA  Young D.C.;
RT  "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT  fetus.";
RL  Clin. Immunol. Immunopathol. 87:184-192(1998).
DR  EMBL; AF035031; AAD56267.1; -.
DR  HSSP; P80362; 1WTL.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; ig; 1.
DR  SMART; SM00406; IGv; 1.
FT  NON_TER   1      1
FT  NON_TER   108    108
SQ  SEQUENCE  108 AA;  11834 MW;  9F9C5A92EBA96EEA CRC64;
```

alignment_scores:
```
        Quality:  368.00         Length:   107
        Ratio:    4.044          Gaps:       0
Percent Similarity: 85.047   Percent Identity: 65.421
```

alignment_block:
US-09-019-441-3 x Q9UL83

Align seq 1/1  to: Q9UL83  from: 1  to: 108

```
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka K., Matsuura K., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
DR   EMBL; AK002514; BAB22154.1; -.
SQ   SEQUENCE   211 AA;   23182 MW;   1A5FFA0F8BA50163 CRC64;

alignment_scores:
            Quality: 367.00                Length:     104
              Ratio:   3.989                 Gaps:       0
Percent Similarity:  88.462    Percent Identity:  65.385

alignment_block:
US-09-019-441-3 x Q91XL0

Align seg 1/1  to: Q91XL0  from: 1  to: 211

76  ATGACCCAGTCTCCATCTTCCCTGTCTGCATCGTAGGGGACAGAGTCAC  125
    ||||||||||||||||||||||||||||||::::||||||   |||||
1   MetThrGlnSerProAlaSerLeuSerValSerValGluThrValTh   17

126 CATCACTGCGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATC  175
    ||||||||||||||||||||::::|||        |||  ||||||||
17  rIleThrCysArgAlaSerGluAsnIleTyrSerAsnLeuAlaTrpTyrG  34

176 AGCAGAAACCAGGAAAAGTCCTAAGCTCCTGATCTATGTTGCATCCAGT  225
    ||||||||   |||||:::|||::|||||||||||:||:::||::::::
34  lnGlnLysGlnGlyLysSerProGlnLeuLeuValTyrAlaAlaThrAsn  50

226 TTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGA  275
    |||    ||||||||||||||||||||||||:|||||||||||||:::
51  LeuAlaAspGlyValProSerArgPheSerGlySerGlySerGlyThrGl  67

276 GTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTTTGCGACTTATT  325
    :::::::|||  ||||||||||||:||||||||||||::||||||||||
67  nTyrSerLeuLysIleAsnSerLeuGlnSerGluAspPheGlySerTyrP  84

326 ACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAAGGACCAAG  375
    :||  :::  :::|||||||||||||||||||  ||||||||
84  heCysGlnHisPheTrpGlyThrProArgThrPheGlyGlyGlyThrLys  100

376 GTGGAAATCAAA  387
    ::||||||||
101 LeuGluIleLys  104
```

```
67  GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCGTAGGGGA  116
    ::::|||   |||||||||||||||||||||||||||:::|||   |||::
1   GluIleValMetThrGlnSerProAlaThrLeuSerValSerProGlyGl  17

117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAA  166
    :|||:|||:||:|:|||||||||||||||||||:::|||       |||
17  uArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerAsnLeuA  34

167 ATTGGTATCAGCAGAAACCAGGAAAGCTCCTAAGCTCCTGATCTATGTT  216
    ||||||||||||||||||||||||||||||||||||||:::||||||||
34  laTrpTyrGlnGlnLysProGlyGlnAlaProArgLeuLeuIleTyrCys  50

217 GCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC  266
    |||||:::         ::|||||||||||||||||||||||||||||||
51  AlaSerThrArgAlaThrGlyIleProAlaArgPheSerGlySerGlySe  67

267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTTG  316
    ||||||||||:||:|||||:::|||||||||||||||||  |||||||
67  rGlyThrGluPheThrLeuThrIleSerSerLeuGlnPheGluAspPheA  84

317 CGATTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA  366
    ||:::||||||||     :||   :::|||       ||  ||||||||
84  laValTyrTyrCysGlnHisPheTrpAsnAsnTyrAsnTrpProPheThrPheGlyGlyPro 100

367 GGGACCAAGGTGGAAATCAAA  387
    ||||||||||||:::|||||
101 GlyThrLysValAspIleLys  107
```

```
seq_name: sp_rodent:Q91XL0

seq_documentation_block:
ID   Q91XL0      PRELIMINARY;      PRT;      211 AA.
AC   Q91XL0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ADULT MALE KIDNEY cDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE   CLONE:0610010P20, FULL INSERT SEQUENCE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=KIDNEY;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA   Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima A.,
RA   Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
RA   Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
RA   Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y.,
RA   Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
RA   Toya T., Yamamura Y., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX   MEDLINE=21085560; PubMed=11217851;
RA   RIKEN FANTOM Consortium.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [4]
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OM of: US-09-019-441-3 to: Pending_Patents_AA_New:*    out_format : pfs

Date: Sep 23, 2002  9:59 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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 -Q=/cgn2_1/USPTO_spool/US09019441/runat_23092002_095258_6341/app_query.fasta_1.1860
 -DB=Pending_Patents_AA_New -QFMT=fastan -SUFFIX=rapn
 -GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
 -LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
 -XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
 -YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=US09019441 @CGN1_1_60 -NCPU=6 -ICPU=3 -LONGLOG
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Search information block:
Query: US-09-019-441-3
Query length: 387
Database: Pending_Patents_AA_New:*
Database sequences: 949130
Database length: 267991220
Search time (sec): 353.570000

score_list:

| Sequence | Strd | Orig | ZScore | EScore | Len | Documentation |
|---|---|---|---|---|---|---|
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| /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-107543 | + | 600.50 | 1024.50 | 1.1e-48 | | |
| /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-206-008-639 | + | 595.00 | 1012.19 | 3.7e-48 | 2 | |
| /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-831-805A-10 | + | 594.50 | 1010.14 | 4.2e-48 | 2 | |
| /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-107484 | + | 592.00 | 1010.52 | 7.0e-48 | | |
| /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-831-805A-1 | + | 590.50 | 1003.30 | 1.0e-47 | 23 | |
| /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-81820 | + | 588.00 | 1004.06 | 1.7e-47 | | |
| /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-12240 | + | 586.00 | 1001.04 | 2.6e-47 | | |
| /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-12255 | + | 586.00 | 1000.64 | 2.6e-47 | | |
| /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-65658 | + | 581.00 | 991.97 | 7.7e-47 | | |
| /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-71040 | + | 578.50 | 983.80 | 1.4e-46 | | |
| /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-71830 | + | 578.00 | 987.11 | 1.5e-46 | | |
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; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE:  2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
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;   ORGANISM: Homo sapiens
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; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
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;   TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;   FILE REFERENCE: PT253C1N
;   CURRENT APPLICATION NUMBER: US/10/206,008
;   CURRENT FILING DATE: 2002-07-29
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      ;   APPLICANT: INCYTE PHARMACEUTICALS, INC.       seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-107484
      ;   APPLICANT: YUE, Henry
      ;   APPLICANT: TANG, Y. Tom                        seq_documentation_block:
      ;   APPLICANT: CORLEY, Neil C.                     ; Sequence 107484, Application US/09791537
      ;   APPLICANT: GUEGLER, Karl J.                    ; GENERAL INFORMATION:
      ;   APPLICANT: GORGONE, Gina A.                    ;   APPLICANT: Bionomix, Inc.
      ;   APPLICANT: BAUGHN, Mariah R.                   ;   APPLICANT: Debe, Derek
      ;   APPLICANT: LU, Dyung Aina M.                   ;   APPLICANT: Danzer, Joseph
      ;   APPLICANT: LAL, Preeti                         ;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
      ;   APPLICANT: HILLMAN, Jennifer L.                ;   TITLE OF INVENTION: METHODS OF USE THEREOF
      ;   APPLICANT: YANG, Junming                       ;   FILE REFERENCE: 261/210
      ;   TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS   ;   CURRENT APPLICATION NUMBER: US/09/791,537
      ;   FILE REFERENCE: PF-0643 PCT                    ;   CURRENT FILING DATE: 2001-02-22
      ;   CURRENT APPLICATION NUMBER: US/09/831,805A      ;   NUMBER OF SEQ ID NOS: 153055
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      Percent Similarity: 94.615    Percent Identity: 90.000    1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTGCTGCTCTGGCT 50
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      alignment_block:                                        1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17
      US-09-019-441-3 x US-09-831-805A-10
                                                                51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGT 100
      Align seg 1/1  to: US-09-831-805A-10  from: 1  to: 237    ||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34
        1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTGCTGCTCTGGCT 50
          ||||||||||||||||||||||||||||||||||||||||||||||||||   101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
        1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17      ||||||||||:::||||||||||||||||||||||||||||||||||||||
                                                                34 erAlaSerValGlyAspArgValThrPheThrCysArgAlaSerGlnThr 50
       51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGT 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||   151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
       17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34      |||   ::||||||||||||||||||||||||||||||||||||||||||
                                                                51 IleAlaThrPheLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67
      101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
          |||||||||:::||||||||||||||||||||||||||||||||:::||||   201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGT 250
       34 erAlaSerValGlyAspArgValThrPheThrCysArgAlaSerGlnSer 50      ||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgP 84
      151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
          ||(|)|||||||||||||||||||||||||||||||||||||||||||     251 TCAGCGGCAGTGGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
                                                                   ||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                84 heSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
```

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 301 CAGCCTGAAGATTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
     |||||||||||||||||||||||| ||| |||||| ||
 101 GlnProGluAspPheAlaThrTyrCysGlnLeuSerTyrSerIlePr 117

 351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
     | |||||||||||||||||||||||||||||
 117 oTrpThrPheGlyGlnGlyThrLysValGluIleLys 129
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-831-805A-1

seq_documentation_block:
; Sequence 1, Application US/09831805A
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: GORGONE, Gina A.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: LAL, Preeti
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: YANG, Junming
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
; FILE REFERENCE: PF-0643 PCT
; CURRENT APPLICATION NUMBER: US/09/831,805A
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 09/195,853; unassigned; 60/113,635; 60/128,194
; PRIOR FILING DATE: 1998-11-19; 1998-11-19; 1998-12-22; 1999-04-07
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO: 079785CD1
US-09-831-805A-1

alignment_scores:
       Quality:   590.50      Length:      130
       Ratio:     4.801       Gaps:        1
Percent Similarity: 94.615    Percent Identity: 89.231

alignment_block:
US-09-019-441-3 x US-09-831-805A-1

Align seg 1/1  to: US-09-831-805A-1  from: 1  to: 237

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   1 ATGGACAATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCGTCTCTGGCT 50
     |||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetAspMetArgValProAlaGlnLeuLeuLeuGlyLeuLeuLeuTrpLe 17

  51 CCCAGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
     | |||||||||||||||||||||||||||||||||||||||||||||
  17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34

 101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
     |||||||||||||||||||||||||||||||||||:::||:::|
  34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50

 151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
     ||| |||||||||||||||||||||||||||||||||||||||||||
  51 IleSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67

 201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGT 250
     ||||||||||||||||||||||||||||||||||::||::||
  67 sLeuLeuIleTyrAlaAlaSerLeuGlnSerGlyValProSerArgP 84
```

```
 251 TCAGGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
     |||||||||||||||||||||||::||||||||||||::|||||||||
  84 heSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

 301 CAGCCTGAAGATTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
     ||||||||||||||||||||||| || ||||| ||
 101 GlnProGluAspPheAlaThrTyrCysGlnLeuSerTyrSerThrPr 117

 351 TCGG...ACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
     |   |||||||||||||||||:::::||||||||
 117 oProIleThrPheGlyGlnGlyThrArgLeuGluIleLys 130
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-81820

seq_documentation_block:
; Sequence 81820, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 81820
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-81820

alignment_scores:
       Quality:   588.00      Length:      129
       Ratio:     4.820       Gaps:        0
Percent Similarity: 94.574    Percent Identity: 88.372

alignment_block:
US-09-019-441-3 x US-09-791-537-81820

Align seg 1/1  to: US-09-791-537-81820  from: 1  to: 129

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   1 ATGGACAATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCGTCTCTGGCT 50
     |||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetAspMetArgValProAlaGlnLeuLeuLeuGlyLeuLeuLeuTrpLe 17

  51 CCCAGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
     |||||||||||||||||||||||||||||||||||||||||||||||
  17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34

 101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
     ||||||||||||||||||||||||||||||||||||||||||||||
  34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnAsn 50

 151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
     |||  ||||||||||||||||||||||||||||||||||||||||||
  51 IleIleSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67

 201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGT 250
     |||||||::||||||||||||||||||||||||||||::::|||
  67 sLeuLeuMetTyrAlaAlaSerLeuGlnSerGlyValProAlaArgP 84

 251 TCAGGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
     |||||||||||||||||||:::||||||||||||::|||||||||
  84 heValGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

 301 CAGCCTGAAGATTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
     |||||||||||||||||||||  ||  |||||  :::||
 101 GlnProGluAspPheAlaThrTyrTyrCysGlnThrTyrSerAlaPr 117

 351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
```

## Right column

```
117 oLeuThrPheGlyGlyThrLysValGluIleLys 129
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-12274

alignment_scores:
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    Quality:  586.00              Length:           123
    Ratio:    4.966               Gaps:             0
Percent Similarity:  95.935    Percent Identity:  92.683
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alignment_block:
US-09-019-441-3 x US-09-791-537-12274

Align seg 1/1  to: US-09-791-537-12274  from: 1  to: 123

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  19 GCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCCAGATGTGA  68
     |||||||||||||||||||||||||||||||||||| ||||||||
   1 AlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuArgGlyAlaArgCysAs  17

  69 CATCCAGATGACCCAGTCTCCATCTCCTGTGTCTGCATCTGTAGGGGGACA 118
     |||||||||||||||||||||||||||||||||||||||||||| ||||||
  17 pIleGlnMetThrGlnSerProSerProValSerAlaSerValGlyAspA  34

 119 GAGTCACCATCACTTGCAGGGCAAGTCAGAGCATTAGGTATTATTTAAAT 168
     ||||||||||||||||||:::|:| ||||||||| |||||||
  34 rgValThrIleThrCysArgAlaSerGlnSerIleSerSerTyrLeuAsn  50

 169 TGGTATCAGCAGAAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGC 218
     ||||||||||||||||||||||||:::|||||||||||||||:::|
  51 TrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrAlaAl  67

 219 ATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTG 268
     |||||||||||||||||||||||||||||||||||||||||||
  67 aSerSerLeuGlnSerGlyValProSerArgPheSerGlySerGlySerG  84

 269 GGACAGACAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTTTGCG 318
     |||||||::::||||||||||||||||||||||||||||||
  84 lyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheAla 100

 319 ACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAAGG 368
     ||||||||||||| ||| |||||||||||||||||||||||
 101 ThrTyrTyrCysGlnGlnSerTyrSerThrProArgThrPheGlyGlnGl 117

 369 GACCAAGGTGGAAATCAAA 387
     |||||||||||||
 117 yThrLysValGluIleLys 123
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-12255

## Left column

```
  | |||||||   ||||||||||||||||
117 oLeuThrPheGlyGlyThrLysValGluIleLys 129
```

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-12274

alignment_scores:
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    Quality:  586.00              Length:           128
    Ratio:    4.843               Gaps:             0
Percent Similarity:  94.531    Percent Identity:  89.062
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alignment_block:
US-09-019-441-3 x US-09-791-537-12255

Align seg 1/1  to: US-09-791-537-12255  from: 1  to: 129

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   4 GACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCC  53
     ||||||||||||||||||||||||||||||||||||||||
   1 AspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuAr  17

  54 AGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGTCTG 103
     ||||||||||||||||||||||||||||||||||||||||||::
  17 gGlyAlaArgCysAspIleGlnMetThrGlnSerProSerProSerLeuSerT  34

 104 CATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATT 153
     ::|||||||  ||||||||||||||||||||||||||||||:|||
  34 hrSerLeuGlyAspArgValThrIleThrCysArgAlaSerGlnSerIle  50

 154 AGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCT 203
     ||||||||||||||||||||||||||||||||||||||||||||||
  51 GlyThrTyrLeuAsnTrpTyrTyrGlnGlnLysProGlyLysAlaProLysPh  67

 204 CCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 253
     :|||||||  ||||||||||||||||||||||||||||||||||
  67 eLeuIleTyrGlyAlaSerLeuGlnSerGlyValProSerArgPheS  84

 254 GCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAG 303
     |||||||||||||||||:::|||||||||::::||||||||||||||
  84 erGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGln 100

 304 CCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCG 353
     |||||||||||||||||| ||| |||||||::::||||||||
 101 ProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProPr 117

 354 GACGTTCGGCCAAGGACCAAGGTGGAAATCAAA 387
     |||||||||  ||||||||||||||
 117 oThrPheGlyGlyThrLysValGluIleLys 128
```

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-65658

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; SEQ ID NO 65658
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-65658

alignment_scores:
      Quality:  581.00             Length:       131
      Ratio:    4.802              Gaps:           1
Percent Similarity: 92.366    Percent Identity: 87.786

alignment_block:
US-09-019-441-3 x US-09-791-537-65658          ..

Align seg 1/1 to: US-09-791-537-65658   from: 1  to: 131

  1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGCTCCTTCTGCTCTGGCT  50
    |||||  ||||||||:::||||||||||||||||||||||||||||||||
  1 MetAspThrArgValProThrArgLeuLeuGlyLeuLeuLeuLeuTrpLe  17

 51 CCCAGGTGCCAGATGACATCCAGATGACCCAGTCTCCATCTTCCCTGT  100
    |  ||||||||||||||||||||||||||||||||||||||||||||||
 17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS  34

101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC  150
    |||||||||||||||||||||||||||||||||||||||||||||:::
 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer  50

151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA  200
    |||  |||||||||||||||||||||||||||||||||||||||||||||
 51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy  67

201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGT  250
    ||||||||||||||||||||||:::||||||||||||||||||||||||
 67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgP  84

251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG  300
    ||||||||||||||||||||||||:::||||||||||||:||||||||
 84 heSerGlySerGlyThrGlyPheThrLeuThrIleSerSerLeu  100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC  350
    ||||||||||||||||||||||||||:::|||||||  ||||||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnSerTyrSerProPr  117

351 T......CGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA  387
          |||||||||||||||||||||||||||||||||
117 oProValTyrThrPheGlyGlnGlyThrLysLeuGluIleLys  131

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-71040

seq_documentation_block:
; Sequence 71040, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT:  Bionomix, Inc.
; APPLICANT:  Debe, Derek
; APPLICANT:  Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE:  2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71040
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-71040

alignment_scores:
      Quality:  578.50             Length:
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                                      Ratio:   4.781            Gaps:           1
                            Percent Similarity:  93.077    Percent Identity: 89.231

                            alignment_block:
                            US-09-019-441-3 x US-09-791-537-71040          ..

                            Align seg 1/1 to: US-09-791-537-71040   from: 1  to: 210

                              1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGCTCCTTCTGCTCTGGCT  50
                                |||||||||||||||||||||||||||||||||||||||||||||  ||
                              1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuArgLe  17

                             51 CCCAGGTGCCAGATGACATCCAGATGACCCAGTCTCCATCTTCCCTGT  100
                                |||  |||||||||||||||||||||||||||||||||||||||||||||
                             17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS  34

                            101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC  150
                                |||||||||||||||||||||||||||||||||||||||||||||:::
                             34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer  50

                            151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA  200
                                |||  |||||||||||||||||||||||||||||||||||||||||||||
                             51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy  67

                            201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGT  250
                                ||||||||||||||||||||:::||||||||||||||||||||||||
                             67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgP  84

                            251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG  300
                                ||||||||||||||||||||||:::||||||||||||:||||||||
                             84 heSerGlySerGlyThrGlySerGlyThrAspPheThrLeuThrIleSerSerLeu  100

                            301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC  350
                                ||||||||||||||||||||||:::||||||  ||  ||||
                            101 GlnProGluAspPheAlaSerTyrTyrCysGlnSerTyrArgThrPr  117

                            351 TCGG...ACGTTCGGCCAAGGACCAAGGTGGAAATCAAA  387
                                |  |||||||||||||||||||||||||||||||||||||
                            117 oAlaTrpThrPheGlyLnGlyThrLysValGluIleLys  130

                            seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-71830

                            seq_documentation_block:
                            ; Sequence 71830, Application US/09791537
                            ; GENERAL INFORMATION:
                            ; APPLICANT:  Bionomix, Inc.
                            ; APPLICANT:  Debe, Derek
                            ; APPLICANT:  Danzer, Joseph
                            ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
                            ; TITLE OF INVENTION: METHODS OF USE THEREOF
                            ; FILE REFERENCE: 261/210
                            ; CURRENT APPLICATION NUMBER: US/09/791,537
                            ; CURRENT FILING DATE:  2001-02-22
                            ; NUMBER OF SEQ ID NOS: 153055
                            ; SOFTWARE: PatentIn version 3.0
                            ; SEQ ID NO 71830
                            ; LENGTH: 127
                            ; TYPE: PRT
                            ; ORGANISM: Homo sapiens
                            US-09-791-537-71830

                            alignment_scores:
                                  Quality:  578.00             Length:       124
                                  Ratio:    4.898              Gaps:           0
                            Percent Similarity: 95.161    Percent Identity: 90.323

                            alignment_block:
                            US-09-019-441-3 x US-09-791-537-71830          ..

                            Align seg 1/1 to: US-09-791-537-71830   from: 1  to: 127

                             16 CCCGCTCAGCTCCTGGGGCTCCTTCGCTCTGCTCTCCAGGTGCCAGATG  65
```

```
                    |||||||||||||||||||||||||       ||||||||
        1 ProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuArgGlyAlaArgCy  17

       66 TGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGG 115
          |||:||||||:::|||||||||||||||||||||||||||||||||||||
       17 sAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyA  34

      116 ACAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTA 165
          ||||||||||||||||||||||||||||||||||||||:::||   ||||
       34 sPArgValThrIleThrCysArgAlaSerGlnSerIleSerAsnTyrLeu  50

      166 AATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGT 215
          |||||||||||||||:::|||||||||||||||||||||||||||:::||
       51 AsnTrpTyrGlnArgLysProGlyLysAlaProLysLeuLeuIleTyrAl  67

      216 TGCATCCAGTTGCAAAGTGGGTCCCATCAAGGTTCAGCGGCAGTGGAT 265
          :||||||||||||||||||||:|||||||||||||||||| |||||||||
       67 aAlaSerLeuGlnSerGlyValProSerArgPheSerGlySerGlyS  84

      266 CTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGATTT 315
          ||||||:::||||||||||||||||||||||||||||||||:: |||||||
       84 erGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPhe  100

      316 GGCACTTATTACTGTCTACAGGTTTATAGTAGTACCCCTCGGACGTTCGGCCA 365
          |||||||||||| ||  |:::||||||    ||||||||||||||
      101 AlaThrTyrTyrCysGlnGlnSerTyrAsnThrProTrpThrPheGlyGl  117

      366 AGGGACCAAGGTGGAAATCAAA 387
          ||||||||||||||||||||||
      117 nGlyThrLysValGluIleLys 124

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-56448

seq_documentation_block:
; Sequence 56448, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
;   SEQ ID NO 56448
;   LENGTH: 128
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-56448

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        Ratio:    4.898                      Gaps:          0
Percent Similarity:  95.161       Percent Identity: 90.323

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       66 TGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGG 115
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       17 sAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyA  34

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      216 TGCATCCAGTTGCAAAGTGGGTCCCATCAAGGTTCAGCGGCAGTGGAT 265
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seq_documentation_block:
; Sequence 107469, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
;   SEQ ID NO 107469
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-107469

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        Ratio:    4.817                      Gaps:          0
Percent Similarity:  93.023       Percent Identity: 88.372

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; Sequence 74071, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT:  Bionomix, Inc.
; APPLICANT:  Debe, Derek
; APPLICANT:  Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE:  2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74071
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-74071
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        Quality:  578.00          Length:     129
        Ratio:      4.817         Gaps:         0
Percent Similarity:  93.023    Percent Identity:  88.372
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Date: Sep 23, 2002 10:00 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

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; GENERAL INFORMATION:
;   APPLICANT: LAKE, PHILIP
;   APPLICANT: OSTBERG, LARS
;   TITLE OF INVENTION:   HUMAN ANTIBODIES AGAINST
;   TITLE OF INVENTION:   VARICELLA-ZOSTER VIRUS
;   NUMBER OF SEQUENCES:  4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Townsend and Townsend Khourie and Crew
;     STREET:  379 Lytton Avenue
;     CITY:  Palo Alto
;     STATE:  California
;     COUNTRY:  US
;     ZIP:  94301
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0,  Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/217,918
;     FILING DATE:  24-MAR-1994
;     CLASSIFICATION:  530
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Smith, William M
;     REGISTRATION NUMBER:  30,223
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (415) 326-2400
;     TELEFAX:  (415) 326-2422
; INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  129 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-217-918-2

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;    TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
;    NUMBER OF SEQUENCES: 28
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;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/470,139
;    FILING DATE: 06 JUNE-1995
;    CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;    NAME: TRUJILLO, DOREEN YATKO
;    REGISTRATION NUMBER: 35,719
;    REFERENCE/DOCKET NUMBER: CARP-0044
;   INFORMATION FOR SEQ ID NO: 26:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 128 amino acids
;    TYPE: amino acid
;    STRANDEDNESS: single
;    TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-470-139-26

alignment_scores:
     Quality: 534.00     Length: 127
     Ratio: 4.643     Gaps: 0
Percent Similarity: 90.551    Percent Identity: 81.102

alignment_block:
US-09-019-441-3 x US-08-470-139-26

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201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGT 250
    ||||:::|||||    ||||||:::||||||||||||||||||||||||||
 67 sLeuMetIleTyrLysAlaSerIleLeuGluAsnGlyValProSerArgP  84

251 TCAGCGGCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
    |||||||||||||||||||||||||||||||||:::|||||  |||||||
 84 heSerGlySerGlyThrGluPheThrLeuThrIleSerSerLeu 100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
    |||||||||||||||||||||||||||||||    || :::  ||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrLysSerTyrPr 117

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
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117 oTrpThrPheGlyGlnGlyThrLysValGluIleLys 129
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seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-157-101A-5

seq_documentation_block:
; Sequence 5, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
;   APPLICANT: KURIHARA, TATSUYA
;   APPLICANT: MATSUKURA, SHIGEKAZU
;   APPLICANT: TSURUOKA, NOBUO
;   APPLICANT: ARIMA, KENJI
;   APPLICANT: NISHIHARA, TATSURO
;   TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION
;   TITLE OF INVENTION: PLASMIDS THEREFOR
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;    ADDRESSEE: PILLSBURY, MADISON & SUTRO
;    STREET: 1100 NEW YORK AVENUE, N.W.
;    CITY: WASHINGTON
;    STATE: D.C.
;    COUNTRY: USA
;    ZIP: 20005
;   COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/157,101A
;    FILING DATE: 05-APR-1994
;    CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;    NAME: TITUS, MARLANA K
;    REGISTRATION NUMBER: 35843
;    REFERENCE/DOCKET NUMBER: 9437/204199
;   TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 202-861-3711
;    TELEFAX: 202-822-0944
;    TELEX: 6714627 CUCH
;   INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 236 amino acids
;    TYPE: amino acid
;    STRANDEDNESS: single
;    TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-157-101A-5

alignment_scores:
     Quality: 551.00     Length: 129
     Ratio: 4.669     Gaps: 0
Percent Similarity: 91.473    Percent Identity: 82.946

alignment_block:
US-09-019-441-3 x US-08-157-101A-5

## Left column

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Align seg 1/1 to: US-08-470-139-26   from: 1 to: 128

  7 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGG  56
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  1 MetSerValProThrGlnValLeuGlyLeuLeuLeuLeuTrpLeuThrArAs  17

 57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT 106
    |||||||||||||||||||||||||||||||||||||||||||||||||
 17 pAlaArgCysAspIleGlnMetThrGlnSerProSerLeuSerAlaS  34

107 CTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGG 156
    |||||||||||||||||||||||||||||::|||  |||
 34 erValGlyAspArgValThrIleThrCysLeuAlaSerGluGlyIleSer  50

157 TATTATTTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCT 206
    |||||||||||||||||||||||||||||||||||||||||||
 51 SerTyrLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLe  67

207 GATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGTTCAGCG 256
    ||||| |||::|||||||||::|||||||||||||||||||
 67 uIleTyrGlyAlaAsnSerLeuGlnThrGlyValProSerArgPheSerG  84

257 GCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT 306
    ||||||||:::|||||||:::|||||||||:||||||||||||
 84 lySerGlySerAlaThrAspTyrThrLeuThrIleSerSerLeuGlnPro 100

307 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAC 356
    |||||||||||||||||||||::||| |||::|| ||::::||
101 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrLysPheProAsnTh 117

357 GTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    |||||||||||||||||||||||:::|||
117 rPheGlyGlnGlyThrLysValGluValLys 127
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seq_documentation_block:
; Sequence 26, Application US/09347061
; Patent No. 6316227
; GENERAL INFORMATION:
;   APPLICANT: Bodmer, Mark
;   APPLICANT: Athwal, Diljeet Singh
;   APPLICANT: Emtage, John Spencer
;   TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
;   FILE REFERENCE:  CARP-0071
;   CURRENT APPLICATION NUMBER: US/09/347,061
;   CURRENT FILING DATE: 1999-07-02
;   NUMBER OF SEQ ID NOS:  28
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
;   LENGTH: 128
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;     NAME/KEY: misc_feature
;     OTHER INFORMATION: No. 6316227el Sequence
US-09-347-061-26

alignment_scores:
          Quality:  534.00              Length:  127
          Ratio:   4.643                 Gaps:    0
Percent Similarity:  90.551    Percent Identity: 81.102

alignment_block:
US-09-019-441-3 x US-09-347-061-26

Align seg 1/1 to: US-09-347-061-26   from: 1 to: 128

  7 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGG  56
    ||| |||||:||:|||:||||||||||||||||||||||||||||||||
  1 MetSerValProThrGlnValLeuGlyLeuLeuLeuLeuTrpLeuThrArAs  17

## Right column

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 57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT 106
    |||||||||||||||||||||||||||||||||||||||||||||||||
 17 pAlaArgCysAspIleGlnMetThrGlnSerProSerLeuSerAlaS  34

107 CTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGG 156
    |||||||||||||||||||||||||||||::|||   |||
 34 erValGlyAspArgValThrIleThrCysLeuAlaSerGluGlyIleSer  50

157 TATTATTTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCT 206
    |||||||||||||||||||||||||||||||||||||||||||
 51 SerTyrLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLe  67

207 GATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGTTCAGCG 256
    ||||| |||::|||||||||::|||||||||||||||||||
 67 uIleTyrGlyAlaAsnSerLeuGlnThrGlyValProSerArgPheSerG  84

257 GCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT 306
    ||||||||:::|||||||:::|||||||||:||||||||||||
 84 lySerGlySerAlaThrAspTyrThrIleSerSerLeuGlnPro 100

307 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAC 356
    |||||||||||||||||||||::||| |||::|| ||::::||
101 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrLysPheProAsnTh 117

357 GTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    |||||||||||||||||||||||:::|||
117 rPheGlyGlnGlyThrLysValGluValLys 127
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seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-569-147-80

seq_documentation_block:
; Sequence 80, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
;   APPLICANT:
;     TITLE OF INVENTION:  HUMANISED ANTIBODIES
;     NUMBER OF SEQUENCES:  95
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz &
;       ADDRESSEE:  No. 6180377Iris, LLP
;       STREET:  One Liberty Place - 46th Floor
;       CITY:  Philadelphia
;       STATE:  PA
;       COUNTRY:  U.S.A.
;       ZIP:  19103
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0,  Version #1.25  (EPO)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/569,147
;       FILING DATE:  25-March-1996
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Trujillo, Doreen Yatko
;       REGISTRATION NUMBER:  35,719
;       REFERENCE/DOCKET NUMBER:  CARP-0047
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 568-3100
;       TELEFAX:  (215) 568-3439
; INFORMATION FOR SEQ ID NO:  80:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  128 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-569-147-80

alignment_scores:
          Quality:  530.00              Length:  127

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                    Ratio:  4.569            Gaps:                 0
Percent Similarity: 91.339    Percent Identity: 81.102

alignment_block:
US-09-019-441-3 x US-08-569-147-80

Align seg 1/1  to: US-08-569-147-80  from: 1 to: 128

    7 ATGAGGGTCCCCGCTCAGCTCCTGGGCTCCTTCTGCTTCTGGCTCCCAGG  56
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    1 MetSerValProThrGlnValLeuGlyLeuLeuLeuLeuLeuTrpLeuThrAs  17

   57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT 106
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   17 pAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaS  34

  107 CTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGG 156
      ||||||||||||||||||||||||||||||:::::::::|||
   34 erValGlyAspArgValThrIleThrCysArgAlaSerGlnAsnIleTyr  50

  157 TATTATTTAAATTGGTATCAGCAGAGAAACCAGGAAAAGTCCTAAGCTCCT 206
      | |||||||||||||||||||||||||||||||||||||||||||
   51 AsnAsnLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeu  67

  207 GATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCG 256
      |:::||:::||||| ||     :::||||||||||||||||||||||
   67 uValTyrAlaAlaThrAsnLeuAlaAspGlyValProSerArgPheSerG  84

  257 GCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT 306
      ||||||||||||||:::::||||||||:||||||||||||||||||||
   84 lySerGlySerGlyThrGlnTyrThrLeuThrIleSerSerLeuGlnPro 100

  307 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAC 356
      ||||||||||||||||||||:||||||||||||||||||||||||||||
  101 GluAspPheAlaThrTyrTyrCysGlnHisLeuTrpSerProTyrTh 117

  357 GTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
      ||||||||||||||||||||||||||||||
  117 rPheGlyGlyGlyThrLysValGluIleLys 127

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-569-147-78

seq_documentation_block:
; Sequence 78, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
;   APPLICANT:
;     TITLE OF INVENTION:  HUMANISED ANTIBODIES
;     NUMBER OF SEQUENCES:  95
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz &
;       ADDRESSEE:  No. 6180377ris, LLP
;       STREET:  One Liberty Place - 46th Floor
;       CITY:  Philadelphia
;       STATE:  PA
;       COUNTRY:  U.S.A.
;       ZIP:  19103
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0,  Version #1.25  (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/569,147
;     FILING DATE:  25-March-1996
;     CLASSIFICATION:  536
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Trujillo, Doreen Yatko
;     REGISTRATION NUMBER:  35,719
;     REFERENCE/DOCKET NUMBER:  CARP-0047
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (215) 568-3100
;     TELEFAX:   (215) 568-3439
; INFORMATION FOR SEQ ID NO:  78:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  128 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-569-147-78
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                    Ratio:  4.569            Gaps:                 0
Percent Similarity: 91.339    Percent Identity: 81.102

alignment_block:
US-09-019-441-3 x US-08-569-147-80

Align seg 1/1  to: US-08-569-147-80  from: 1 to: 128

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    1 MetSerValProThrGlnValLeuGlyLeuLeuLeuLeuLeuTrpLeuThrAs  17

   57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT 106
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   17 pAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaS  34

  107 CTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGG 156
      ||||||||||||||||||||||||||||||:::::::::|||
   34 erValGlyAspArgValThrIleThrCysArgAlaSerGlnAsnIleTyr  50

  157 TATTATTTAAATTGGTATCAGCAGAGAAACCAGGAAAAGTCCTAAGCTCCT 206
      | |||||||||||||||||||||||||||||||||||||||||||
   51 SerAsnLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeu  67

  207 GATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCG 256
      |:::||:::||||| ||     :::||||||||||||||||||||||
   67 SerAsnLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeu  67

  257 GCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT 306
      ||||||||||||||:::::||||||||:||||||||||||||||||||
   67 uIleTyrAlaAlaSerAsnLeuAlaAspGlyValProSerArgPheSerG  84

  307 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAC 356
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   84 lySerGlySerGlyThrGlnTyrThrLeuThrIleSerSerLeuGlnPro 100

  357 GTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
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  101 GluAspPheAlaThrTyrTyrCysGlnHisPheTrpThrProTrpAl 117

  117 aPheGlyGlyGlyThrLysValGluIleLys 127

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-136-315-8

seq_documentation_block:
; Sequence 8, Application US/09136315B
; Patent No. 6228360
; GENERAL INFORMATION:
;   APPLICANT:  CO, MAN SUNG
;   APPLICANT:  VASQUEZ, MAXIMILLIANO
;   TITLE OF INVENTION:  ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND
;   TITLE OF INVENTION:  FACTOR MONOCLONAL ANTIBODY
;   FILE REFERENCE:  0010-0933-0
;   CURRENT APPLICATION NUMBER:  US/09/136,315B
;   CURRENT FILING DATE:  1998-08-19
;   NUMBER OF SEQ ID NOS:  8
;   SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-136-315-8

alignment_scores:
       Quality:   520.00         Length:        127
         Ratio:    4.483         Gaps:            0
Percent Similarity: 91.339    Percent Identity: 77.953

alignment_block:
US-09-019-441-3 x US-09-136-315-8

Align seg 1/1  to: US-09-136-315-8  from: 1 to: 127
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alignment_scores:
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        Quality:    519.00              Length:      127
        Ratio:        4.474              Gaps:          0
Percent Similarity:  91.339    Percent Identity: 78.740
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alignment_block:
US-09-019-441-3 x US-08-569-147-78        ..

Align seg 1/1 to: US-08-569-147-78    from: 1 to: 128

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  1 MetSerValProThrGlnValLeuGlyLeuLeuLeuLeuTrpLeuThrArs  17

 57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT 106
    |||||||||||||||||||||||||||||||||||||||||||||||||
 17 pAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaS  34

107 CTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGG 156
    |||||||||||||||||||||||||||||:::::::||||||
 34 erValGlyAspArgValThrIleThrCysArgAlaSerGlnAsnIleTyr  50

157 TATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCT 206
    ||||||||:::||||  :::||||||||||||||||:::::||||
 51 SerAsnLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProGlnLeuLe  67

207 GATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGTTCAGCG 256
    |||::||||||:::|||   :::||::||||||||||||||||||
 67 uIlePheAlaAlaSerAsnLeuAlaAspGlyValProSerArgPheSerG  84

257 GCAGTGGATCTGGGACAGAGTTCACTCTCACCACGTCAGCAGCCTGCAGCCT 306
    |||||||||||||||:::::||||||||||||||||:::|||||||
 84 lySerGlySerGlyThrGlnTyrThrLeuThrIleSerSerLeuGlnPro 100

307 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAC 356
    ||||||||||||||||||||||||| :::  :::||||::::||
101 GluAspPheAlaThrTyrTyrCysGlnHisPheTrpThrThrProTrpAl 117

357 GTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    :|||||||||||||||||||||||||||
117 aPheGlyGlnGlyThrLysValGluIleLys 127
```

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-259-372A-14

seq_documentation_block:
; Sequence 14, Application US/08259372A
; Patent No. 5565354
; GENERAL INFORMATION:
;   APPLICANT: Ostberg, Lars G.
;   TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
;   TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
;   NUMBER OF SEQUENCES: 16
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend and Crew LLP
;     STREET: Two Embarcadero Center, Eighth Floor
;     CITY: San Francisco
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/259,372A
;     FILING DATE: 14-JUN-1994
;     CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/871,426
;     FILING DATE: 21-APR-1992

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;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/676,036
;     FILING DATE: 27-MAR-1991
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/538,796
;     FILING DATE: 15-JUN-1990
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/192,754
;     FILING DATE: 11-MAY-1988
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 06/925,196
;     FILING DATE: 31-OCT-1986
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 06/904,517
;     FILING DATE: 05-SEP-1986
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Smith, William M.
;     REGISTRATION NUMBER: 30,223
;     REFERENCE/DOCKET NUMBER: 11823-50-7
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (415) 326-2400
;     TELEFAX:    (415) 576-0300
; INFORMATION FOR SEQ ID NO:  14:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 128 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-259-372A-14

alignment_scores:
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        Quality:    518.00              Length:      127
        Ratio:        4.544              Gaps:          0
Percent Similarity:  89.764    Percent Identity: 79.528
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alignment_block:
US-09-019-441-3 x US-08-259-372A-14        ..

Align seg 1/1 to: US-08-259-372A-14    from: 1 to: 128

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  1 MetArgProValAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPheProGl  17

 57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT 106
    |::::||||||||||||||||||||||||||||:::||||:::||||||
 17 ySerArgCysAspIleGlnMetThrGlnSerProSerSerValSerAlaS  34

107 CTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGG 156
    ||||||||||||||||:::||||||||||||||||
 34 erValGlyAspArgValThrValThrCysArgAlaSerGlnGlyIleSer  50

157 TATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCT 206
    :::|||  ||||||||||||||||||||||||||||||||||||||
 51 SerTrpLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLe  67

207 GATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCG 256
    |||||||||||||||||||||||:::||::||||||||||||||||
 67 uIleHisAlaAlaSerLeuGlnSerGlyValProSerArgPheIleG  84

257 GCAGTGGATCTGGGACAGAGTTCACTCTCACCCTCAGCAGCCTGCAGCCT 306
    ||||||||||||||||||:::::||||||||||::::|||||||
 84 lySerGlySerGlyThrAspPheThrLeuThrIleThrSerLeuGlnAla 100

307 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAC 356
    ||||||||||||||||||||||| ||:::  ||| ||  ||
101 GluAspPheAlaThrTyrTyrCysGlnLysAlaAspSerLeuProPheTh 117

357 GTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    :|||||||||||||||||||:::||||
117 rPheGlyGlyGlyThrLysValAspPheLys 127
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seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-468-671-14

seq_documentation_block:
; Sequence 14, Application US/08468671
; Patent No. 5648077
GENERAL INFORMATION:
.; APPLICANT: Ostberg, Lars G.
.; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
.; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
.; NUMBER OF SEQUENCES: 16
.; CORRESPONDENCE ADDRESS:
.;   ADDRESSEE: Townsend and Townsend and Crew LLP
.;   STREET: Two Embarcadero Center, Eighth Floor .
.;   CITY: San Francisco
.;   STATE: CA
.;   COUNTRY: USA
.;   ZIP: 94111-3834
.; COMPUTER READABLE FORM:
.;   MEDIUM TYPE: Floppy disk
.;   COMPUTER: IBM PC compatible
.;   OPERATING SYSTEM: PC-DOS/MS-DOS
.;   SOFTWARE: Patentin Release #1.0, Version #1.30
.; CURRENT APPLICATION DATA:
.;   APPLICATION NUMBER: US/08/468,671
.;   FILING DATE: 06-JUN-1995
.;   CLASSIFICATION: 424
.; PRIOR APPLICATION DATA:
.;   APPLICATION NUMBER: US 08/259,372
.;   FILING DATE: 14-JUN-1994
.;   APPLICATION NUMBER: US 07/871,426
.;   FILING DATE: 21-APR-1992
.; PRIOR APPLICATION DATA:
.;   APPLICATION NUMBER: US 07/676,036
.;   FILING DATE: 27-MAR-1991
.; PRIOR APPLICATION DATA:
.;   APPLICATION NUMBER: US 07/538,796
.;   FILING DATE: 15-JUN-1990
.; PRIOR APPLICATION DATA:
.;   APPLICATION NUMBER: US 07/192,754
.;   FILING DATE: 11-MAY-1988
.; PRIOR APPLICATION DATA:
.;   APPLICATION NUMBER: US 06/925,196
.;   FILING DATE: 31-OCT-1986
.; PRIOR APPLICATION DATA:
.;   APPLICATION NUMBER: US 06/904,517
.;   FILING DATE: 05-SEP-1986
.; ATTORNEY/AGENT INFORMATION:
.;   NAME: Smith, William M.
.;   REGISTRATION NUMBER: 30,223
.;   REFERENCE/DOCKET NUMBER: 11823-50-7
.; TELECOMMUNICATION INFORMATION:
.;   TELEPHONE: (415) 326-2400
.;   TELEFAX: (415) 576-0300
.; INFORMATION FOR SEQ ID NO: 14:
.; SEQUENCE CHARACTERISTICS:
.;   LENGTH: 128 amino acids
.;   TYPE: amino acid
.;   TOPOLOGY: linear
.;   MOLECULE TYPE: protein
US-08-468-671-14

alignment_scores:
      Quality:   518.00            Length:   127
      Ratio:     4.544             Gaps:     0
Percent Similarity: 89.764     Percent Identity: 79.528

alignment_block:
US-09-019-441-3 x US-08-468-671-14
Align seg 1/1  to: US-08-468-671-14  from: 1  to: 128

   7 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCCTGCTCCCCAGG 56
     |||||   |||||||||||||||||||||||||||::|||||
   1 MetArgProValAlaGlnLeuLeuGlyLeuLeuLeuLeuLeuTrpPheProGl 17

  57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT 106
     |::|||||||||||||||||||||||||||::||||||
  17 ySerArgCysAspIleGlnMetThrGlnSerProSerSerValSerAlaS 34

 107 CTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGG 156
     ||||||||||||||||||||::||||||||||||   |||
  34 erValGlyAspArgValThrValThrCysArgAlaSerGlnGlyIleSer 50

 157 TATTATTAAATTGGTATCAGCAGAAAACCAGGAAAAGCTCCTAAGCTCCT 206
     ::|||   ||||||||||||||||||||||||||||
  51 SerTrpLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLe 67

 207 GATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCG 256
     |||::::|||||||||||||||||||||||||||||   |
  67 uIleHisAlaAlaSerSerLeuGlnSerGlyValProSerArgPheIleG 84

 257 GCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT 306
     |||||||||||||::|:||||||||||::::|||||||   :|||||||
  84 lySerGlySerGlyThrAspPheThrLeuThrIleThrSerLeuGlnAla 100

 307 GAAGATTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAC 356
     ||||||||||||||||   |||::   || |||   ||| ||
 101 GluAspPheAlaThrTyrTyrCysGlnGlnAlaAspSerLeuProPheTh 117

 357 GTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
     ||||||||||||||||:::::||
 117 rPheGlyGlyGlyThrLysValAspPheLys 127

seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-836-561-71

seq_documentation_block:
; Sequence 71, Application US/08836561
; Patent No. 6018032
GENERAL INFORMATION:
.; APPLICANT: KOIKE, Masamichi
.; APPLICANT: FURUYA, Akiko
.; APPLICANT: NAKAMURA, Kazuyasu
.; APPLICANT: IIDA, Akihiro
.; APPLICANT: ANAZAWA, Hideharu
.; APPLICANT: HANAI, No. 6018032uo
.; APPLICANT: TAKATSU, Kiyoshi
.; TITLE OF INVENTION: Antibody Against Human Interleukin-5
.; TITLE OF INVENTION: Receptor Alpha Chain
.; NUMBER OF SEQUENCES: 106
.; CORRESPONDENCE ADDRESS:
.;   ADDRESSEE: Pennie & Edmonds LLP
.;   STREET: 1155 Avenue of the Americas
.;   CITY: New York
.;   STATE: NY
.;   COUNTRY: USA
.;   ZIP: 10036
.; COMPUTER READABLE FORM:
.;   MEDIUM TYPE: Diskette
.;   COMPUTER: IBM Compatible
.;   OPERATING SYSTEM: DOS
.;   SOFTWARE: FastSEQ Version 2.0
.; CURRENT APPLICATION DATA:
.;   APPLICATION NUMBER: US/08/836,561
.;   FILING DATE: 09-MAY-1997
.;   CLASSIFICATION: 424
.; PRIOR APPLICATION DATA:
.;   APPLICATION NUMBER: JP 232384/95
.;   FILING DATE: 11-SEP-1995
.; ATTORNEY/AGENT INFORMATION:
.;   NAME: Lawrence, III, Stanton T
.;   REGISTRATION NUMBER: 25,736
.;   REFERENCE/DOCKET NUMBER: 7005-115-999
.; TELECOMMUNICATION INFORMATION:
.;   TELEPHONE: 212-790-9090
.;   TELEFAX: 212-869-9741

; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 71:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 127 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-836-561-71

alignment_scores:
         Quality:  516.00          Length:     127
         Ratio:      4.649          Gaps:         0
Percent Similarity:  87.402    Percent Identity:  81.102

alignment_block:
US-09-019-441-3 x US-08-836-561-71    ..

Align seg 1/1  to: US-08-836-561-71  from:  1  to: 127

   7 ATGAGGGTCCCCGCTCCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGG  56
     ||  ||||::::||||||||||||||| ||||||   :::
   1 MetMetSerAlaGlnPheLeuGlyLeuLeuLeuLeuCysPheGlnAs  17

  57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT  106
     |||||||||||||||||||||||||||||||:::||||||||||||||||
  17 pIleArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaS  34

 107 CTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAGTCAGGACATTAGG  156
     |||||||||||||||||||||||||| :::||:::||||:
  34 erValGlyAspArgValThrIleThrCysGlyThrSerGluAspIleIle  50

 157 TATTATTTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCT  206
     |||||||||||||||||||||||||||||||||||||||||||||||
  51 AsnTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLe  67

 207 GATCTATGTTGCATCCAGTTGCAAAGTGGGTCCCATCAAGGTTCAGCG  256
     ||||||   :::||  ||||||||||||||||||||||||||||||||
  67 uIleTyrHisThrSerArgLeuGlnSerGlyValProSerArgPheSerG  84

 257 GCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT  306
     |||||||||||||||||:::||||||:::||||||||||||||||||||
  84 lySerGlyHisGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro  100

 307 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAC  356
     ||||||||||||||||||||||||| |||:::  ||||  || ||
 101 GluAspPheAlaThrTyrTyrCysLeuGlnGlyTyrThrLeuProTyrTh  117

 357 GTTCGGCCAAGGGACCAAGGTGGAAATCAAA  387
     ||||||||||||||||||||||||||||||
 117 rPheGlyGlnGlyThrLysValGluIleLys  127

seq_name: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:US-08-976-183A-46

seq_documentation_block:
; Sequence 46, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
;  APPLICANT: King, David J.
;  APPLICANT: Adair, John R.
;  APPLICANT: Owens, Raymond J.
;  TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
;  TITLE OF INVENTION: ANTIGEN
;  NUMBER OF SEQUENCES: 55
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: FOLEY & LARDNER
;   STREET: 3000 K. Street, N.W., Suite 500
;   CITY: Washington, D.C.
;   COUNTRY: USA
;   ZIP: 20007
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/976,183A
;  FILING DATE:
; PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US/08/595,848
;  FILING DATE:  02-FEB-1996
;  APPLICATION NUMBER: PCT/GB93/02529
;  FILING DATE:  10-DEC-1993
; PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: GB 9225853.2
;  FILING DATE:  10-DEC-1993
; PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 9315249.4
;  FILING DATE:  22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
;  NAME: Bernhard D. Saxe
;  REGISTRATION NUMBER: 28,665
;  REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
;  TELEPHONE:  (202) 672-5300
;  TELEFAX:  (202) 672-5399
;  TELEX:  904136
; INFORMATION FOR SEQ ID NO:  46:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 138 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: YES
US-08-976-183A-46

alignment_scores:
         Quality:  511.00          Length:     127
         Ratio:      4.443          Gaps:         0
Percent Similarity:  90.551    Percent Identity:  76.378

alignment_block:
US-09-019-441-3 x US-08-976-183A-46    ..

Align seg 1/1  to: US-08-976-183A-46  from:  1  to: 138

   7 ATGAGGGTCCCCGCTCCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGG  56
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   8 MetSerValProThrGlnValLeuGlyLeuLeuLeuLeuTrpLeuThrAs  24

  57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT  106
     |||||||||||||| ||||||  ||||||||||||||||||||||:::|
  24 pAlaArgCysAspIleGlnMetThrGlnSerProSerLeuSerValS  41

 107 CTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGG  156
     ||||||||||||||||||||||:::||:::|||||||||||||||||||
  41 erValGlyAspArgValThrIleThrCysAlaSerGlnAsnValArg  57

 157 TATTATTTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCT  206
     |||||||||||||||||||||||| ::|||||||||||||||||||
  58 ThrValAlaLaTrpTyrGlnGlnLysProGlyLeuAlaProLysThrLe  74

 207 GATCTATGTTGCATCCAGTTGCAAAGTGGGTCCCATCAAGGTTCAGCG  256
     ||||||||  :::||||:::  |||||||||||||||||||||||||
  74 uIleTyrLeuAlaSerAsnArgHisThrGlyValProSerArgPheSerG  91

 257 GCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT  306
     ||||||||||||||||||||||:::||||||||||||||||||||||
  91 lySerGlySerGlyThrAspPheThrIleSerSerLeuGlnPro  107

 307 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAC  356
     ||||||  :::||||||  :::|||||||  |||  ||  ||
 108 GluAspSerIleAlaThrTyrPheCysLeuGlnHisTrpSerTyrProLeuTh  124

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357 GTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
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124 rPheGlyGlnGlyThrLysValGluValLys 134
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seq_name: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:US-08-812-586-16

seq_documentation_block:
; Sequence 16, Application US/08812586
; Patent No. 6048704
; GENERAL INFORMATION:
;  APPLICANT: Martin David Tilson
;  TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
;  TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYM (AAA)
;  TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
;  NUMBER OF SEQUENCES: 61
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Cooper & Dunham LLP
;   STREET: 1185 Avenue of the Americas
;   CITY: New York
;   STATE: New York
;   COUNTRY: U.S.A.
;   ZIP: 10036
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/812,586
;   FILING DATE: 07-MAR-1997
;   CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;   NAME: White, John P.
;   REGISTRATION NUMBER: 28,678
;   REFERENCE/DOCKET NUMBER: 0575/53862-A
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 278-0400
;   TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 16:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 235 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-812-586-16

alignment_scores:
        Quality:     511.00          Length:        129
        Ratio:         4.482         Gaps:            0
Percent Similarity:  88.372      Percent Identity: 88.519

alignment_block:
US-09-019-441-3 x US-08-812-586-16

Align seg 1/1  to: US-08-812-586-16  from: 1  to: 235

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1 ATGGACATGAGGGTCCCCCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCT 50
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1 MetAspMetArgValProAlaProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17

51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
   ||||||||||||||||::::::||||||||||||||||||||||||||||
17 uProGlyAlaArgCysAlaIleArgIleAlaGlnSerProSerLeuS 34

101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
    |||||||::|||||||||||||||||||||||||||||||||||||||||
34 erAlaSerThrGlyAspArgValThrIleThrCysArgAlaSerGlnGly 50

151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    |||  |||||| |||||||||||||||||||||::||||||::|||
51 IleSerAsnTyrLeuAlaTrpTyrGlnGlnLysProGlyGlnAlaProAr 67
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201 GTTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGT 250
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67 gLeuLeuIleTyrAspAlaSerArgArgAlaThrGlyIleProAspArgP 84

251 TCAGGCGCAGTGGATCTGGACAGAGAGTTCACTCTCACCGTCAGCAGCCTG 300
    ||||||||||||||||||||||||||:::|||||||||||||||::|||
84 heSerGlySerGlyThrAspPheThrLeuThrIleSerArgLeu 100

301 CAGCCTGAAGATTTGGCCACTTATTACTGTCTACAGGTTTATAGTACCCC 350
    ::|||||||||||||||::|||||  |||||||   ||   |||:::|||
101 GluProGluAspPheAlaValTyrTyrGlyGlnTyrGlySerSerPr 117

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    |  |||||| |||||||||||||||||||||||||||
117 oLeuThrPheGlyGlyGlyThrLysValGluIleLys 129
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seq_name: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:US-08-579-378A-18

seq_documentation_block:
; Sequence 18, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
;  APPLICANT: Co, Man Sung
;  TITLE OF INVENTION: Humanized Antibodies Reactive with
;  TITLE OF INVENTION: L-Selectin
;  NUMBER OF SEQUENCES: 20
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew
;   STREET: One MarketPlaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/579,378A
;   FILING DATE: 27-DEC-1995
;   CLASSIFICATION: 424
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/160,074
;   FILING DATE: 30-NOV-1993
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/983,946
;   FILING DATE: 01-DEC-1992
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP 95112895.8
;   FILING DATE: 17-AUG-1995
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP 95114696.8
;   FILING DATE: 19-SEP-1995
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Liebescheutz, Joe O.
;   REGISTRATION NUMBER: 37,505
;   REFERENCE/DOCKET NUMBER: 11823-002220
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-326-2400
;   TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 131 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-579-378A-18

alignment_scores:
        Quality:     508.00          Length:        131

Percent Similarity: 88.550    Percent Identity: 75.573

Ratio: 4.379    Gaps: 1

alignment_block:
US-09-019-441-3 x US-08-579-378A-18

Align seg 1/1  to: US-08-579-378A-18  from: 1 to: 131

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  1 MetGluThrAspThrIleLeuLeuTrpValLeuLeuTrpValProGl  17

 57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT 106
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 17 ySerThrGlyAspIleGlnMetThrGlnSerProSerSerLeuSerAlaS  34

107 CTGTAGGGGACAGAGTCACCACCACTTGCCAGGGCAAGTCAGGACATTAGG 156
    |||||||||||||||||||||||||||||:||:|::|||
 34 erValGlyAspArgValThrIleThrCysLysAlaSerGlnSerValAsp  50

157 TAT........TATTTAAATTGGTATCAGCAGAAACCAGGAAAAGC 194
    |||        ||:::|||||||||||||||||||||||||||||
 51 TyrAspGlySerTyrMetAsnTrpTyrGlnGlnLysProGlyLysAl  67

195 TCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCAT 244
    |||||||||||||||||:||||::|
 67 aProLysLeuLeuIleTyrAlaAlaSerAsnLeuGluSerGlyIlePros  84

245 CAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGC 294
    |||||||||||||||||||||||||||::|||||||||::::||
 84 erArgPheSerGlySerGlyThrAspPheThrLeuThrIleSer 100

295 AGCCTGCAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAG 344
    |||||||||||||||||||||||| ||| :: :::
101 SerLeuGlnProAlaAspPheAlaThrTyrTyrCysLeuGlnValTyrAsnGl 117

345 TACCCCTCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    :  ||||||||||||||||||||||||||||||||||||
117 uAspProTrpThrPheGlyGlnGlyThrLysValGluIleLys 131
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seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-461-284-2

alignment_scores:
         Quality:  506.00              Length:   131
           Ratio:    4.325              Gaps:     1
Percent Similarity:  89.313    Percent Identity:  74.809

alignment_block:
US-09-019-441-3 x US-08-461-284-2

Align seg 1/1  to: US-08-461-284-2  from: 1 to: 133

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  1 MetSerValProThrGlnValLeuGlyLeuLeuLeuTrpLeuThrAs  17

 57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT 106
    ||||||||||||||||||::::|||||||::||||::::||||||||
 17 pAlaArgCysAspIleGlnLeuThrGlnSerProSerThrLeuSerAlaS  34

107 CTGTAGGGGACAGAGTCACCATCACTTGCCAGGGCAAGTCAGGACATTAGG 156
    |||||||||||||||||||||||||||||::||::||
 34 erValGlyAspArgValThrIleThrCysArgAlaSerGluSerLeuAsp  50

157 TATTAT........TTAAATTGGTATCAGCAGAAAACCAGGAAAAGC 194
    |||||||        |||:::||||||||||||||||||||||||||
 51 AsnTyrGlyIleArgPheLeuThrTrpPheGlnGlnLysProGlyLysAl  67

195 TCCTAAGCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCAT 244
    ||||||||||||||::||||:::::||      |||||||||||
 67 aProLysLeuLeuMetTyrAlaAlaSerAsnGlnGlySerGlyValPros  84

245 CAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGC 294
    |||||||||||||||||||||||||||::||||||||||:::|||
 84 erArgPheSerGlySerGlyThrGlyPheThrLeuThrIleSer 100

295 AGCCTGCAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAG 344
    |||||||||||||||||||||||||||||  ||: :: ::
101 SerLeuGlnProAlaAspPheAlaThrTyrTyrCysGlnGlnThrLysGl 117

345 TACCCCTCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    ::: |||    ::||||||||||||||||||||||||||::|||
117 uValProTrpSerPheGlyGlnGlyThrLysValGluValLys 131
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seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-462-939-2

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        TITLE OF INVENTION:  Conjugates of Methyltrithio Antitumor
        TITLE OF INVENTION:  Agents and Intermediates for Their Synthesis
        NUMBER OF SEQUENCES:  4
        CORRESPONDENCE ADDRESS:
          ADDRESSEE:  American Cyanamid Company
          STREET:  One Cyanamid Plaza
          CITY:  Wayne
          STATE:  New Jersey
          COUNTRY:  United States
          ZIP:  07470-8426
        COMPUTER READABLE FORM:
          MEDIUM TYPE:  Floppy disk
          COMPUTER:  IBM PC compatible
          OPERATING SYSTEM:  PC-DOS/MS-DOS
          SOFTWARE:  PatentIn Release #1.0,  Version #1.25
        CURRENT APPLICATION DATA:
          APPLICATION NUMBER:  US/08/462,939
          FILING DATE:
          CLASSIFICATION:  435
        PRIOR APPLICATION DATA:
          APPLICATION NUMBER:  US 08/253,877
          FILING DATE:  03-JUN-1994
        ATTORNEY/AGENT INFORMATION:
          NAME:  Jackson, Herbert G.
          REGISTRATION NUMBER:  24,476
          REFERENCE/DOCKET NUMBER:  32,368
        TELECOMMUNICATION INFORMATION:
          TELEPHONE:  201-831-3142
          TELEFAX:  201-831-3305
        INFORMATION FOR SEQ ID NO: 2:
          SEQUENCE CHARACTERISTICS:
            LENGTH:  133 amino acids
            TYPE:  amino acid
            TOPOLOGY:  linear
          MOLECULE TYPE:  protein
US-08-462-939-2
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alignment_scores:
          Quality:   506.00                Length:    131
          Ratio:       4.325                 Gaps:       1
Percent Similarity:  89.313        Percent Identity:  74.809

alignment_block:
US-09-019-441-3 x US-08-462-939-2    ..

Align seq 1/1  to: US-08-462-939-2  from: 1  to: 133

   7 ATGAGGGTCCCCGCTCAGCTCCTCGGGGCTCCTTCGCTCTGGCTCCCCAGG  56
     |||  ||||||::|||::|||||||||||||||||||||||||||||||||
   1 MetSerValProThrGlnValLeuGlyLeuLeuLeuLeuTrpLeuThrAs  17

  57 TGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT  106
     |||||||||||||||:::||||||||:::|||||||||:::||||||||
  17 pAlaArgCysAspIleGlnLeuThrGlnSerProSerThrLeuSerAlaS  34

 107 CTGTAGGGGACAGAGTCACCATCACTTGCCAGGGCCAAGTCAGGACATTAGG  156
     ||||||||||||||||||||||||||||||||||||||::::::::
  34 erValGlyAspArgValThrIleThrCysArgAlaSerGluSerLeuAsp  50

 157 TATTAT..........TTAAATTGGTATCAGCAGAAACCAGGAAAGC  194
     |||              |||::|||::|||||||||||||||||||
  51 AsnTyrGlyIleArgPheLeuThrTrpPheGlnGlnLysProGlyLysAl  67

 195 TCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCAT  244
     ||||||||||||:::||||::::             ||||||||||||
  67 aProLysLeuMetTyrAlaAlaSerAsnGlnGlySerGlyValProS  84

 245 CAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGC  294
     |||||||||||||||||||||||||||||||::|||
  84 erArgPheSerGlySerGlyThrGlyPheThrLeuThrIleSer  100

 295 AGCCTGCAGCCTGAAGATTTGCGACTTATTACTGTCTACCAGGTTTATAG  344
```

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                |||||||||||::::::|||||||||||||||||||||||  |||::::::  :::
          101 SerLeuGlnProAspPheAlaThrTyrTyrCysGlnThrLysGl  117

          345 TACCCCTCGGACGTTCGGCCCAAGGGACCAAGGTGGAAATCAAA  387
               ::::|||    ::||||||||||||||||||::::||
          117 uValProTrpSerPheGlyGlnGlyThrLysValGluValLys  131
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OM of: US-09-019-441-4 to: PIR_71:*     out_format : pfs

Date: Sep 23, 2002 10:02 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09019441/runat_23092002_095258_6306/app_query.fasta_1.1860
-DB=PIR_71 -QFMT=fastan -SUFFIX=rpr -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -USER=US09019441 @CGN1_1.227
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-019-441-4
Query length: 411
Database: PIR_71:*
Database sequences: 283138
Database length: 96089334
Search time (sec): 132.110000

score_list:

| Sequence | Strd | Orig | ZScore | EScore | Len | ! Documentation |
|---|---|---|---|---|---|---|
| pir2:S31666 | + | 546.50 | 889.04 | 1.4e-41 | 138 | ! Ig heavy chain v region - human |
| pir2:S05271 | + | 538.50 | 874.95 | 7.6e-41 | 160 | ! Ig heavy chain precursor - huma |
| pir2:S31686 | + | 529.50 | 861.31 | 5.0e-40 | 140 | ! Ig heavy chain v region - human |
| pir2:S31588 | + | 528.50 | 859.69 | 6.1e-40 | 140 | ! Ig heavy chain v region - human |
| pir2:S31699 | + | 526.50 | 855.77 | 9.3e-40 | 134 | ! Ig heavy chain v region - human |
| pir2:S70442 | + | 518.00 | 842.63 | 5.4e-39 | 140 | ! Ig heavy chain precursor V regi |
| pir2:S31587 | + | 517.00 | 841.22 | 6.7e-39 | 136 | ! Ig heavy chain precursor V regi |
| pir2:A60943 | + | 517.00 | 840.44 | 6.7e-39 | 151 | ! Ig heavy chain precursor V regi |
| pir2:S31669 | + | 516.00 | 839.33 | 8.3e-39 | 141 | ! Ig heavy chain v region - human |
| pir2:I37781 | + | 514.50 | 837.00 | 1.1e-38 | 139 | ! Ig heavy chain v region - human |
| pir2:S22657 | + | 513.50 | 835.32 | 1.4e-38 | 140 | ! Ig heavy chain precursor V regi |
| pir2:S31679 | + | 512.50 | 834.02 | 1.7e-38 | 134 | ! Ig heavy chain v region - human |
| pir2:A30532 | + | 511.50 | 832.07 | 2.1e-38 | 140 | ! Ig heavy chain precursor V-III |
| pir2:S78054 | + | 511.00 | 831.42 | 2.3e-38 | 137 | ! Ig heavy chain precursor V-D-J |
| pir2:S31674 | + | 507.00 | 824.81 | 5.4e-38 | 139 | ! Ig heavy chain v region - human |
| pir2:S31701 | + | 503.50 | 818.42 | 1.2e-37 | 137 | ! Ig heavy chain v region - human |
| pir2:S31598 | + | 502.50 | 817.72 | 1.4e-37 | 135 | ! Ig heavy chain precursor V-III |
| pir2:A34964 | + | 499.00 | 813.09 | 2.9e-37 | 117 | ! Ig heavy chain precursor V-III |
| pir2:A45953 | + | 498.00 | 811.47 | 3.5e-37 | 117 | ! Ig heavy chain precursor V-III |
| pir2:S11239 | + | 496.00 | 806.63 | 5.3e-37 | 145 | ! Ig heavy chain v region - human |
| pir1:H3HU26 | + | 494.00 | 804.97 | 8.2e-37 | 117 | ! Ig heavy chain precursor V-III |
| pir2:I37778 | + | 490.00 | 797.41 | 1.9e-36 | 135 | ! variable region (VDJ) (clone |
| pir2:I37603 | + | 485.50 | 790.26 | 4.8e-36 | 132 | ! Ig heavy chain precursor V-III |
| pir2:S21979 | + | 484.00 | 788.79 | 6.6e-36 | 116 | ! Ig heavy chain V-gene (clone WH |
| pir2:S60296 | + | 483.50 | 786.79 | 7.2e-36 | 136 | ! Ig heavy-chain variable region |
| pir2:S31678 | + | 482.50 | 785.01 | 8.9e-36 | 139 | ! Ig heavy chain v region - human |
| pir2:B34964 | + | 482.00 | 785.47 | 9.9e-36 | 117 | ! Ig heavy chain precursor V-III |
| pir2:I37780 | + | 482.00 | 783.78 | 9.8e-36 | 147 | ! variable region (VDJ) (clone |
| pir2:S21980 | + | 481.00 | 783.85 | 1.2e-35 | 117 | ! Ig heavy chain V-gene (clone WH |
| pir2:S31688 | + | 480.50 | 782.03 | 1.4e-35 | 134 | ! Ig heavy chain v region - human |
| pir2:S16847 | + | 480.50 | 781.92 | 1.4e-35 | 136 | ! Ig heavy chain precursor V-III |
| pir2:PL0098 | + | 479.50 | 780.63 | 1.7e-35 | 130 | ! Ig heavy chain precursor V-III |
| pir2:S17079 | + | 478.00 | 778.97 | 2.3e-35 | 117 | ! Ig heavy chain V-gene (clone HH |
| pir2:S31590 | + | 477.00 | 776.40 | 2.8e-35 | 133 | ! Ig heavy chain v region - human |
| pir2:A30561 | + | 476.50 | 775.31 | 3.1e-35 | 138 | ! Ig heavy chain precursor V-III |
| pir2:S17080 | + | 473.50 | 771.73 | 5.9e-35 | 116 | ! Ig heavy chain V-gene (clone HH |
| pir2:S31601 | + | 467.50 | 761.13 | 2.0e-34 | 130 | ! Ig heavy chain v region - human |
| pir2:S09258 | + | 467.50 | 760.69 | 2.0e-34 | 138 | ! Ig heavy chain precursor V-regi |
| pir2:B28966 | + | 466.50 | 760.35 | 2.5e-34 | 116 | ! Ig heavy chain precursor V-regi |
| pir2:B26471 | + | 465.50 | 756.72 | 3.1e-34 | 152 | ! Ig heavy chain precursor V regi |
| pir2:S69340 | + | 465.50 | 753.06 | 3.0e-34 | 249 | ! Ig heavy chain VHIII-D-JH-CH |
| pir2:B56701 | + | 463.50 | 754.91 | 4.7e-34 | 138 | ! Ig heavy chain V region prec |
| pir2:S31120 | + | 463.00 | 754.80 | 5.2e-34 | 114 | ! Ig heavy chain - human |
| pir2:S12557 | + | 461.50 | 752.23 | 7.1e-34 | 116 | ! Ig heavy chain - human (frag |
| pir2:PT0369 | + | 461.00 | 750.74 | 7.9e-34 | 127 | ! Ig gamma chain precursor V r |

seq_name: pir2:S31666

seq_documentation_block:
Ig heavy chain v region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31666
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from t
A;Reference number: S31585
A;Accession: S31666
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-138 <CUI>
A;Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
             Quality:   546.50                      Length:    140
             Ratio:     4.372                        Gaps:        2
Percent Similarity:     89.286      Percent Identity:  76.429

alignment_block:
US-09-019-441-4 x S31666

Align seg 1/1  to: S31666    from: 1  to: 138

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  1 ATGGAGTTGGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGT  50
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  1 MetGluPheGlyLeuSerTrpLeuPheLeuVaLAlaiLeuLeuLysGlyVa  17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCCTTGGCCAAAGCCTG  100
    |||||||||||||||||||::||||||||||||||||||||:::||||
 17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuVaLGlnProG  34

101 GGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC  150
    ||||||||||||||||||||||||||||          ||||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly.......PheThrPhe  48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA  200
    ::::::||| |||:::|||||||||||||||||||||||||:|||||||
 49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl  65

201 GTGGGTCTCAGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT  250
    ||||||||| ||||::|||||| |||:::|||||||:||||||||
 65 uTrpValSerAlaIleSerGlySerGlySerThrTyrTyrAlaAspS  82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGGCCAACAACACACTG  300
    ::||||||||||||||||||||||||||||||||||||||||||||||||
 82 erValLysGlyArgPheThrIleSerArgArgAspAsnSerLysAsnThrLeu  98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACGACGGCTGCTCTATTACTG  350
    :::||||||||||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaVaLTyrTyrCy  115

351 TGCGAGCTTGACTACAGGG........TCTGACTCCTGGGGCCAGGGAG  391
    ||||::       |||||:       ||||||||:::||
115 sAlaLysAlaArgThrGlyTyrTyrPheAspLeuTrpGlyArgGlyThrf  132

392 TCCTGGTCACCGTCTCCTCA  411
    ||||||||||||||||||||
132 hrLeuValThrValSerSer  138
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seq_name: pir2:S05271

seq_documentation_block:
Ig heavy chain precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996
C;Accession: S05271; S04602
R;Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A;Reference number: S05270
A;Accession: S05271
A;Molecule type: mRNA
A;Residues: 1-160 <KIS1>
A;Cross-references: EMBL:X14584
R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
A;Reference number: S04601; MUID:89296497
A;Accession: S04602
A;Molecule type: mRNA
A;Residues: 1-144 <KIS2>
A;Cross-references: EMBL:X14584
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality:        538.50              Length:   146
Ratio:            4.308              Gaps:       2
Percent Similarity:  85.616        Percent Identity:  72.603

alignment_block:
US-09-019-441-4 x S05271

Align seg 1/1 to: S05271 from: 1 to: 160

1    ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTGTTCCTCTTTTGAAAGGTGT   50
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1    MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa   17

51   CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTGCAAAGCCTG   100
     ||||||||||||||||||||||||||||||||||:|||||||:::||||
17   lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG   34

101  GGGGGTCCCTGAGACTCTGGTGCGCCAGCCTCCGGGTTCAGGTTCACCTTC   150
     |||||||||||||||||||||||||:::||||          |||||||
34   lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe   48

151  AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA   200
     ::::::|||  ||||:||||||||||||||||||||||||||
49   SerThrTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl   65

201  GTGGGTCTCACCTATTAGTAGTAGTGGTAGTATCCCACAGTACGCAGACT   250
     |||||||  |||||||||||||||:|||
65   uTrpValSerAlaIleSerGlySerGlyGlyGlnInAlaProGlyLysGlyLeuGl   82

251  CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG   300
     ||||:|||||||| |||:|||||||||
82   erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu   98

301  TTTCTTCAAATGAACAGCCTGAGGACACGGCTGTCTATTACTG   350
     ::::|||||||||||||||||||||::::|||||
99   TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy   115

351  TGCGAGCTTGCGACTACA..........GGGTCTG   373
     |||::: ::::: :::::                   |||
115  sAlaLysAlaAlaValArgGlyValIleSerPheTyrTyrTyrTyrGlyMetA   132

374  ACTCCTGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA   411
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132  spValTrpGlyGlnGlyThrThrValThrValSerSer   144

seq_name: pir2:S31686

seq_documentation_block:
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31686
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from t
A;Reference number: S31585
A;Accession: S31686
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-140 <CUI>
A;Cross-references: EMBL:Z14205; NID:g30969; PIDN:CAA78574.1; PID:g30970
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality:        529.50              Length:   142
Ratio:            4.202              Gaps:       3
Percent Similarity:  88.732        Percent Identity:  74.648

alignment_block:
US-09-019-441-4 x S31686

Align seg 1/1 to: S31686 from: 1 to: 140

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1    MetGluPheGlyLeuSerTrpLeuSerLeuValAlaIleLeuLeuLysGlyVa   17

51   CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTTGGTGCAAAGCCTG   100
     ||||||||||||||||||||||||||||||||||||||:|||||:::|||
17   lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProG   34

101  GGGGGTCCCTGAGACTCTGGTGCGCGCAGCCTCCGGGTTCAGGTTCACCTTC   150
     ||||||||||||||||||||  ||||||||||||          |||||||
34   lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe   48

151  AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA   200
     ::|||||||||||||||||||:::|||
49   SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl   65

201  GTGGGTCTCACCTATTAGTAGTAGTGGTGATCCCACAGTACGCAGACT   250
     |||||||  ||||||::|||
65   uTrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyrSerAspS   82

251  CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG   300
     ||||:|||||||||| |||:|||||||||
82   erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu   98

301  TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG   350
     ||||||||:|||||||||||||||||||||||::||||
99   TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy   115

351  TGCGAGC.......TTGACTACAGGGGTCT.........GACTCCTGGGGCC   385
     |||::     ::::|||   :|||||||||
115  sAlaLysCysProPheAlaGlyGlySerProSerPheAspTyrTrpGlyG   132

386  AGGGAGTCCTGGTCACCGTCTCCTCA   411
     ||||::|||||||||||||||||||||
132  InGlyThrLeuValThrValSerSer   140

seq_name: pir2:S31588

seq_documentation_block:
Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31588
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31588
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
A;Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
        Quality:  528.50          Length:     142
        Ratio:      4.262          Gaps:         2
Percent Similarity:  87.324       Percent Identity:  73.944

alignment_block:
US-09-019-441-4 x S31588

Align seg 1/1  to: S31588  from: 1  to: 140

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  1 ATGGAGTTTGGGCTGAGCTGGGTTTCCTTGTTCCTCTTTGAAAGGTGT 50
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  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuArgGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTCGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
    ||||||||||||||||||||::|||||||||||||||||||||
 17 lGlnCysGluValGlnLeuLeuSerGlyGlyGlyLeuValGlnProG 34

101 GGGGTCCCTGAGACTCTGCTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    |||||||||||||| ||||||||||    |||||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    ::::::||| ||::||||||||||||||||||::||||
 49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTGGTGATCCCACATGGTACGCGCAGACT 250
    ||||||||| ||:::||||||||||||||    ::||||||
 65 uTrpValSerAlaIleSerGlySerGlyThrTyrTyrAlaAspS 82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG 300
    ||||||||||||::||||||::||||||||||:::||||||||||
 82 erValLysGlyArgPheThrIleSerArgAspAspSerLysAsnThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
    :::::||||||||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

351 TGCGAGCTTGACTACAGGGTCT..........GACTCCTGGGGCC 385
    ||||::: ||||||||||||            |||||||
115 sAlaLysAspHisAspTyrSerAsnTyrIleTyrPheAspTyrTrpGlyG 132

386 AGGGAGTCCTGGTCACCGTCTCCTCA 411
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132 lnGlyThrLeuValThrValSerSer 140
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seq_name: pir2:S31699

seq_documentation_block:
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31699
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the

---

A;Reference number: S31585
A;Accession: S31699
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <CUI>
A;Cross-references: EMBL:Z14201; NID:g30961; PIDN:CAA78570.1; PID:g30962
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
        Quality:  526.50          Length:     137
        Ratio:      4.351          Gaps:         2
Percent Similarity:  88.321       Percent Identity:  75.912

alignment_block:
US-09-019-441-4 x S31699

Align seg 1/1  to: S31699  from: 1  to: 134

```
  1 ATGGAGTTTGGGCTGAGCTGGGTTTCCTTGTTCCTCTTTGAAAGGTGT 50
    ||||||||||||||||||||||||||||||||::||::::||||
  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGGAGTCTGGGGCGGCTTGGCAAAGCCTG 100
    |||||||||||||||||||||::|||||||||||||||||||| |||
 17 lGlnCysGluValGlnLeuLeuSerGlyGlyGlyLeuValHisProG 34

101 GGGGTCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    |||||||||||| |||||||||||    |||||||||
 34 lyGlySerLeuArgLeuSerCysAlaSerGly......PheThrPhe 48

151 AATAACTACTACATGGACTGGGTCCCCCAGGCTCCAGGGCAGGGGCTGGA 200
    ::::||| ||::|||||||||||||||||||::||||
 49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    ||||||||| ||:::||||||||||||||    ::|||||
 65 uTrpValSerAlaIleSerGlySerGlyThrTyrTyrSerAspS 82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG 300
    |||||||||||::||||||::||||||||||:||||||||||||
 82 erValLysGlyArgPheThrIleSerArgAspAspSerLysAsnThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
    :::::||||||||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

351 TGCGAGCTTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGTCA 400
    ||| |||||||||||||:::||||||
115 sAlaArg...TrpArgAspLeuAspTyrTrpGlyGlnGlyThrLeuValT 131

401 CCGTCTCCTCA 411
    ||||||||
131 hrValSerSer 134
```

seq_name: pir2:S70442

seq_documentation_block:
Ig heavy chain precursor V region (mu) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C;Accession: S70442
R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of
A;Reference number: S70442; MUID:93024508
A;Accession: S70442
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
          Quality:   518.00              Length:     141
          Ratio:     4.281               Gaps:         2
Percent Similarity:  85.816    Percent Identity: 73.759

alignment_block:
US-09-019-441-4 x S70442    ..

Align seg 1/1  to: S70442  from: 1 to: 140

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  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGT  50
    ||||||||||||||||||||||||||||||||||||||||||:::||||||
  1 MetGluPheGlyLeuSerTrpValPheLeuValAlaLeuLeuLeuArgGlyVa  17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTTGGCAAAGCCTG 100
    ||||||:::||||||||||||||||||||||||||||:::::||:||||
 17 lGlnCysGlnValGlnLeuValGluSerGlyGlyGlyValValGlnProG  34

101 GGGGGTCCCTGAGACTCTGGTGCAGCCTCCGGGTTCAGGTTCACCTTC  150
    ||||||||||||||| |||||||||          ||||||||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    ::||||||  ||| ||||||||||||||||||:::||||||||||||
 49 SerAsnTyrGlyMetHisTrpValArgGlnAlaProGlyLysGlyLeuGl  65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    ||||||||||||       ::||||:::||||||||||||||||
 65 uTrpValAlaPheIleArgTyrAspGlySerAsnLysTyrTyrAlaAspS  82

251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
    ||||||||||||||||||||||||||||||||||::||||::||||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu  98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
    :::|||||||||||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  115

351 TGCGAGC..........TTGACTACAGGGTCTGACTCCTGGGGCCAGG 388
    ||||                    ::||| ||| ||||||||
115 sAlaArgAspHisIleValGlyAlaThrArgTyrPheAspTyrTrpGlyGlnG 132

389 GAGTCCTGGTCACCGTCTCCTCA 411
    ||:||||||||||||||||||||
132 lyThrLeuValThrValSerSer 139
```

seq_name: pir2:S31587

seq_documentation_block:
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31587
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31587
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-136 <CUI>
A;Cross-references: EMBL:Z14189; NID:g31005; PIDN:CAA78558.1; PID:g31006
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-114/Domain: immunoglobulin homology <IMM>

alignment_scores:
          Quality:   517.00              Length:     138
          Ratio:     4.169               Gaps:         2

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Percent Similarity: 89.855    Percent Identity: 72.464

alignment_block:
US-09-019-441-4 x S31587    ..

Align seg 1/1  to: S31587  from: 1 to: 136

```
 10 GGGCTGAGCTGGGTTTCCTTGTTCCTCTTTTGAAAGGTGTCCAGTGTGA. 59
    ||||||||||||||||||||||||||      :::||:||||||||||||||
  1 GlyLeuSerTrpValPheLeuValAlaLeuLeuLeuGluGlyValGlnCysGl  17

 60 GGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTTGGCAAAGCCTGGGGGGTCCC 109
    |||||||||||||||||||||||||||||::|||::||||||||||||||
 17 uValGlnLeuValGluSerGlyGlyGlyGlyLeuValGlnProGlyGlySerL  34

110 TGAGACTCTGGTGCAGCCTCCGGGTTCAGGTGCACCTTCAATAACTAC 159
    ||||||   |||||||||||||||||     ...PheThrPheSerSerTyr  48
 34 euArgLeuSerCysAlaAlaSerGly......PheThrPheSerSerTyr  48

160 TACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGCTGGAGTGGGTCTC 209
    :::||||||||||||||||||||||||::||||||||||||||||||
 49 TrpMetSerTrpValArgGlnAlaProGlyLysGlyLeuGluTrpValAl  65

210 ACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACTCCGTGAAGG 259
    :::|||:::|||:||  :::||||||||||||||||||||||
 65 aAsnIleLysGlnSerGlyGluLysTyrTyrValAspSerValLysG  82

260 GCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTGTTTCTTCAA 309
    ||||||||||||||||||||||::||||:::||||::||||||
 82 lyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeuTyrLeuGln  98

310 ATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTT 359
    ||||||||||||||||||||||||||||||||||||||||||||||
 99 MetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArgGl  115

360 GACTACAGGGTCT..........GACTCCTGGGGCCAGGGAGTCCTGG 397
    ||||||            |||   ||||||||||||||||:::|
115 yLeuThrGlyAlaThrAspAlaPheAspIleTrpGlyGlnGlyThrMetV 132

398 TCACCGTCTCCTCA 411
    ||||||||||||||
132 alThrValSerSer 136
```

seq_name: pir2:A60943

seq_documentation_block:
Ig heavy chain precursor V region (clone HN.14) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: A60943; A48165
R;Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.; Alt, F.W.; Kabat, E.A
J. Neuroimmunol. 30, 245, 1990
A;Title: Molecular cloning of a human immunoglobulin heavy chain variable (V-H) regio
A;Reference number: A60943; MUID:91036050
A;Accession: A60943
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-151 <DES>
R;Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.; Alt, F.W.; Kabat, E.A
J. Neuroimmunol. 26, 35-41, 1990
A;Title: Molecular cloning of a human immunoglobulin heavy chain variable (V-H) regio
A;Reference number: A48165; MUID:90094677
A;Accession: A48165
A;Molecule type: mRNA
A;Residues: 1-36,'M',38-62,'AR',67-151 <DE2>
A;Note: this sequence has been corrected in reference A60943
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
          Quality:   517.00              Length:     145

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                  Ratio:   4.238              Gaps:      3
Percent Similarity:  84.138      Percent Identity:  72.414

alignment_block:
US-09-019-441-4 x A60943

Align seg 1/1  to: A60943  from:  1  to: 151

  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGTTCCTCTTTTGAAAGGTGT  50
    ||||||  ||||||  ||||||||||||||||||  ||||||::||||
  1 MetGluPheGlyLeuSerTrpValPheLeuValAlaLeuValArgGlyVa  17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
    ||||||::|||||||||||||||||||||||||  |||||:::||||||
 17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyValGlnProG     34

101 GGGGTCCCTGAGACTCTGGTGCGCCAGCCTCCGGGTTCAGGTTCACCTTC 150
    ||  ||||||||||  ||||||||||||||||||
 34 lyThrSerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

151 AATAACTACTACATGGACTGGGTCCGCCAGCCTCCAGGGTCCAGGGCTGGA 200
    :::::||| |||::||||||||||||||||  ||||||||
 49 SerArgTyrGlyMetHisTrpValArgGlnAlaProGlyLysGlyLeuGl  65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGGCAGACT 250
    ||||||||| ||  |||||||||||||||||||||||||
 65 uTrpValSerIleSerSerSerSerTyrIleTyrTyrAlaAsps         82

251 CCGTGAAGGGCCGAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG 300
    :||||||| ||||||||||||||||::||||||||||||
 82 erValSerValIleSerPheAspGlyGlyThrLysTyrTyrAlaAspS    98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACCACGGCTCTCTATTACTG 350
    :||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluArgAspLeuAlaValTyrTyrCy 115

351 TGCCAGC.............TTGACTACAGGGTCT...........GACT 376
    ||||||||| :||
115 sAlaLysLysAlaAlaSerThrGlySerGlyValAspPheAspT        132

377 CCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
    |||||||||||::||||||||||||||||||
132 yrTrpGlyGlnGlyThrLeuValThrValSerSer                 143

seq_name: pir2:S31669

seq_documentation_block:
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31669
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31669
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-141 <CUI>
A;Cross-references: EMBL:Z14212; NID:g30959; PIDN:CAA78581.1; PID:g30960
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
      Quality:  516.00              Length:    143
        Ratio:    4.195              Gaps:        3
Percent Similarity:  86.014      Percent Identity:  74.126

alignment_block:
US-09-019-441-4 x S31669
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Align seg 1/1  to: S31669  from:  1  to: 141

  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGTTCCTCTTTTGAAAGGTGT  50
    ||||||  ||||||  :::||||::||||
  1 MetGluProGlyLeuArgTrpValPheLeuValAlaIleLeuGluGlyVa  17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
    |||||||:::||||||||||||||||||||||::||||||
 17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValLysProG  34

101 GGGGTCCCTGAGACTCTGGTGCGCCAGCCTCCGGGTTCAGGTTCACCTTC 150
    ||||||||||| ||||||||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

151 AATAACTACTACATGGACTGGGTCCGCCAGCCTCCAGGGTCCAGGGCTGGA 200
    :::::||| |||::||||||||||||||||||||
 49 SerSerTyrSerMetAsnTrpValArgGlnAlaProGlyLysGlyLeuGl  65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGGCAGACT 250
    |||||||||| |||||||||||::|||
 65 uTrpValSerIleSerSerSerSerTyrIleTyrTyrAlaAsps         82

251 CCGTGAAGGGCCGAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG 300
    |||||||||::|||||||||||||||:::||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu  98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
    :||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

351 TGCG.....AGCTTGACTACAGGGTCT...........GACTCCTGGG 382
    |||| :::::
115 sAlaArgGlyArgHisLeuThrGlyGluLysGlyTyrPheAspLeuTrpG 132

383 GCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
    ||::||||||||||||||||
132 lyArgGlyThrLeuValThrValSerSer 141

seq_name: pir2:I37781

seq_documentation_block:
Ig variable region (VDJ) (clone T21-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C;Accession: I37781; S25475
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed b
A;Reference number: A36876; MUID:94119917
A;Accession: I37781
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <RES>
A;Cross-references: EMBL:X67908; NID:g33580; PIDN:CAA48106.1; PID:g33581
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;35-118/Domain: immunoglobulin homology <IMM>

alignment_scores:
      Quality:  514.50              Length:    139
        Ratio:    4.116              Gaps:        2
Percent Similarity:  89.928      Percent Identity:  71.223

alignment_block:
US-09-019-441-4 x I37781

Align seg 1/1  to: I37781  from:  1  to: 139

  4 GAGTTTGGGCTGAGCTGGGTTTTCCTCGTTCCTCTTTTGAAAGGTGTCCA  53
    |||||||||||||||||||  :::||||:||||||
  3 GluPheGlyLeuSerTrpValPheLeuValAlaIleLeuGluGluGlyValGl  19

 54 GTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGG 103
```

```
                 ||||||||||||||||||||||||||||| :||||||||
      19 nCysGluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyG  36

     104 GGTCCCTGAGACTCTGGTCGCGCAGCTTCCGGGTTCACCTTCAAT 153
         |||||||||||||       |||||||||||::||||| :::
      36 lySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPheSer  50

     154 AACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCTGGAGTG 203
         ::||||||:::|||::||||||||||||||||||||||
      51 SerTyrTrpMetSerTyrValArgGlnLeuProGlyLysGlyLeuGluTr  67

     204 GGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGTACGGCAGACTCCG 253
         |||::::::::||::::   ::|||  :::|||::|||||
      67 pValAlaAsnIleLysGlnAspGlySerGluLysTyrTyrValAspSerV  84

     254 TGAAGGGCAGATTCACCATCTCCAGAGAGACGCCAACAACACACTGTTT 303
         :::|||||||||||||||||||||||||||::||:||||||||
      84 aLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeuTyr  100

     304 CTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCGTCTATTACTGTGC 353
         ||||||||||||||||||||||||||||||||||||||
     101 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAl  117

     354 GAGCTTGACTACAGGGTCT........GACTCCTGGGGCCAGGAGTCC 394
         |   ::||||:::             ::  |||||||||:::::
     117 aArgLeuThrThrGlySer......AspSerTrpGlyGlnGlyThrM  134

     395 TGGTCACCGTCTCCTCA 411
         :::|||||||||||||
     134 etValThrValSerSer 139
```

seq_name: pir2:S22657

seq_documentation_block:
Ig heavy chain precursor V region (O-81VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 06-Feb-1998
C;Accession: S22657
R;Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.
Nucleic Acids Res. 20, 2601, 1992
A;Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-a
A;Reference number: S22657; MUID:92285150
A;Accession: S22657
A;Molecule type: mRNA
A;Residues: 1-140 <HIR>
A;Cross-references: EMBL:X59134
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
    Quality: 513.50                  Length: 137
    Ratio: 4.108                     Gaps: 2
Percent Similarity: 91.241     Percent Identity: 71.533

alignment_block:
US-09-019-441-4 x S22657

Align seg 1/1 to: S22657   from: 1 to: 140

     1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTGCCCTTTTTGAAAGGTGT 50
       ||||||||||||||||||||||||||  ::||||:|||
     1 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleLeuGluGlyGlyVa 17

    51 CCAGTGTGAGGTGCAGCTGGTGCAGTCTGGGGCCGGCTTGGCAAAGCCTG 100
       ||||||:|||||||||||||||||||:||||||||||||:::|||
    17 lGlnCysGluValGlnLeuValGlyLeuValAlaIleLeuGluLeuGlyVa 34

   101 GGGGGTCCCTGAGACTCTGGTCGCGCAGCTCCGGGGTTCAGGTTCACCTTC 150
       ||  |||||||||||||||||||||||||||||||||
```

---

```
                    :||||||||||||||||||||| :||||||||
      34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

     151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
         :::::::::|||   |||||||||::::|||||||:::   ||||
      49 SerSerHisTrpMetThrTrpValArgGlnThrProGlyLysArgLeuGl 65

     201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGTACGGCAGACT 250
         |||||||  |||||||||||||||:::||:   ::||||||||
      65 uTrpValAlaAsnValLysGlnAspGlySerAlaArgTyrTyrAlaAspS 82

     251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
         |||||||||||||||||||||||||||||||||||||||||||
      82 erValArgGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu 98

     301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCCTGTCTATTACTG 350
         :::|||||||||||||||||||||||::|||::|||||||||||
      99 TyrLeuGlnMetAsnSerLeuArgAlaAspAspThrAlaValTyrTyrCy 115

     351 TGCGAGCTTGACTACAGGGTCTGACTCCTGGGGCCAGGAGTCCTGGTCA 400
         ||    :|||||   |||    ::|||||||||||||:-|||||:|
     115 sAlaArg...SerThrGlyIleAspTyrTrpGlyGlnGlyThrLeuValT 131

     401 CCGTCTCCTCA 411
         :::||||||||
     131 hrValSerSer 134
```

seq_name: pir2:S31679

seq_documentation_block:
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31679
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from t
A;Reference number: S31585
A;Accession: S31679
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <CUI>
A;Cross-references: EMBL:Z14203; NID:g30965; PIDN:CAA78572.1; PID:g30966
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
    Quality: 512.50                  Length: 137
    Ratio: 4.271                     Gaps: 2
Percent Similarity: 87.591     Percent Identity: 74.453

alignment_block:
US-09-019-441-4 x S31679

Align seg 1/1 to: S31679   from: 1 to: 134

     1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTGCCCTTTTTGAAAGGTGT 50
       ||||||||||||||||||||||||||:::||||::|||
     1 MetGlyPheGlyLeuSerTrpValPheLeuValAlaLeuLeuGluArgGlyVa 17

    51 CCAGTGTGAGGTGCAGCTGGTGCAGTCTGGGGCCGGCTTGGCAAAGCCTG 100
       ||||||:|||||||||||::||||||:||||||||||||||::|||
    17 lGlnCysGlnValGlnLeuValGluSerGlyGlyGlyLeuValGlnProG 34

   101 GGGGGTCCCTGAGACTCCTGGTCGCGCAGCCTCCGGGGTTCAGGTTCACCTTC 150
       ||     ||||||||||||||||||||||||::::|||
    34 lyArgSerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

   151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
       :::::|||:::   |||||||||::::||||||||:::  ||||
    49 SerSerTyrAlaMetHisTrpValArgGlnAlaProGlyLysGlyLeuGl 65
```

seq_name: pir2:A30532

seq_documentation_block:
Ig heavy chain precursor V-III region (38) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 18-Oct-1996
C;Accession: A30532
R;Meeker, T.C.; Grimaldi, J.C.; O'Rourke, R.; Loeb, J.; Juliusson, G.; Einhorn, S.
J. Immunol. 141, 3994-3999, 1988
A;Title: Lack of detectable somatic hypermutation in the V region of the Ig H chain gene
A;Reference number: A30532; MUID:89035542
A;Accession: A30532
A;Molecule type: DNA
A;Residues: 1-140 <MEE>
C;Genetics:
C;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;20-140/Product: Ig heavy chain V-III region 38 #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
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       Quality:     511.50            Length:    142
       Ratio:         4.263           Gaps:        2
Percent Similarity:  84.507    Percent Identity: 72.535
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alignment_block:
US-09-019-441-4 x A30532

Align seg 1/1  to: A30532  from: 1  to: 140

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  1 ATGGAGTTTGGGCTGAGCTGGGTTTCCTTGTTCCTCTTTGAAAGGTGT 50
    |||||||||||||||||||||||::  ::||||||||
  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTCGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
    |||||||||||||||||||  ::|||||::|||
 17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuAlaLysProG 34

101 GGGGGTCCCTGAGACTCTGTGCGCCAGCCTCCGGGTTCAGTTCACCTTC 150
    |||||||||||||  |||||||   |||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    :::|||||| ||:::||||||||||::|||||
 49 SerAsnTyrTyrMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGTACGCAGACT 250
    |||||||| ||||||        :::||||::||
 65 uTrpValSerIleSerGlySerAspGlyGlyThrTyrTyrTyrThrAlaS 82
```

---

```
251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
    ||||||||||||||||||||||||||:::||:::||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACGCACCGGTCTCTATTACTG 350
    ::|||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

351 TGCCAGC..........TTGACTACAGGGTCTGACTCCTGGGGCC 385
    |||:::  ||
115 sAlaGlnAsnMetGlyAspIleArgLeuThrProLeuAlaTyrTrpGlyG 132

386 AGGGAGTCCTGGTCACCGTCTCCTCA 411
    |||||||||||||||||||||
132 lnGlyThrLeuValThrValSerSer 140
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seq_name: pir2:S78054

seq_documentation_block:
Ig heavy chain precursor V-D-J region (clone mAB 60VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78054; S23719
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78054
A;Molecule type: mRNA
A;Residues: 1-137 <HAR>
A;Cross-references: EMBL:X54435; NID:g37812; PIDN:CAA38304.1; PID:g37813
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notk
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- an
patient.
A;Reference number: S23716; MUID:9031262
A;Accession: S23719
A;Molecule type: mRNA
A;Residues: 20-116 <HAW>
A;Cross-references: EMBL:X54435
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-137/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IMM>

alignment_scores:
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       Quality:     511.00            Length:    140
       Ratio:         4.121           Gaps:        3
Percent Similarity:  88.571    Percent Identity: 72.143
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alignment_block:
US-09-019-441-4 x S78054

Align seg 1/1  to: S78054  from: 1  to: 137

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  1 ATGGAGTTTGGGCTGAGCTGGGTTTCCTTGTTCCTCTTTGAAAGGTGT 50
    |||||||||||||||||||||||||::  ::||||||||
  1 MetGluPheGlyLeuAsnTrpValPheLeuValAlaIleLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGGCAAAGCCTG 100
    ||||||||||||||||||||||  ||:::|||
 17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProG 34

101 GGGGGTCCCTGAGACTCTCCTGTGCGCCAGCTCTGGGTTCACCTTC 150
    ||||||||||||||  |||||  ||||||
 34 lyGlySerLeuArgLeuSerCysValValSerGly......PheProPhe 48

151 AATAACTACTACATGGACTGGTAGTAGTGGTGATCCCACATGGTACCAGACT 200
    ::::|||||  ||||||||     :::|||||::||
 49 SerThrTyrTrpMetHisTrpValArgGlnThrProGlyLysGlyLeuVa 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTGATCCCAGACT 250
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```
       ||||||::  |||::::|||  |||        |||||||||
    65 lTrpValAlaMetIleAsnSerGlyGlyThrGlyThr...TyrAlaAspS  81

   251 CCGTGAAGGCAGATTCACCATCTCCAGAGAACGCCAACAACACACTG  300
       ||||||||||||||||||||||||:|||||||::|||||||||
    81 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeu  97

   301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG  350
       ::||||||||||||||||||||||||::|||||||||:||||||||||
    98 TyrLeuGlnMetAsnSerLeuArgAlaAspAlaValAlaValTyrTyrCy  114

   351 TGCGAGCTTG........ACTACAGGGTCTGACTCCTGGGGCCAGGGAG  391
       |||| ::: :::::   |||||||||||||||:
   114 sAlaArgIleGlyGlyThrAsnSerProAspSerTrpGlyGlnGlyT  131

   392 TCCTGGTCACCGTCTCCTCA  411
       ::|||||||||||||||||
   131 hrLeuValThrValSerSer  137

seq_name: pir2:S31674

seq_documentation_block:
Ig_heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31674
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31674
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <CUI>
A;Cross-references: EMBL:Z14204; NID:g30967; PIDN:CAA78573.1; PID:g30968
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
            Quality:  507.00         Length:     141
              Ratio:    4.225          Gaps:       2
Percent Similarity: 85.106   Percent Identity: 72.340

alignment_block:
US-09-441-4 x S31674

Align seg 1/1  to: S31674  from: 1  to: 139

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     1 MetGluLeuGlyLeuSerTrpValPheLeuValAlaLeuLeuArgGlyVa  17

    51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
       |||||||||||||||||||||||||||||||||::::::|:|||
    17 lGlnCysValGlnLeuValGluSerGlyGlyGlyLeuValGlnProG  34

   101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC  150
       || |||||||| |||||||| ||||||||| ||||||||  |||||||
    34 lyArgSerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

   151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA  200
       ::::::|||  ||| |||||||||||||||||||  ::||||||||
    49 SerSerTyrGlyMetHisTrpValArgGlnAlaProCysLysGlyLeuGl  65

   201 GTGGGTCTCACGTATTAGTAGTAGTAGTAGTTGGTGATCCCACCATGGTACGCAGACT  250
       |||||||    |||||||||   ::::||||||:::::|||
    65 uTrpValAlaValIleSerTyrAspGlySerAsnLysTyrTyrAlaAspS  82

   251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGGCCAACAACACACTG  300
       |||||||||||||||||||||||||||  ::::|||||||
    82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu  98
```

```
   301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGAGGACACGGCTGTCTATTACTG  350
       ::||||||||||||||||||||||||||||||||||||||||||||||||
    99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  115

   351 TGCGAGCTTGACTACAGGG.........TCTGACTCCTGGGGCCAGG  388
       ||||:::            |||  |||||||||||||||||
   115 sAlaLysAlaGlyLeuGlyPheAsnTrpPheAspProTrpGlyGlnG  132

   389 GAGTCCTGGTCACCGTCTCCTCA  411
       |:::||||||||||||||||||
   132 lyThrLeuValThrValSerSer  139
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OM of: us-09-019-441-4 to: SwissProt_40:*    out_format : pfs
Date: Sep 23, 2002 10:24 AM
About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=framet_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_Spool/US09019441/runat_23092002_095259_6394/app_query.fasta_1.1860
-DB=SwissProt_40 -QFMT=fastan -SUFFIX=rsp -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09019441_QCGN_1_91 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-019-441-4
Query length: 411
Database: SwissProt_40:*
Database sequences: 105224
Database length: 38719550
Search time (sec): 62.410000

score_list:
Sequence                 Strd Orig   ZScore EScore   Len ! Documentation
SwissProt_40:HV3C_HUMAN   +  494.00  855.65 4.9e-40  117 ! P01764 homo sapiens (human)
SwissProt_40:HV05_CARAU   +  466.50  808.13 2.2e-37  116 ! P19181 carassius auratus (go
SwissProt_40:HV16_MOUSE   +  438.00  757.37 1.3e-34  136 ! P01783 mus musculus (mouse)
SwissProt_40:HV55_MOUSE   +  423.00  732.76 3.5e-33  117 ! P18526 mus musculus (mouse)
SwissProt_40:HV58_MOUSE   +  421.00  722.50 5.4e-33  117 ! P18529 mus musculus (mouse)
SwissProt_40:HV54_MOUSE   +  417.00  722.37 1.3e-32  117 ! P18525 mus musculus (mouse)
SwissProt_40:HV59_MOUSE   +  411.00  711.99 5.0e-32  117 ! P18530 mus musculus (mouse)
SwissProt_40:HV53_MOUSE   +  406.00  703.33 1.5e-31  117 ! P18524 mus musculus (mouse)
SwissProt_40:HV3A_HUMAN   +  406.00  702.96 1.5e-31  122 ! P01762 homo sapiens (human)
SwissProt_40:HV26_MOUSE   +  405.50  700.60 1.7e-31  144 ! P01795 mus musculus (mouse)
SwissProt_40:HV3T_MOUSE   +  402.00  696.48 3.7e-31  116 ! P01781 mus musculus (mouse)
SwissProt_40:HV3B_HUMAN   +  401.00  694.91 4.6e-31  114 ! P01763 homo sapiens (human)
SwissProt_40:HV3G_HUMAN   +  400.00  692.57 5.8e-31  122 ! P01768 homo sapiens (human)
SwissProt_40:HV3J_HUMAN   +  397.50  688.32 1.0e-30  121 ! P01771 homo sapiens (human)
SwissProt_40:HV01_RAT     +  396.50  685.15 1.3e-30  142 ! P01805 rattus norvegicus (rat)
SwissProt_40:HV3H_HUMAN   +  393.00  680.45 2.7e-30  122 ! P01769 homo sapiens (human)
SwissProt_40:HV3E_HUMAN   +  388.50  672.81 7.4e-30  120 ! P01766 homo sapiens (human)
SwissProt_40:HV36_MOUSE   +  383.50  664.46 2.2e-29  116 ! P01806 mus musculus (mouse)
SwissProt_40:HV02_CANFA   +  382.50  662.65 2.8e-29  117 ! P01785 canis familiaris (dog
SwissProt_40:HV31_HUMAN   +  382.50  662.50 2.8e-29  119 ! P01770 homo sapiens (human)
SwissProt_40:HV32_MOUSE   +  381.50  661.08 3.5e-29  115 ! P01801 mus musculus (mouse)
SwissProt_40:HV3F_HUMAN   +  380.50  659.35 4.3e-29  120 ! P01767 homo sapiens (human)
SwissProt_40:HV3U_HUMAN   +  378.00  654.64 7.6e-29  120 ! P01772 homo sapiens (human)
SwissProt_40:HV3K_HUMAN   +  378.00  654.20 7.6e-29  126 ! P01765 homo sapiens (human)
SwissProt_40:HV3D_HUMAN   +  376.50  652.42 1.1e-28  115 ! P01796 homo sapiens (human)
SwissProt_40:HV27_MOUSE   +  374.50  649.12 1.6e-28  113 ! P01799 mus musculus (mouse)
SwissProt_40:HV30_MOUSE   +  374.50  649.12 1.6e-28  113 ! P01798 mus musculus (mouse)
SwissProt_40:HV29_MOUSE   +  371.50  643.93 3.2e-28  113 ! P01800 mus musculus (mouse)
SwissProt_40:HV31_MOUSE   +  371.50  643.93 3.2e-28  113 ! P01802 mus musculus (mouse)
SwissProt_40:HV33_MOUSE   +  370.50  642.04 4.0e-28  115 ! P01784 canis familiaris (dog
SwissProt_40:HV01_CANFA   +  370.00  641.25 4.4e-28  114 ! P18528 canis familiaris (dog
SwissProt_40:HV57_MOUSE   +  369.00  640.88 5.4e-28   98 ! P18528 mus musculus (mouse)
SwissProt_40:HV28_MOUSE   +  368.50  638.73 6.2e-28  113 ! P01797 mus musculus (mouse)
SwissProt_40:HV3L_HUMAN   +  365.50  633.08 1.2e-27  119 ! P01773 homo sapiens (human)
SwissProt_40:HV03_CARAU   +  365.00  632.36 1.4e-27  117 ! P19180 carassius auratus (go
SwissProt_40:HV20_MOUSE   +  362.00  626.80 2.7e-27  122 ! P01789 mus musculus (mouse)
SwissProt_40:HV18_MOUSE   +  359.50  622.39 4.6e-27  123 ! P01787 mus musculus (mouse)
SwissProt_40:HV21_MOUSE   +  359.00  621.60 5.2e-27  122 ! P01790 mus musculus (mouse)
SwissProt_40:HV56_MOUSE   +  357.50  621.06 7.0e-27   97 ! P18527 mus musculus (mouse)
SwissProt_40:HV34_MOUSE   +  357.00  619.69 7.1e-27  113 ! P01803 mus musculus (mouse)
SwissProt_40:HV37_MOUSE   +  357.00  618.36 8.0e-27  119 ! P01807 mus musculus (mous
SwissProt_40:HV17_MOUSE   +  356.50  617.65 8.9e-27  117 ! P01786 mus musculus (mous
SwissProt_40:HV23_MOUSE   +  356.50  617.20 9.0e-27  123 ! P01792 mus musculus (mous
SwissProt_40:HV3P_HUMAN   +  356.00  616.63 1.0e-26  119 ! P01777 homo sapiens (huma
SwissProt_40:HV19_MOUSE   +  355.50  615.47 1.1e-26  123 ! P01788 mus musculus (mous

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seq_documentation_block:
ID   HV3C_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01764;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-III region VH26 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81101090; PubMed=6450418;
RA   Matthyssens G., Rabbitts T.H.;
RT   "Structure and multiplicity of genes for the human immunoglobulin
RT   heavy chain variable region.";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; J00236; AAA53516.1; -.
DR   EMBL; M35415; AAA58735.1; -.
DR   PIR; A02047; H3HU26.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V-III REGION VH26.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12582 MW;  E826733F1A3CB0F1 CRC64;

alignment_scores:
                   Quality:    494.00              Length:  118
                   Ratio:      4.491               Gaps:      1
Percent Similarity:  93.220       Percent Identity:  79.661

alignment_block:
US-09-019-441-4 x HV3C_HUMAN

Align seg 1/1  to: HV3C_HUMAN   from: 1 to: 117

    1 ATGGAGTTGGGCTGAGCTGGGTTTCCTTGTTCCTCTTTTGAAAGGTGT 50
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    1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17

   51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGGCAAAGCCTG 100
      |||||||||||||||||||||||||||||||||||||:|||||||||||||
   17 lGlnCysGluValGlnLeuLeuLeuSerGlyGlyGlyLeuValGlnProG 34

  101 GGGGGTCCCTGAGACTCTGGTGCCGCAGCCTCCGGGTTCACCTTC 150
      ||||||||||||||||||||||||||:||||||||  ||||||||
   34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

  151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
      :::::|||| ||||:||||||:||||||:||||||||:::||||||
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 49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65
    ||||||||||||||||||||||||||||||||||||||||||| :::||||
 17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuGlnProG 34

201 GTGGGTCTCACGTATTAGTAGTGGTGATCCCCACATGGTACGCAGACT 250        101 GGGGTCCCTGAGACTCTGGTCGCCAGCCTCCGGTTCACCTTC 150
    ||||||||||||::::||||| |||::||::||||                         ||||||||||||| ||||||||||||||        |||||
 65 uTrpValSerAlaIleSerGlyGlySerThrTyrTyrGlyAspS 82            34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrVal 48

251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG 300       151 AATAACTACTACCATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    ||||||||||||||||||||||||| :::||::||:::|||||||              ::::: ||||||:::||||||| |||||||||||||||||||||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98      49 SerSerAsnTyrMetSerTrpValArgGlnProProGlyLysGlyLeuGl 65

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350      201 GTGGGTCTCACGTATTAGTAGTGGTGATCCCCACATGGTACGCAGACT 250
    ::::||||||||||||||||||||||||||||||||||||||||||||||         |||::||| ||| ||||||||||||:::||:::|||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115     65 uTrpValSerValIleTyrSerGlyGlySer...ThrTyrTyrAlaAspS 81

351 TGCG 354                                                    251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG 300
    |||                                                         ||||||||||||||||||||||:::||::||::::||||||||
115 sAla 116                                                    81 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 97

seq_name: SwissProt_40:HV05_CARAU                             301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
                                                                 :::||||||||||||||||||||||||||||||||||||||||||||||
seq_documentation_block:                                      98 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 114
ID   HV05_CARAU     STANDARD;        PRT;     116 AA.
AC   P19181;                                                  351 TGCG 354
DT   01-NOV-1990 (Rel. 16, Created)                               |||
DT   01-NOV-1990 (Rel. 16, Last sequence update)              114 sAla 115
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 5A precursor.                    seq_name: SwissProt_40:HV16_MOUSE
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;    seq_documentation_block:
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;   ID   HV16_MOUSE    STANDARD;        PRT;     136 AA.
OC   Cypriniformes; Cyprinidae; Carassius.                    AC   P01783;
OX   NCBI_TaxID=7957;                                         DT   21-JUL-1986 (Rel. 01, Created)
RN   [1]                                                      DT   21-JUL-1986 (Rel. 01, Last sequence update)
RP   SEQUENCE FROM N.A.                                       DT   15-JUL-1999 (Rel. 38, Last annotation update)
RX   MEDLINE=88144476; PubMed=3125551;                        DE   Ig heavy chain V region MOPC 21 precursor (Fragment).
RA   Wilson M.R., Middleton D., Warr G.W.;                    OS   Mus musculus (Mouse).
RT   "Immunoglobulin heavy chain variable region gene evolution: structure    OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RT   and family relationships of two genes and a pseudogene in a teleost       OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RT   fish.";                                                  OX   NCBI_TaxID=10090;
RL   Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).        RN   [1]
DR   PIR; B28966; B28966.                                     RP   SEQUENCE FROM N.A.
DR   InterPro; IPR003006; Ig_MHC.                             RX   MEDLINE=81234548; PubMed=6788376;
DR   InterPro; IPR003596; Ig_v.                               RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
DR   Pfam; PF00047; ig; 1.                                    RA   Baltimore D.;
DR   SMART; SM00406; IGv; 1.                                  RT   "Heavy chain variable region contribution to the NPb family of
KW   Immunoglobulin V region; Signal.                         RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
FT   SIGNAL         1      19                                 RL   Cell 24:625-637(1981).
FT   CHAIN         20     116    IG HEAVY CHAIN V REGION 5A.   RN   [2]
FT   DOMAIN        20      49    FRAMEWORK-1.                  RP   SEQUENCE OF 17-136.
FT   DOMAIN        50      54    COMPLEMENTARITY-DETERMINING-1.    RX   MEDLINE=77100368; PubMed=401950;
FT   DOMAIN        55      68    FRAMEWORK-2.                  RA   Adetugbo K., Milstein C., Secher D.S.;
FT   DOMAIN        69      84    COMPLEMENTARITY-DETERMINING-2.    RT   "Molecular analysis of spontaneous somatic mutants.";
FT   DOMAIN        85     116    FRAMEWORK-3.                  RL   Nature 265:299-304(1977).
FT   DISULFID      41     114    BY SIMILARITY.                CC   -!- This SWISS-PROT entry is copyright. It is produced through a collaboration
FT   NON_TER      116     116                                 CC       between the Swiss Institute of Bioinformatics and the EMBL outstation -
SQ   SEQUENCE    116 AA;   12808 MW;  9C2279E2DF199B12 CRC64;    CC       the European Bioinformatics Institute. There are no restrictions on its
                                                              CC       use by non-profit institutions as long as its content is in no way
alignment_scores:                                            CC       modified and this statement is not removed. Usage by and for commercial
      Quality:    466.50       Length:     118               CC       entities requires a license agreement (See http://www.isb-sib.ch/announce/
        Ratio:     4.401         Gaps:       2               CC       or send an email to license@isb-sib.ch).
Percent Identity:   89.831    Percent Identity:  78.814       CC
Percent Similarity: 89.831                                   DR   EMBL; J00522; AAD15290.1; -.
                                                              DR   PIR; A02066; GIMS21.
alignment_block:                                             DR   HSSP; P01772; 2FB4.
US-09-019-441-4 x HV05_CARAU        ..                       DR   InterPro; IPR003006; Ig_MHC.
                                                              DR   InterPro; IPR003596; Ig_v.
Align seg 1/1  to: HV05_CARAU   from: 1  to: 116             DR   Pfam; PF00047; ig; 1.
                                                              DR   SMART; SM00406; IGv; 1.
  1 ATGGAGTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGT 50      KW   Immunoglobulin V region; Signal.
    | |||||||| |||||||||||||||||||| :::||||||||||||||||       FT   NON_TER       1       1
  1 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleAlaIleLysGlyVa 17   FT   SIGNAL       <1      16

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
```

```
FT  CHAIN      17   136   IG HEAVY CHAIN V REGION MOPC 21.
FT  DOMAIN    115   119   D SEGMENT.
FT  DOMAIN    120   136   JH4 SEGMENT.
FT  DISULFID   38   112
FT  CONFLICT   75    78   HYAD -> DYAH (IN REF. 2).
FT  CONFLICT   89    90   DN -> ND (IN REF. 2).
FT  CONFLICT  115   115   W -> H (IN REF. 2).
FT  CONFLICT  120   120   Y -> W (IN REF. 2).
FT  NON_TER   136   136
SQ  SEQUENCE  136 AA;   15071 MW;   2276A98DBDBF7016 CRC64;

alignment_scores:
                    Quality:   438.00              Length:  137
                    Ratio:     3.876               Gaps:    2
Percent Similarity: 82.482     Percent Identity: 65.693

alignment_block:
US-09-019-441-4 x HV16_MOUSE   ..

Align seg 1/1   to: HV16_MOUSE   from: 1   to: 136

 13 CTGAGCTGGTTTCCTTGTTCCTCTTTTGAAAGGTGTCCAGTGTGAGGT 62
    |||:::   |||||||||    :::||||||||||||||:::||
  2 LeuAsnLeuValPheLeuValLeuIleLeuLysGlyValGlnCysAspVa 18

 63 GCAGCTGGTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGA 112
    |||||||||||||||||||:::||||::::||||||||||
 18 lGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlySerArgL 35

113 GACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTAC 162
    ::|||   |||||||||||||        |||||||||
 35 ySerLeuSerCysAlaAlaSerGly......PheThrPheSerPheGly 49

163 ATGGACTGGGTCCGCCAGGCTCCAGGCAGGGGCTGGAGTGGGGTCTCACG 212
    |||   ||||||||||||||||   ::||||||||||||||::::
 50 MetHisTrpValArgGlnAlaProGlyLysGlyLeuGluTrpValAlaTy 66

213 TATTAGTAGTGGTGATCCCACATGCTACGCAGACTCCGTGAAGGGCA 262
    |||||||:::::::   |||||||::::||||||||||
 66 rIleSerSerGlySerSerThrLeuHisTyrAlaAspThrValLysGlyA 83

263 GATTCACCATCTCCAGAGAGAACCGCCAACAACACACTGTTTCTTCAAATG 312
    |||||||||||||   ||||||||||||||:::|||
 83 rgPheThrIleSerArgAspAsnProLysAsnThrLeuPheLeuGlnMet 99

313 AACAGCCTGAGAGCTGAGGACACGGCGTCTATTACTGTGCGAGCTTGAC 362
    ::||||||||||:::|||||||||:::::||||||||||
100 ThrSerLeuArgSerGluAspThrAlaMetTyrTyrCysAlaArgTrpGl 116

363 TACA..........GGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCA 400
    :::            ||  |||||||||:::   ||||
116 yAsnTyrProTyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValT 133

401 CCGTCTCCTCA 411
    |||||||||||
133 hrValSerSer 136
```

seq_name: SwissProt_40:HV55_MOUSE

```
KW  Immunoglobulin V region; Signal.
FT  SIGNAL      1    19
FT  CHAIN      20   117   IG HEAVY CHAIN V REGION 345.
FT  DOMAIN     20    49   FRAMEWORK-1.
FT  DOMAIN     50    54   COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN     55    68   FRAMEWORK-2.
FT  DOMAIN     69    85   COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN     86   117   FRAMEWORK-3.
FT  DISULFID   41   115   BY SIMILARITY.
FT  NON_TER   117   117
SQ  SEQUENCE  117 AA;   12902 MW;   49380E4627ACA99A CRC64;

alignment_scores:
                    Quality:   423.00              Length:  118
                    Ratio:     4.067               Gaps:    1
Percent Similarity: 88.136     Percent Identity: 69.492

alignment_block:
US-09-019-441-4 x HV55_MOUSE   ..

Align seg 1/1   to: HV55_MOUSE   from: 1   to: 117

  1 ATGGAGTTGGGCTGAGCTGGGTTTCCTTGTTCCTCTTTGAAAGGTGT 50
    |||:||||||||    ::|||||||    ||||||||||
  1 MetAsnPheGlyLeuArgLeuIlePheLeuValLeuThrLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
    |:::|||||||||||||||  :::||||||||||||||||||||||
 17 lLysCysGluValGlnLeuValGluSerGlyGlyGlyLeuValLysProG 34

101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    ||||||||||||||||||        |||:::|||:::||
 34 lyGlySerLeuLysSerCysAlaAlaSerGly......PheAlaPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGCAGGGGCCTGGA 200
    :::::|||   |||||||||||||||||:::||     ||||
 49 SerSerTyrAspMetSerTrpValArgGlnThrProGlyLysArgLeuGl 65

201 GTGGGTCTCAGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    ||||||   |||||||||||||||||::::||||||||||
 65 uTrpValAlaTyrIleSerSerSerGlyGlyGlySerThrTyrProAspT 82

251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
    :::||||||||||||||||||||||||:::||||::|||
 82 hrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
    :::||||||||||::::|||||::::||||||||||:::||||||
 99 PheLeuGlnMetSerSerLeuLysSerGluAspThrAlaMetTyrTyrCy 115

351 TGCG 354
    ||||
115 sAla 116
```

seq_name: SwissProt_40:HV58_MOUSE

DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 5-76 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/CJ.
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during
RT   the primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
CC   -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR   PIR; JT0505; HVMS57.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM004006; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V REGION 5-76.
FT   DOMAIN       20     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE    117 AA;  12991 MW;  93A04782B78B8FA0 CRC64;

alignment_scores:
          Quality:   421.00                Length:   118
          Ratio:       4.010               Gaps:       1
Percent Similarity:   88.983   Percent Identity:   70.339

alignment_block:
US-09-019-441-4 x HV58_MOUSE  ..

Align seg 1/1  to: HV58_MOUSE  from: 1  to: 117

    1 ATGGAGGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGT 50
      |||:::|||  ||||||||||||    :::|||||||||   ::||||||||||||
    1 MetAsnPheValLeuSerLeuileLeuPheLeuAlaLeuileLeuLysGlyVa 17

   51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGCAAAGCCTG 100
      |||||||||||||||||||  |||||||||||:||||||||||||:::||||  ||||
   17 lGlnCysGluValHisLeuValGluSerGlyGlyGlyLeuValLysProG 34

  101 GGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
      |||||||||||  |||:::|||  ||||||||| |||||||||   |||||||
   34 lyGlySerLeuLysLeuSerCysValValSerGly......PheThrPhe 48

  151 AATAACTACTACATGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
      ||:::||| |||::|||||||||||||:||||||||||   ::: ||||
   49 AsnLysTyrAlaMetSerTrpValArgGlnThrProGluLysArgLeuGl 65

  201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
      ||||||||| |||||||:::|||  ||:::|||   |||:::|| ||||
   65 uTrpValAlaThrIleSerAsnGlyGlyGlyGlySerThrTyrTyrProAspS 82

  251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG 300
      |||||||||||||||||||:::|||||||||||:::|||||||||||
   82 erValLysGlyArgPheThrIleSerArgArgAsnAlaGlyAsnThrLeu 98

  301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACACGCGTTGTCTATTACTG 350
      ||||||||:::|||:::||||||||||||||:::|||||||||  :: |||||
   98 TyrLeuGlnMetSerSerLeuArgSerGluAspThrAlaMetTyrTyrCy 115

  351 TGCG 354

---

115 sAla 116
    |||

seq_name: SwissProt_40:HV54_MOUSE

seq_documentation_block:
ID   HV54_MOUSE   STANDARD;      PRT;   117 AA.
AC   P18525;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 5-84 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/CJ.
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during
RT   the primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
CC   -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR   PIR; JT0505; HVMS84.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V REGION 5-84.
FT   DOMAIN       20     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE    117 AA;  12872 MW;  23405CB6A469861 CRC64;

alignment_scores:
          Quality:   417.00                Length:   118
          Ratio:       3.971               Gaps:       1
Percent Similarity:   88.983   Percent Identity:   67.797

alignment_block:
US-09-019-441-4 x HV54_MOUSE  ..

Align seg 1/1  to: HV54_MOUSE  from: 1  to: 117

    1 ATGGAGGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGT 50
      |||:::||||||||||||   :::||||||||   ::|||||||||||
    1 MetAsnPheGlyLeuSerLeuileLeuPheLeuValLeuValLeuLysGlyVa 17

   51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGCAAAGCCTG 100
      |||||||||||||||||||||||||||||||:||||||||||||:::||||  ||||
   17 lLeuCysGluValLysLeuValGluSerGlyGlyGlyLeuValGlnProG 34

  101 GGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
      |||||||||||||||:::|||  ||||||||| |||||||||   |||||||
   34 lyGlySerLeuLysLeuSerCysAlaAlaSerGly......PheThrPhe 48

  151 AATAACTACTACATGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
      ::::::||| |||::|||||||||||||:||||||||||   ::: ||||
   49 SerSerTyrThrMetSerTrpValArgGlnThrProGluLysArgLeuGl 65

  201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
      ||||||||| |||||||:::|||  ||:::|||   |||:::|| ||||
   65 uTrpValAlaTyrIleSerAsnGlyGlyGlyGlySerThrTyrTyrProAspT 82

```
251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAACGCCAACAACACACTG 300
    ::|||||||||||||||||||||||||||||||::||::|||
 82 hrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnAsnLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGGTCTCTATTACTG 350
    ::|||||:::|||||||:::|||||||||||||::||||||
 99 TyrLeuGlnMetSerSerLeuLysSerGluAspThrAlaMetTyrTyrCy 115

351 TGCG 354
    |||
115 sAla 116

seq_name: SwissProt_40:HV59_MOUSE

seq_documentation_block:
ID  HV59_MOUSE    STANDARD;      PRT;    117 AA.
AC  P18530;
DT  01-NOV-1990 (Rel. 16, Created)
DT  01-NOV-1990 (Rel. 16, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig heavy chain V region 7-39 precursor.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/CJ;
RX  MEDLINE=89279149; PubMed=2499654;
RA  Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT  "Early onset of somatic mutation in immunoglobulin VH genes during
RT  the primary immune response.";
RL  J. Exp. Med. 169:2007-2019(1989).
CC  -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR  PIR; JT0507; HVMS39.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; ig; 1.
DR  SMART; SM00406; IGv; 1.
KW  Immunoglobulin V region; Signal.
FT  SIGNAL       1     19
FT  CHAIN       20    117     IG HEAVY CHAIN V REGION 7-39.
FT  DOMAIN      20     49     FRAMEWORK-1.
FT  DOMAIN      50     54     COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN      55     68     FRAMEWORK-2.
FT  DOMAIN      69     85     COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN      86    117     FRAMEWORK-3.
FT  DISULFID    41    115     BY SIMILARITY.
FT  NON_TER    117    117
SQ  SEQUENCE  117 AA;  12972 MW;  D5CA4167D0F1774F CRC64;

alignment_scores:
       Quality:    411.00              Length:    118
       Ratio:        4.029             Gaps:        1
Percent Similarity:  86.441      Percent Identity: 68.644

alignment_block:
US-09-019-441-4 x HV59_MOUSE  ..

Align seg 1/1  to: HV59_MOUSE  from: 1  to: 117

  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTGAAAGGTGT 50
    |||::||||||||||||||| ::|||||||  ::||||||||||
  1 MetAsnPheGlyLeuSerLeuIlePheLeuValLeuIleLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGCAAAGCCTG 100
    |||||||||||::   ||||||||||||||||||||  ::|||||
 17 lGlnCysGluValLysTrpValGluSerGlyGlyGlySerValLysProG 34

101 GGGGTCCCTGAGACTCTGGTGCGCCAGCCTCCGGGTTCCAGGTTCACCTTC 150
    ||||||||||::::|||  |||||||||||  ||||||||
 34 lyGlySerLeuLysLeuSerCysGluAlaSerGly......PheThrPhe 48
```

```
151 AATAACTACTACATGACTGGGTCCGCAGGCTCCCAGGCAGGGCTGGA 200
    :::|||||   |||:::|||||||||||||||||||  :::  ||||
 49 SerAsnTyrGlyMetSerTrpValArgGlnThrProGluLysArgLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    |||||::   |||||::::   :::   ||:::|||   ||:::|||    ||||
 65 uTrpValAlaSerIleSerGlyGlyValSerTyrThrTyrTyrProAspS 82

251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACCACTG 300
    |||||||||||||||||||||||||||||||||||::|||::|||
 82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnAsnLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACGCGGCTGTCTATTACTG 350
    :::||||||||||||||| ::|||||||||||:::||||||||||||
 99 TyrLeuGlnMetAsnSerLeuThrSerGluAspThrAlaLeuTyrTyrCy 115

351 TGCG 354
    |||
115 sAla 116

seq_name: SwissProt_40:HV53_MOUSE

seq_documentation_block:
ID  HV53_MOUSE    STANDARD;      PRT;    117 AA.
AC  P18524;
DT  01-NOV-1990 (Rel. 16, Created)
DT  01-NOV-1990 (Rel. 16, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig heavy chain V region RF precursor.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/CJ;
RX  MEDLINE=89279149; PubMed=2499654;
RA  Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT  "Early onset of somatic mutation in immunoglobulin VH genes during
RT  the primary immune response.";
RL  J. Exp. Med. 169:2007-2019(1989).
CC  -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR  PIR; JT0503; HVMSRF.
DR  HSSP; P01810; 2FBJ.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; ig; 1.
DR  SMART; SM00406; IGv; 1.
KW  Immunoglobulin V region; Hybridoma; Signal.
FT  SIGNAL       1     19
FT  CHAIN       20    117     IG HEAVY CHAIN V REGION RF.
FT  DOMAIN      20     49     FRAMEWORK-1.
FT  DOMAIN      50     54     COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN      55     68     FRAMEWORK-2.
FT  DOMAIN      69     85     COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN      86    117     FRAMEWORK-3.
FT  DISULFID    41    115     BY SIMILARITY.
FT  NON_TER    117    117
SQ  SEQUENCE  117 AA;  12866 MW;  2CE3295F390F725B CRC64;

alignment_scores:
       Quality:    406.00              Length:    118
       Ratio:        3.942             Gaps:        1
Percent Similarity:  87.288      Percent Identity: 66.949

alignment_block:
US-09-019-441-4 x HV53_MOUSE  ..

Align seg 1/1  to: HV53_MOUSE  from: 1  to: 117

  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTGAAAGGTGT 50
```

Align seg 1/1  to: HV3A_HUMAN  from: 1  to: 122

```
   58 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCCGCTTGGCAAAGCCTGGGGGTC
      ::||||||||||:||||||||||||||||||||||::||||||||||||||
    1 GlnValGlnLeuValGlnSerGlyGlyGlyLeuValLysProGlyGlySe  17

  108 CCTGAGACTCTGTGCGCAGCCTCCGGTTCAGTTCACCTTCAATAACT 157
      ||||||||  |||::||||||||       |||:::||::::::||
   17 rLeuArgLeuSerCysValAlaSerGly......PheSerPheArgAspP  32

  158 ACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTC 207
      :||||||||||||||||:::||||||||||  ||||**||||:::||||
   32 heTyrMetSerTrpIleArg***ThrProGlyLysGlyLeu***TrpVal  48

  208 TCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGGACTCCGTGAA 257
      |||  |||::||||||::::   |||||||||||||||||:||||||
   49 SerTyrIleGlyGlySerThrLeuTyrTyrAlaAspSerValTy  65

  258 GGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTGTTTCTTC 307
      ||||||||||||||||||||||||||||||::::||||||:::||
   65 sGlyArgPheThrIleSerArgAspAsnAlaGlnLysSerLeuTyrLeu*  82

  308 AAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 357
      ::||:::||||||||||||||||||||:||||||||||||||||||||
   82 **Met***SerLeuArgThr*****ThrAlaValTyrTyrCysAlaAla  98

  358 TTG.............ACTACAGGGTCGACTCCTGGGGCCAGGG 389
      |||             :::  |||||||||| ||||||||
   99 Thr*******Phe***TrpSerSerLeu***TyrTrpGly***Gl  115

  390 AGTCCTGGTCACCGTCCTCA 411
      |  |||||||||||||||||
  115 y***LeuValThrValSerSer 122
```

seq_name: SwissProt_40:HV26_MOUSE

seq_documentation_block:
```
ID   HV26_MOUSE   STANDARD;          PRT;    144 AA.
AC   P01795;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region M167 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9358330; PubMed=6101208;
RA   Kim S., Davis M., Sinn E., Patten P., Hood L.;
RT   "Antibody diversity: somatic hypermutation of rearranged VH genes.";
RL   Cell 27:573-581(1981).
RN   [2]
RP   SEQUENCE OF 20-142.
RX   MEDLINE=76222762; PubMed=819932;
RA   Rudikoff S., Potter M.;
RT   "Size differences among immunoglobulin heavy chains from
RT   phosphorylcholine-binding proteins.";
RL   Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC       THAT BINDS PHOSPHORYLCHOLINE.
```

```
DR   EMBL; J00516; AAC18867.1; -.
DR   PIR; A02071; AVMS67.
```

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```
   |||::|||||||||                    ::||||||||||
    1 MetAsnPheGlyLeuArgLeuIlePheLeuLeuValLeuValLysGlyVa  17

   51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCCGCTTGGCAAAGCCTG 100
      |  |||::||::||||||||||||||||||||||||||::::|||  |
   17 lLeuCysAspValLysLeuValGluSerGlyGlyGlyLeuValLysLysLeuG  34

  101 GGGGTCCCTGAGACTCTGTGCGCAGCCTCCGGTTCAGTTCACCTTC 150
      |||||||  |:|::|||        |||||||||  |||||||||
   34 lyGlySerLeuLysLeuSerCysAlaAlaSerGly......PheThrPhe  48

  151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
      ::::::||||||||||||||||||:::|||||||||  ::: |||||
   49 SerSerTyrTyrMetSerTrpIleArgGlnThrProGluLysArgLeuGl  65

  201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
      ||  ||||::::||||:::|||        ||::::||  |||:||
   65 uLeuValAlaAlaIleAsnSerAsnGlyLySerThrTyrTyrProAspT  82

  251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
      :::||||||||||||||||||||||||||||:::||||||:::||||||
   82 hrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeu  98

  301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
      ::||||||||||||::::|||||||  |||||||||::::|||||||||
   99 TyrLeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuTyrTyrCy  115

  351 TGCG 354
      ||||
  115 sAla  116
```

seq_name: SwissProt_40:HV3A_HUMAN

seq_documentation_block:
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ID   HV3A_HUMAN   STANDARD;          PRT;    122 AA.
AC   P01762;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-III region TRO.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (MYELOMA PROTEIN TRO).
RX   MEDLINE=76023781; PubMed=809331;
RA   Kratzin H., Altevogt P., Ruban E., Kortt A., Staroscik K.,
RA   Hilschmann N.;
RT   "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.),
RT   II. The amino acid sequence of the H-chain, alpha-type, subgroup III:
RT   structure of the complete IgA-molecule.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
CC   -!- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
DR   PIR; A02045; A1HUTR.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13472 MW;  2E21A11DA04D80F9 CRC64;
```

alignment_scores:
```
      Quality:   406.00         Length:    124
      Ratio:       3.794        Gaps:        2
      Percent Similarity: 86.290      Percent Identity: 60.484
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alignment_block:
US-09-019-441-4 x HV3A_HUMAN  ..

```
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    144       IG HEAVY CHAIN V REGION M167.
FT   CONFLICT    125    125       N -> D (IN REF. 2).
FT   NON_TER     144    144
SQ   SEQUENCE    144 AA;  16219 MW;  BECB4A2C956CF769 CRC64;

alignment_scores:
          Quality:   405.50                  Length:     146
          Ratio:       3.557                  Gaps:         3
Percent Similarity:  78.082    Percent Identity:  56.164

alignment_block:
US-09-019-441-4 x HV26_MOUSE

Align seg 1/1  to: HV26_MOUSE   from: 1  to: 144

    1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGT  50
      ||:::::::  |||::|||||||||||||::::  |||||  |||||
    1 MetLysMetTrpLeuAsnTrpValPheLeuLeuThrLeuHisGlyIl  17

   51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
      :|||||||||||||||||||||::|||||||||:::|||||::|
   17 eGlnCysGluValLysValValGluSerGlyGlyGlyLeuValGlnProG  34

  101 GGGGTCCCCTGAGACTCTGGTGCGCGCAGCCTCCGGGTTCACCTTCACCTTC  150
      ||||||||||||||||  |||||:::||||     ||||||
   34 lyGlySerLeuArgLeuSerCysAlaThrSerGly......PheThrPhe  48

  151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA  200
      ::::::||||:::||||::||||||||||||||:::|||||:::    ||||
   49 SerAspPheTyrMetGluTrpValArgGlnThrProGlyLysArgLeuGl  65

  201 GTGGGTC.....TCACGTATTAGTAGTAGTGGTGATCCCACATGGTACG  244
      ||||||  ||||||  :::::::     ||:||  |||:
   65 uTrpIleAlaSerArgSerLysAlaHisAspTyrArgThrGluTyrS  82

  245 CAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAACGCCAACAAC  294
      ::  |||||||||||||  :::|||||||:::::::::::::||::
   82 erAlaSerValLysGlyArgPheIleValSerArgAspThrSerGlnSer  98

  295 ACACTGTTTCTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTA  344
      :::|||||::::|||||||||:::|||||||||||||||||||:::|
   99 ValLeuTyrLeuGlnMetAsnAlaLeuArgAlaGluAspThrAlaThrTy  115

  345 TTACTGTGCG...........AGCTTGACTACAGGGTCTG  373
      |||||||:|              |||||:||
  115 rTyrCysThrArgAspAlaAspTyrGlyAsnSerTyrPheGlyTyrPheA  132

  374 ACTCCTGGGGCCAGGGAGTCCTGGTCACCGTGTCCTCCTCA  411
      ||  |||||  |||:::||||||||||||||||||
  132 spValTrpGlyAlaGlyThrThrValThrValSerSer  144

seq_name: SwissProt_40:HV3T_HUMAN

seq_documentation_block:
ID   HV3T_HUMAN      STANDARD;      PRT;    116 AA.
AC   P01781;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-III region GAL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
```

```
RP   SEQUENCE.
RX   MEDLINE=75059123; PubMed=4803843;
RA   Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT   "The primary structure of a monoclonal IgM-immunoglobulin
RT   (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
RT   type), subgroup H III. Architecture of the complete IgM-molecule.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN   [2]
RP   REVISION TO THE COMPOSITION OF 28-33.
RA   Hilschmann N.;
RL   Submitted (JUN-1975) to the PIR data bank.
CC   -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC       MACROGLOBULIN.
DR   PIR; A02064; M3HUGL.
DR   HSSP; P01772; 2IG2.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   NON_TER     116    116
SQ   SEQUENCE    116 AA;  12730 MW;  2C67CA9AAAAA1282 CRC64;

alignment_scores:
          Quality:   402.00                  Length:     118
          Ratio:       3.980                  Gaps:         1
Percent Similarity:  85.593    Percent Identity:  67.797

alignment_block:
US-09-019-441-4 x HV3T_HUMAN

Align seg 1/1  to: HV3T_HUMAN   from: 1  to: 116

   58 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGTC  107
      |||||||||||||||||||||||||||||  ||||::::::||||||  ||
    1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyArgSe  17

  108 CCTGAGACTCTGGTGCGCGCAGCCTCCGGGTTCAGGTTCAATTCAATAACT  157
      |||||||||  ||||||||||||  ||  :||||||  :::
   17 rLeuArgLeuSerCysAlaAlaSerGly......Phe***Phe******L  32

  158 ACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTC  207
      |||  |||||||||||||||||||||||||||||||||||||||||
   32 euGlyMetThrTrpValArgGlnAlaProGlyLysGlyLeuGluTrpVal  48

  208 TCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACTCCGTGAA  257
      :::::||||:::|||::  |||:::  ||:|||::::||||||||||||||
   49 AlaAsnIleLys******GlySer******TyrValAspSerValLy  65

  258 GGGCAGATTCACCATCTCCAGAGAACGCCAACAACACACACTGTTTCTTC  307
      ||||||||||||:::::::|||||||||||||||:::||:  ||||||
   65 sGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeuTyrLeuG  82

  308 AAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC  357
      |||||||||||||||||:::|||||||||||||||||||||||||||
   82 lnMetAsnSerLeuArgValGluAspThrAlaLeuTyrTyrCysAlaArg  98

  358 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC  407
      |||:::||  |||::|||||||||||||||||||||||||||||||
   99 GlyTrpGlyGlyGlyAspTyrTrpTrpGlyGlnGlyThrLeuValThrValSe  115

  408 CTCA  411
      ||::
  115 rThr  116

seq_name: SwissProt_40:HV3B_HUMAN

seq_documentation_block:
ID   HV3B_HUMAN      STANDARD;      PRT;    114 AA.
AC   P01763;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
```

```
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-III region WEA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83273707; PubMed=6410398;
RA   Goni F., Frangione B.;
RT   "Amino acid sequence of the Fv region of a human monoclonal IgM
RT   (protein WEA) with antibody activity against 3,4-pyruvylated
RT   galactose in Klebsiella polysaccharides K30 and K33.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC       AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC       WALDENSTROM'S MACROGLOBULINEMIA.
DR   PIR; A02046; M3HUWE.
DR   HSSP; P01772; 2IG2.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER     114    114
SQ   SEQUENCE     114 AA;  12256 MW;  D88294F8418A07B7 CRC64;

alignment_scores:
             Quality:    401.00          Length:     120
               Ratio:      3.856           Gaps:       3
  Percent Similarity:    86.667   Percent Identity:  67.500

alignment_block:
US-09-019-441-4 x HV3B_HUMAN       ..

Align seg 1/1  to: HV3B_HUMAN  from: 1  to: 114

  58 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGTC 107
     :::|||||||||||::||||||  ||||||||:::::|||||||||||||
   1 GlnValGlnLeuValAspSerGlyGlyGlyLeuValGluProGlyGlySe 17

 108 CCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGTTCACCTTCAATAACT 157
     ||||||||   ||:||||||||||||| |||:: |||: |||:::|
  17 rLeuArgLeuSerCysSerAlaSerGlyPheThrPheSerAlaAsnAsp. 33

 158 ACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTC 207
     ||||||||||||||||:::::||||||||||||||::|||||||||||||
  34 ....MetAsnTrpValArgGlnAlaProGlyLysGlyLeuGluTrpLeu 48

 208 TCACGTATTAGTAGTGGTGATCCCACCATGTGACCAGACTCCGTGAA 257
     |||  ||:::::||||||::|:  ::|||||||||||||||||||||
  49 SerPheIleGlySerGlySerThrIleTyrTyrAlaAspSerValLy 65

 258 GGGCAGATTCACCATCTCCAGAGAACACGCCAACAACACTGTTTCTTC 307
     ||||||||||||||||||||||||||::::||:|||:::|||||||||
  65 sGlyArgPheThrIleSerArgAsn***SerLysAsnSerLeuTyrLeuG 82

 308 AAATGAACAGCCTGAGAGCTGAGGACACGCCGTCCTGGTGGTCTCGTCAC 401
     ||||||||||||||||||::|||||||::|||||||||||||||||
  82 lnMetSerSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArg 98

 358 .....TTGACTACAGGGTCTGACTCCTGGGGCCAGGAGTCCGTCAC 401
       ||                :::|||||||||||:::||||||||||
  99 GlyTrpLeuLeu.........AsnTrpGlyGlnGlyThrLeuValTh 111

 402 CGTCTCCTCA 411
     ||||||||||
 111 rValSerSer 114

seq_name: SwissProt_40:HV3G_HUMAN
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seq_documentation_block:
ID   HV3G_HUMAN      STANDARD;       PRT;       122 AA.
AC   P01768;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-III region CAM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=81013859; PubMed=6774332;
RA   Lehman D.W., Putnam F.W.;
RT   "Amino acid sequence of the variable region of a human mu chain:
RT   location of a possible JH segment.";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC   -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC       PATIENT WITH MACROGLOBULINEMIA.
DR   PIR; A02051; M3HUAM.
DR   HSSP; P01772; 2IG2.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER     122    122
SQ   SEQUENCE     122 AA;  13668 MW;  A42D0F17D252F1C2 CRC64;

alignment_scores:
             Quality:    400.00          Length:     124
               Ratio:      3.922           Gaps:       2
  Percent Similarity:    82.258   Percent Identity:  63.710

alignment_block:
US-09-019-441-4 x HV3G_HUMAN       ..

Align seg 1/1  to: HV3G_HUMAN  from: 1  to: 122

  58 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGTC 107
     :::|||||||||||::||||||  ||||||||:::::|||||||||||||
   1 GlnValGlnLeuValGluSerGlyGlyGlyVaIVaI***ProGlyArgSe 17

 108 CCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGTTCACCTTCAATAACT 157
     |||||||| ||:||||||||||||||          |||:::::||||
  17 rLeuArgLeuSerCysAlaAlaSerGly......PheThrPheSerAsnT 32

 158 ACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTC 207
     ||  ||| ||||||||:::::||||||||:::||||||||||||||||||
  32 yrAlaMetHisTrpValArgGlnProProGlyLysGlyLeuGluTrpVal 48

 208 TCACGTATTAGTAGTGGTGATCCCACCATGTGATCCAGACTCCGAGCTGAA 257
     ::: |||||  |||||| |::|:|||||||||:::|||||||:||||||
  49 AlaValIleSerTyr***Gly***Lys***TyrTyrAla***SerValLy 65

 258 GGGCAGATTCACCATCTCCAGAGAACGCCAACAACACTGTTTCTTC 307
     |||||||||||||||||||||||||||::||:||:::|||||||||
  65 sGlyArgPheThrIleSerArgAsp***SerLys***ThrLeuTyrLeuG 82

 308 AAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCG... 354
     ||||||||||||||||||::||||||||::|||||||||||||||||
  82 lnMetAsnSerLeuArgAlaGlu***ThrAlaValTyrTyrCysAlaArg 98

 355 ...........AGCTTGACTACAGGGTCTGACTCCTGGGGCCAGG 389
        ::          :::|||||||||||:::||||||||
  99 AspArgProLeuTyrGly***TyrArgAlaPheAsnTyrTrpGlyGlnGl 115

 390 AGTCCTGGTCACCGTCTCCTCA 411
     |:::||||||||||||||||||
 115 yThrLeuValThrValSerSer 122
```

seq_name: SwissProt_40:HV3J_HUMAN

seq_documentation_block:
ID   HV3J_HUMAN      STANDARD;      PRT;    121 AA.
AC   P01771;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-III region HIL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79124695; PubMed=420800;
RA   Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT   "Amino acid sequence of the VH region of human myeloma
RT   cryoimmunoglobulin IgG Hil.";
RL   Biochemistry 18:553-560(1979).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC       PROTEIN.
DR   PIR; A02054; G1HUHL.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13566 MW;  480FC53610EF5DAB CRC64;

alignment_scores:
        Quality:   397.50                 Length:       123
        Ratio:     3.822                   Gaps:         3
Percent Similarity:  84.553       Percent Identity:  65.854

alignment_block:
US-09-019-441-4 x HV3J_HUMAN         ..

Align seg 1/1  to: HV3J_HUMAN   from: 1  to: 121

  58 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGTC 107
     ::::||||::|||||||:::::||||||||||:::::::::||||||| ||
   1 GlnValLysLeuValGlnAlaGlyGlyGlyLeuValGlnProGlyArgSe  17

 108 CCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACT 157
     |||||||| ||| |||||||| ||||||||      |||||||::::|||
  17 rLeuArgLeuSerCysIleAlaSerGly......PheThrPheSerAsnT  32

 158 ACTACATGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTC 207
     || ||| |||||||:||| |||||||||||||||:||||||||||||||
  32 yrGlyMetHisTrpValArgGlnAlaProGlyLysGlyLeuGluTrpVal  48

 208 TCACGTATTAGTAGTGGTGGTCATCCACATGGTACGCAGCATCCGTGAA 257
     :::||||||      :||:::::|||||||||||||||||||||||:||
  49 AlaValIleTrpTyrAsnGlySerArgThrTyrTyrGlyAspServalLy  65

 258 GGGCAGATTCACCATCTCCAGAGAGAACGCCACAACCACTGTTTCTTC 307
     ||||||||||||||||||:::|||||||:||:||||||||||:::::::
  65 sGlyArgPheThrIleSerArgAspAsnSerLysArgThrLeuTyrMet*  82

 308 AAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 357
     :::||||||||||||||||||||||||||||||||||||||||||||
  82 **MetAsnSerLeuArgThrGluAspThrAlaValTyrTyrCysAlaArg  98

 358 ..........TTGACTACAGGGTCT...GACTCCTGGGGCCAGGGAGT 392
     ||||||||||   ||| |||||||||||||
  99 AspProAspIleLeuThrAlaPheSerPheAspTyrTrpGlyGlnGlyVa 115

393 CCTGGTCACCGTCTCCTCA 411
    |||||||||||||||||||
115 lLeuValThrValSerSer 121

seq_name: SwissProt_40:HV01_RAT

seq_documentation_block:
ID   HV01_RAT      STANDARD;      PRT;    142 AA.
AC   P01805;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region IR2 precursor.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83064537; PubMed=6292865;
RA   Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;
RT   "Structure and evolution of the heavy chain from rat immunoglobulin
RT   E.";
RL   Nucleic Acids Res. 10:6041-6049(1982).
CC   -!- MISCELLANEOUS: THE MRNA WAS ISOLATED FROM AN IGE-SECRETING
CC       IMMUNOCYTOMA THAT ARISES SPONTANEOUSLY IN LOU/C/WSL RATS.
DR   PIR; A02075; EVRTR2.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    142       IG HEAVY CHAIN V REGION IR2.
FT   NON_TER       1    142
SQ   SEQUENCE   142 AA;  16024 MW;  DE29E6CFE745DF3B CRC64;

alignment_scores:
        Quality:   396.50                 Length:       144
        Ratio:     3.304                   Gaps:         3
Percent Similarity:  83.333       Percent Identity:  52.778

alignment_block:
US-09-019-441-4 x HV01_RAT         ..

Align seg 1/1  to: HV01_RAT   from: 1  to: 142

   1 ATGGAGTTGGCTGAGCTGGTTTTCCTTGTTCCTCTTTTGAAAGTGT  50
     |||::::: |||::::||||::|||||:||| :::||||||||||
   1 MetAspLeuArgLeuThrTyrValPheIleValAlaIleLeuLysGlyVa  17

  51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
     | ||||||||:::|||  |||||||||::||||||||||:||||||:|||
  17 lLeuCysGluValLysLeuGluGlySerGlyGlyLeuValGlnProG  34

 101 GGGGGTCCCTGAGACTCTGGTGCGAGCCTCCGGGTTCAGGTTCACCTTC 150
     ||   |||||||||| |||||| |||||||||||||||||    |||||
  34 lyMetSerValLysSerLeuSerCysAlaThrSerGly......PheThrPhe  48

 151 AATAACTACTACATGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
     :::::||||||||||||:||| |||||||||||||||||||:|||||||
  49 SerAspTyrTrpMetGluTrpValArgGlnAlaProGlyLysGlyLeuGl  65

 201 GTGGGTCTCACGTATTAGTAGTAGTGGTGAT.....CCCACATGGTACG 244
     |||||||::||:::::|||   :::|||||||       ::||:|||
  65 uTrpValAlaGluIleArgAsnLysAlaAsnAsnTyrValAlaTyrYrG  82

 245 CAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAAC 294
     ::  ||||:|||||||||||||||||||||||||||||||||||||||
  82 lyLysSerLeuLysGlyArgPheThrLeuSerArgAspAspSerLysSer  98

```
295 ACACTGTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTA 344
    :::::|||||||||||||||:::::|||||||||||||::::::||
 99 IleValTyrLeuGlnMetAsnAsnIleArgSerGluAspThrGlyIleTy 115

345 TTACTGTGCGAGCTTGACTACAGGGTCTGACTCC..............T 379
    |||||||:::       |||    ::::::                   |
115 rTyrCysSerArgGlyTyrGlyTyrSerGluAsnTrpPheValTyrT 132

380 GGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
    |||||||||||::||||||||||||||||||||
132 rpGlyGlnGlyThrLeuValThrValSerSer 142
```

OM of: US-09-019-441-4 to: SPTREMBL_19:*     out_format : pfs

Date: Sep 23, 2002 10:23 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09019441/runat_23092002_095259_6361/app_query.fasta_1.1860
-DB-SPTREMBL_19 _QFMT=fastan -SUFFIX=rspt -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09019441 @CGN1_1.409 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-019-441-4
Query length: 411
Database: SPTREMBL_19:*
Database sequences: 562222
Database length: 172994929
Search time (sec): 228.280000

score_list:

| Sequence | Strd | Orig | ZScore | EScore | Len | ! Documentation |
|---|---|---|---|---|---|---|
| sp_human:Q96BB9 | + | 532.50 | 1012.41 | 8.0e-49 | 597 | ! Q96bb9 homo sapiens (human). hy |
| sp_human:Q96K68 | + | 503.00 | 956.98 | 1.2e-45 | 494 | ! Q96k68 homo sapiens (human). cc |
| sp_rodent:Q99KA4 | + | 465.00 | 883.42 | 1.5e-41 | 487 | ! Q99ka4 mus musculus (mouse). hy |
| sp_rodent:Q91Z05 | + | 455.00 | 864.30 | 1.8e-40 | 473 | ! Q91z05 mus musculus (mouse). hy |
| sp_rodent:Q91WP5 | + | 449.50 | 853.51 | 7.1e-40 | 479 | ! Q91wp5 mus musculus (mouse). hy |
| sp_rodent:Q91XE1 | + | 442.50 | 839.92 | 4.1e-39 | 480 | ! Q91xe1 mus musculus (mouse). un |
| sp_human:Q9UL71 | + | 437.50 | 843.23 | 1.1e-38 | 121 | ! Q9ul71 homo sapiens (human). my |
| sp_rodent:Q91Z07 | + | 434.50 | 824.28 | 3.0e-38 | 486 | ! Q91z07 mus musculus (mouse). my |
| sp_human:Q9UL91 | + | 429.00 | 826.98 | 8.7e-38 | 118 | ! Q9ul91 homo sapiens (human). my |
| sp_human:Q9HCC1 | + | 423.00 | 815.84 | 3.8e-37 | 112 | ! Q9hcc1 homo sapiens (human). si |
| sp_human:Q9UL90 | + | 421.50 | 812.84 | 5.6e-37 | 113 | ! Q9ul90 homo sapiens (human). my |
| sp_human:Q9UL84 | + | 412.00 | 793.70 | 6.0e-36 | 122 | ! Q9ul84 homo sapiens (human). my |
| sp_human:Q9UL93 | + | 410.50 | 791.26 | 8.6e-36 | 116 | ! Q9ul93 homo sapiens (human). my |
| sp_human:Q9UL72 | + | 410.00 | 790.13 | 9.8e-36 | 118 | ! Q9ul72 homo sapiens (human). my |
| sp_rodent:Q920E7 | + | 401.50 | 773.57 | 8.1e-35 | 119 | ! Q920e7 mus musculus (mouse). pt |
| sp_human:Q9UL88 | + | 394.50 | 759.08 | 4.7e-34 | 131 | ! Q9ul88 homo sapiens (human). my |
| sp_human:Q9Y509 | + | 393.00 | 755.09 | 7.1e-34 | 147 | ! Q9y509 homo sapiens (human). vh |
| sp_human:Q9UL6 | + | 380.00 | 733.99 | 1.6e-32 | 95 | ! Q9ulb6 homo sapiens (human). imu |
| sp_rodent:Q9QYF0 | + | 352.00 | 668.99 | 2.2e-29 | 298 | ! Q9qyf0 mus musculus (mouse). cr |
| sp_human:Q9UL92 | + | 344.00 | 661.96 | 1.3e-28 | 124 | ! Q9ul92 homo sapiens (human). my |
| sp_human:Q9UGP3 | + | 342.50 | 659.71 | 1.9e-28 | 112 | ! Q9ugp3 homo sapiens (human). in |
| sp_rodent:Q9RIA4 | + | 340.00 | 642.01 | 4.7e-28 | 437 | ! Q9ria4 mus musculus (mouse). ga |
| sp_rodent:Q9D8L4 | + | 339.50 | 640.29 | 5.4e-28 | 473 | ! Q9d8l4 mus musculus (mouse). 18 |
| sp_human:Q9UL87 | + | 334.50 | 644.89 | 1.4e-27 | 104 | ! Q9ul87 homo sapiens (human). my |
| sp_human:Q96QS0 | + | 327.00 | 626.34 | 9.6e-27 | 159 | ! Q96qs0 homo sapiens (human). pu |
| sp_human:Q9UL95 | + | 324.50 | 623.76 | 1.7e-26 | 125 | ! Q9ul95 homo sapiens (human). my |
| sp_mammal:Q9N0W4 | + | 322.00 | 618.99 | 3.2e-26 | 124 | ! Q9n0w4 oryctolagus cuniculus (r |
| sp_mammal:Q9N0W6 | + | 319.00 | 613.17 | 6.7e-26 | 124 | ! Q9n0w6 oryctolagus cuniculus (r |
| sp_human:Q9UL94 | + | 310.50 | 597.08 | 5.5e-25 | 119 | ! Q9ul94 homo sapiens (human). my |
| sp_human:Q99LA6 | + | 308.50 | 579.95 | 1.2e-24 | 484 | ! Q99la6 mus musculus (mouse). hy |
| sp_human:Q9BRV0 | + | 308.00 | 578.67 | 1.4e-24 | 500 | ! Q9brv0 homo sapiens (human). hy |
| sp_human:Q91WT1 | + | 307.50 | 578.10 | 1.6e-24 | 481 | ! Q91wt1 mus musculus (mouse). un |
| sp_human:Q96GA6 | + | 302.50 | 566.07 | 5.7e-24 | 614 | ! Q96ga6 mus musculus (mouse). ur |
| sp_rodent:Q924P9 | + | 301.00 | 576.92 | 6.1e-24 | 143 | ! Q924p9 mus musculus (mouse). v3 |
| sp_human:Q99L31 | + | 300.50 | 564.75 | 8.8e-24 | 468 | ! Q99l31 mus musculus (mouse). si |
| sp_rodent:Q99LC4 | + | 300.00 | 563.88 | 1.0e-23 | 463 | ! Q99lc4 mus musculus (mouse). si |
| sp_rodent:Q99M22 | + | 296.50 | 556.78 | 2.4e-23 | 479 | ! Q99m22 mus musculus (mouse). hy |
| sp_rodent:Q924R2 | + | 295.50 | 566.45 | 2.4e-23 | 140 | ! Q924r2 mus musculus (mouse). vh |
| sp_rodent:Q92IC4 | + | 295.00 | 567.09 | 2.6e-23 | 118 | ! Q92ic4 mus musculus (mouse). ar |
| sp_rodent:Q921A6 | + | 295.00 | 560.35 | 3.0e-23 | 241 | ! Q921a6 mus musculus (mouse). ar |

```
sp_invertebrate:Q9GYz2   + 293.50  564.10  3.8e-23  119  ! Q9gyz2 schistosoma japonic
sp_rodent:Q924R5         + 291.00  557.79  7.3e-23  139  ! Q924r5 mus musculus (mouse).
sp_rodent:Q924Q9         + 290.00  555.45  9.4e-23  145  ! Q924q9 mus musculus (mouse).
sp_human:O95973          + 290.00  555.13  9.5e-23  150  ! O95973 homo sapiens (human).
sp_rodent:Q921K1         + 290.00  549.31  1.1e-22  278  ! Q921k1 mus musculus (mouse).
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seq_name: sp_human:Q96BB9

seq_documentation_block:
ID  Q96BB9      PRELIMINARY;      PRT;      597 AA.
AC  Q96BB9;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  HYPOTHETICAL 65.0 KDA PROTEIN.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA  Strausberg R.;
RL  Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; BC015760; AAH15760.1; -.
KW  Hypothetical protein.
SQ  SEQUENCE  597 AA;  65039 MW;  4FCA3ADBECE263D9 CRC64;

alignment_scores:
          Quality:  532.50                    Length:  146
          Ratio:    4.260                      Gaps:    2
Percent Similarity: 85.616     Percent Identity: 71.918

alignment_block:
US-09-441-4 x Q96BB9

Align seg 1/1 to: Q96BB9   from: 1  to: 597

```
  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTTTTGAAAGGTGT 50
    |||||||||||||||||||||||||||||||::|||||| ::|||||||
  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGCGGCCTTGCAAAGCCTG 100
    |||||||||||||||||||||||||||||||||||||||::::|||||||
 17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG 34

101 GGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    |||||||||||||||  ||||||||||||||||     |||::|||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheSerPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    :::|||::|||||||||||||||||||||||||||||||||:||:||||||
 49 SerSerTyrAlaMetAsnTrpValArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTGGTGATCCCACATGGTACGGCAGAGCT 250
    |||||||||| |||||::|||||  ||||||:||:|||||::||:|||||
 65 uTrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyrAlaAspS 82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
    |||||||||||||||::|||::||||||||:||||:||:::|||:||||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerArgAspThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
    ::||::|||||||||||||||||||:||:||||::||:|||::||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

351 TGCGAGCTTGACTACAGGG.................TCTG 373
    ::|||::  ||                       ||||||
115 sAlaLysAspProArgGlyTyrSerAlaSerGlyAsnTyrThrArgGluA 132

374 ACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
    ||  ||||||||||||||||||||||::|||||||||||
```

```
      132 spTyrTrpGlyGlnGlyThrLeuValThrValSerSer 144

seq_name: sp_human:Q96K68

seq_documentation_block:
ID   Q96K68        PRELIMINARY;     PRT;    494 AA.
AC   Q96K68;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CDNA FLJ14473 FIS, CLONE MAMMA1001080, HIGHLY SIMILAR TO HOMO
DE   SAPIENS SNC73 PROTEIN (SNC73) MRNA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MAMMARY GLAND;
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA   Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Chiba S., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA   Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA   Ninomiya K., Iwayanagi T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK027379; BAB55072.1; -.
SQ   SEQUENCE  494 AA;  53088 MW;  9A1D7AEB5AEE4C0E CRC64;

alignment_scores:
           Quality:   503.00                    Length:   143
           Ratio:       4.123                    Gaps:       2
Percent Similarity:   85.315    Percent Identity:   69.930

alignment_block:
US-09-019-441-4 x Q96K68

Align seg 1/1  to: Q96K68  from: 1  to: 494

  1 ATGGAGTTTGGGCTGAGCTCGGTTTTCCTTGTTCCTCTTTTGAAAGGTGT 50
    |||||||:::|||||| ||||||||||  :::||||::||||
  1 MetGluLeuGlyLeuArgTrpValPheLeuValAlaPheLeuGluGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCCGCTGGCAAAGCCTG 100
    |||||||||||||||||||||||||||||||:|||||::||||||
 17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValLysProG 34

101 GGGGGTCCCTGAGACTCTGTGCGCCAGCTCCGGGTTCAGGTTCACCTTC 150
    |||||||||||||||||||| ::|||  ||||||||| :::||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly.....LeuSerPhe 48

151 AATACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    ::::::||| ||:||||||:|||||||||||||||::||||
 49 SerThrTyrAlaMetAsnTrpValArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCCAGACT 250
    ::||||||||  :::||  :::||| ||:||| :::|||||||||||
 65 uTrpValSerSerIleSerSerArgSerAspTyrIleTyrTyrArgAspS 82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAAGAACGCCAACAACACACTG 300
    |||||||||||||||||||::||||||||||||||||:::||||
 82 erValLysGlyArgPheThrIleSerArgArgAspAsnAlaLysAsnLeu 98

301 TTTCTTCAAATGAACAGCTGAGAGCTGAGGACACGACGCTGTCTATTACTG 350
    ::|||||||||||||||||:||||||||||||||||::::||||
 99 TyrLeuGlnMetAsnSerLeuArgValAspAspThrAlaValTyrTyrCy 115

351 TGCG.....................AGCTTGACTACAGGGTCTGACTCCTGG 382
    |||                   ::  :: |||||||||||||
115 sAlaArgAspSerCysAsnGlyAlaIleCysTyrGlyPheSerProTrpG 132
```

```
      383 GCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
          ||||||| :::|||||||||||||||||
      132 lyGlnGlyThrLeuValThrValSerSer 141

seq_name: sp_rodent:Q99KA4

seq_documentation_block:
ID   Q99KA4        PRELIMINARY;     PRT;    487 AA.
AC   Q99KA4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 52.6 KDA PROTEIN.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC004786; AAH04786.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003599; Ig_cl.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE  487 AA;  52554 MW;  7DC8E96DB333077B CRC64;

alignment_scores:
           Quality:   465.00                    Length:   145
           Ratio:       3.908                    Gaps:       2
Percent Similarity:   82.069    Percent Identity:   64.138

alignment_block:
US-09-019-441-4 x Q99KA4

Align seg 1/1  to: Q99KA4  from: 1  to: 487

  1 ATGGAGTTTGGGCTGAGCTCGGTTTTCCTTGTTCCTCTTTTGAAAGGTGT 50
    |||:::|||||||||||| ||||||||||  :::||||||::||||
  1 MetAsnPheGlyLeuSerLeuIlePheLeuValLeuValLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCCGCTTGGCAAAGCCTG 100
    ||||||||||||||||||||||||||||||:||||:::||||||
 17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValLysProG 34

101 GGGGGTCCCTGAGACTCTGTGCGCCAGCCTCCGGGTTCAGGTTCACCTTC 150
    |||||||||||||||||||||| ||||  ||||||||| :::||||
 34 lyGlySerLeuSerLeuSerCysAlaAlaSerGly......PheThrPhe 48

151 AATACTACTACATGGACTGGGTCCGCCAGGCTCCGCCAGGCCAGGGGCTGGA 200
    ::::::||| |||:|||||||||||||||||:::||||||
 49 SerSerTyrAlaMetSerTrpValArgGlnThrProGluLysArgLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCATGGTGGTACGCCAGACT 250
    ||||||:::  ::::||  :::||| |||||  :::|||  :::|||
 65 uTrpValAlaThrIleSerSerAspGlyGlySerTyrThrTyrTyrProAspA 82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
    :::|||||||||||||||||::||||||||||||||||:::|||
 82 snValLysGlyArgPheThrIleSerArgArgAspAsnAlaLysAsnLeu 98
```

```
301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTCTATTACTG 350
    ::|||||||||:::  ||:::||||||||:::|||||||||||:|||||
 99 TyrLeuGlnMetSerHisLeuLysSerGluAspThrAlaMetTyrTyrCy 115

351 TGCGAGCTTGACTACAGGGTCT................GACT 376
    |||||                               |||
115 sAlaArgAspMetGlyGlySerProTyrGlyTyrSerArgPheAspT 132

377 CCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
    |||||||||||:::  :::|||||||||||
132 yrThrGlyIleGlyThrThrIleThrValSerSer 143
```

seq_name: sp_rodent:Q91Z05

seq_documentation_block:
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ID   Q91Z05        PRELIMINARY;       PRT;    473 AA.
AC   Q91Z05;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 51.9 KDA PROTEIN.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010327; AAH10327.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE  473 AA;  51946 MW;  CF625F008932AF12 CRC64;
```

alignment_scores:
```
       Quality:    455.00              Length:   139
       Ratio:        3.991             Gaps:       2
Percent Similarity:  82.014     Percent Identity:  66.906
```

alignment_block:
US-09-019-441-4 x Q91Z05     ..

Align seg 1/1  to: Q91Z05  from: 1  to: 473

```
  1 ATGGAGTTGGGCTGAGCTGGGTTTCCTTGTTCCTCTTTGAAAGGTGT 50
    |||:::  ||::: ||||||||||  ::||||||
  1 MetAspSerArgLeuAsnLeuValPheLeuValLeuIleLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
    ||||||||||||||||||||||||||||||::|||||
 17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValLysProG 34

101 GGGGGTCCCTGAGACTCTGTGCGCAGCCTCCGGGTTCACCTTC 150
    |||||||||  :::|||||:::|||||||
 34 lyGlySerLeuSerValSerCysAlaAlaSerGly......PheThrPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGGCTGGA 200
    ::::||||  |||  ::||||||||
 49 SerAspTyrGlyMetHisTrpValArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTGGTGATCGTACCGCAGACT 250
    :::::||  |||  ::||||||||
 65 uTrpValAlaTyrIleAsnSerGlySerThrThrIleTyrTyrAlaAspT 82

251 CCGTGAAGGGCAGAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG 300
    ::|||||||||:::||||||:::||||||
 82 hrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTCTATTACTG 350
    ||||||||:::|||||||||:::||||||
 99 PheLeuGlnMetThrSerLeuArgSerGluAspThrAlaMetTyrTyrCy 115

351 TGCGAGC......TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCC 394
```

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```
115 sAlaArgGluLeuTrpLeuArgArgIleAspTyrTrpGlyGlnGlyThrT 132

395 TGGTCACCGTCTCCTCA 411
    :::||||||||||
132 hrIleThrValSerSer 137
```

seq_name: sp_rodent:Q91WP5

seq_documentation_block:
```
ID   Q91WP5        PRELIMINARY;       PRT;    479 AA.
AC   Q91WP5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 51.6 KDA PROTEIN.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013656; AAH13656.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE  479 AA;  51603 MW;  ECB2D0877748584F CRC64;
```

alignment_scores:
```
       Quality:    449.50              Length:   139
       Ratio:        3.842             Gaps:       3
Percent Similarity:  84.173     Percent Identity:  64.748
```

alignment_block:
US-09-019-441-4 x Q91WP5     ..

Align seg 1/1  to: Q91WP5  from: 1  to: 479

```
  1 ATGGAGTTGGGCTGAGCTGGGTTTCCTTGTTCCTCTTTGAAAGGTGT 50
    |||:::||||||||:::  ::|||||||||
  1 MetAsnPheGlyLeuThrLeuIlePheLeuValLeuThrLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
    ||||||||||||||||||||||||||||:::||||||
 17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValLysProG 34

101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCACCTTC 150
    ||||||||  :::|||||:::  ||||||
 34 lyGlySerLeuLysValSerCysAlaAlaSerGly......LeuThrPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGGGCTGGA 200
    ::::||||||  :::|||||||  ||||
 49 SerAsnTyrAlaMetSerTrpValArgGlnSerProGluLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTGGTGATCGTACCGCAGACT 250
    ||||||  :::|||||  :::|||
 65 uTrpValAlaAlaIleAsnSerAsnGlyGlyAsnThrTyrTyrSerAspT 82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAAGAACGCCAACAACACTG 300
    :::||||||||  :::|||||:::||||||
 82 hrMetLysGlyArgPheThrIleSerArgAspAsnAlaLysSerThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTCTATTACTG 350
    :::||||||:::|||||||  ||||||||
 99 TyrLeuGlnMetSerSerLeuArgSerGluAspGluAlaPheThrTyrTyrCy 115

351 TGCGAGCTTGACTACAGGGTCT.....GACTCCTGGGGCCAGGGAGTCC 394
    |      |||:::  |||
115 s........ValArgGlyGlyTyrPheAspValTrpGlyAlaGlyThrA 129

395 TGGTCACCGTCTCCTCA 411
```

```
            |||||||||||
        129 laValThrValSerSer 134

seq_name: sp_rodent:Q91XE1

seq_documentation_block:
ID   Q91XE1       PRELIMINARY;       PRT;   480 AA.
AC   Q91XE1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   UNKNOWN (PROTEIN FOR IMAGE:4224494) (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010798; AAH10798.1; -.
FT   NON_TER      1      1
SQ   SEQUENCE    480 AA;   51936 MW;   20B9234EEF2B41ED CRC64;

alignment_scores:
           Quality:    442.50            Length:   139
             Ratio:     3.916              Gaps:     3
Percent Similarity:    81.295     Percent Identity:  66.187

alignment_block:
US-09-019-441-4 x Q91XE1

Align seg 1/1  to: Q91XE1  from: 1  to: 480

  7 TTTGGGCTGAGCTGGTTTTCCTTGTTCCCTCTTTTGAAAGGTGTCCAGTG 56
    |||||||||||  :::|||||||       ::||||||||||||||||||
  2 PheGlyLeuSerLeuIlePheLeuValLeuIleLeuLysGlyValLeuCy 18

 57 TGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGT 106
    |:::||||||||||||||||||||||||||||||||||||::|||||||
 18 sAspValLysLeuValGluSerGlyGlyGlyLeuValLysProGlyGlyLys 35

107 CCCTGAGACTCTGTGCCGCCAGCCTCCGGGTTCAGGTTCACCTTCAATAAC 156
    |||||||| ||||||||||||||   ||||||||   :::||
 35 erLeuArgLeuSerCysAlaAlaSerGly......PheIlePheSerAsn 49

157 TACTACATGGACTGGTCCGCCAGGCCCAGGGGCTGGAGTGGGT 206
    |||||||||||||:::||||||||    :::  |||||||||||
 50 SerTyrMetSerTrpValArgGlnThrProGluLysArgLeuGluTrpVa 66

207 CTCACGTATTAGTAGTGGTGATCCCACATGGTACGCCAGACTCCGTGA 256
    |:::  |||||||:::||||      |||   |||  :::|||||:::|
 66 lAlaThrIleSerAsnSerGlyTyrAlaThrHisTyrProAspSerMetL 83

257 AGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTGTTCTT 306
    |||||||||  ::::|||||||  ::|||||  :::|||  ::|||||
 83 ysGlyArgPheThrIleSerArgAspAsnAlaGlnAsnThrValLeuLeu 99

307 CAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAG 356
    |||||||||||:::|||||||||||||||||||||||||||||||||:::
100 GlnMetThrSerLeuAsnSerGluAspThrAlaValTyrTyrCys..... 114

357 CTTGACTCAGGGTCT..........GACTCCTGGGGCCAGGGAGTCC 394
    |||  :::::            |||||||  ||||||  :::::
115 ...ThrArgGlyAspTyrTyrPheTyrPheAspValTrpGlyAlaGlyThrT 130

395 TGGTCACCGTCTCCTCA 411
    |||||||||||||||||
136 hrValThrValSerSer 135

seq_name: sp_human:Q9UL71
```

```
seq_documentation_block:
ID   Q9UL71       PRELIMINARY;       PRT;   121 AA.
AC   Q9UL71;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035043; AAD56279.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    121    121
SQ   SEQUENCE    121 AA;   13154 MW;   2F045CCFA5D50736 CRC64;

alignment_scores:
           Quality:    437.50            Length:   123
             Ratio:     4.051              Gaps:     3
Percent Similarity:    87.805     Percent Identity:  71.545

alignment_block:
US-09-019-441-4 x Q9UL71

Align seg 1/1  to: Q9UL71  from: 1  to: 121

 58 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGTC 107
    |||||||||||||||||||||||||||||||||||    :::||||||||
  1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySe 17

108 CCTGAGACTCTCGGTGCGCCAGCCTCCGGGTTCAGGTTCACCTTCAATAACT 157
    ||||||||| ||:::||||||||       |||||||||   ::||||::::
 17 rLeuArgLeuPheCysAlaAlaSerGly......PheThrPheAspGlyT 32

158 ACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTC 207
    ||  ||| ||||||||:::||||||||||   ::::|||||||||||||||
 32 yrAlaMetHisTrpValArgGlnAlaProGlyLysGlyLeuGluTrpVal 48

208 TCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCCAGACTCCGTGAA 257
    |||  |||||||:::|||||      |||   |||   :::|||||  ||||
 49 SerLeuIleSerGlyAspGlyGlySerThrTyrTyrAlaAspSerValLy 65

258 GGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTGTTCTTC 307
    ||||||||  :::||||||   ::|||||||  ::|||  :::||||
 65 sGlyArgPheThrIleSerArgAspAsnSerLysAsnSerLeuTyrLeuG 82

308 AAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCG... 354
    |||||||||||:::||||||||||||||||||||||||:::||||||
 82 lnMetAsnSerLeuArgAlaGluAspThrAlaLeuTyrTyrCysAlaLys 98

355 ...AGCTTGACTACA........GGGTCTGACTCCTGGGGCCAGGGAGT 392
    |||||:::::           |||   |||  ||||||  :::
 99 GlyLysValThrThrIleTyrArgArgPheAspIleTrpGlyGlnGlyTh 115

393 CCTGGTCACCGTCTCCTCA 411
    :::|||||||||||||||
115 rMetValThrValSerSer 121
```

seq_name: sp_rodent:Q91Z07

seq_documentation_block:
ID    Q91Z07        PRELIMINARY;        PRT;    486 AA.
AC    Q91Z07;
DT    01-DEC-2001 (TrEMBLrel. 19, Created)
DT    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT    01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE    HYPOTHETICAL 52.7 KDA PROTEIN.
OS    Mus musculus (Mouse).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX    NCBI_TaxID=10090;
RN    [1]
RP    SEQUENCE FROM N.A.
RA    Strausberg R.;
RL    Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; BC010324; AAH10324.1; -.
KW    Hypothetical protein.
SQ    SEQUENCE   486 AA;   52682 MW;   4FEF835125DA870B CRC64;

alignment_scores:
          Quality:    434.50              Length:      145
          Ratio:       3.682              Gaps:          4
Percent Similarity:   81.379      Percent Identity:   61.379

alignment_block:
US-09-019-441-4 x Q91Z07    ..

Align seg 1/1  to: Q91Z07  from: 1  to: 486

  1 ATGGAGTTGGCTGAGCTGGGTTTCCTTGTCCTCTTTTGAAAGGTGT 50
    |||:|||||||||             |||||||||||:||||||
  1 MetAsnPheGlyLeuArgLeuIlePheLeuValAlaLeuLysGlyVa 17

 51 CCAGTGTCAGGTCGAGCTGGCAGCTGGAGCTGGGGGCGGCTTGGCAAAGCCTG 100
    ||||||||||:||||||||||||||||||:||||::||||||
 17 lGlnCysGluValHisLeuValGluSerGlyGlyGlyLeuValLysProG 34

101 GGGGGTCCCTGAGACTCTGGTGCGCAGCTCCGGGTTCAGGTTCACCTTC 150
    ||||:|||||  |||::|:|||||||||||||||||  ||||||
 34 lyGlySerLeuLysLeuSerCysValValSerGlyPheSerPheThr... 49

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    :::||| |||:||||||||||||||:::||||  |||||
 50 ...SerTyrAspMetSerTrpValArgGlnThrProGluArgArgLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    ||||||:|| |||:||:|:||:::  |||| ||:|||||||
 65 uTrpValAlaAlaIleThrSerGlyGlyAsn...ThrTyrTyrProAspA 81

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACACACACTG 300
    ::||||||||||::||||:::::|||||:|| ||||||
 81 snValLysGlyArgPheThrValSerArgAspAsnAlaAsnThrThrLeu 97

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACGTGTCTATTACTG 350
    ::|||||||||  |||||||||||::|||||||||||||
 98 TyrLeuGlnMetSerSerLeuLysSerGluAspThrAlaMetTyrTyrCy 114

351 TGCGGAGC.........TTGACTACAGGGTCT......GACT 376
    |:||       |||||:|||||
114 sValArgProGlyIleProIleTyrTyrTyrSerGlySerTyrPheAspS 131

377 CCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
    |||||||||||::||:  :::||||||||||||
131 erTrpGlyGlnGlyThrThrIleThrValSerSer 142

seq_name: sp_human:Q9UL91

seq_documentation_block:
ID, Q9UL91        PRELIMINARY;        PRT;    118 AA.
AC    Q9UL91;
DT    01-MAY-2000 (TrEMBLrel. 13, Created)
DT    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT    01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE    MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE    (FRAGMENT).
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=98277139; PubMed=9614934;
RA    Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA    Young D.C.;
RT    "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT    fetus.";
RL    Clin. Immunol. Immunopathol. 87:184-192(1998).
DR    EMBL; AF035023; AAD56259.1; -.
DR    HSSP; P01772; 2FB4.
DR    InterPro; IPR003006; Ig_MHC.
DR    InterPro; IPR003596; Ig_v.
DR    Pfam; PF00047; ig; 1.
DR    SMART; SM004406; IGv; 1.
FT    NON_TER      1      1
FT    NON_TER    118    118
SQ    SEQUENCE   118 AA;   12843 MW;   D063949F2AC149D CRC64;

alignment_scores:
          Quality:    429.00              Length:      119
          Ratio:       4.125              Gaps:          2
Percent Similarity:   87.395      Percent Identity:   73.109

alignment_block:
US-09-019-441-4 x Q9UL91    ..

Align seg 1/1  to: Q9UL91  from: 1  to: 118

 58 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCCAAAGCCTGGGGGGTC 107
    |||||||||||||||||||||||||||||||:::||:||||||||||
  1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySe 17

108 CCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACT 157
    |||||||        ||||||||||||  ||||||||||:
 17 rLeuArgLeuSerCysAlaAlaSerGly......PheThrPheSerSerT 32

158 ACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTC 207
    ||  |||::||||||||||||||||||||||||:|||||||||||
 32 yrSerMetAsnTrpValArgGlnAlaProGlyLysGlyLeuGluTrpVal 48

208 TCACGTATTAGTAGTAGTGGTGATCCACCATGGTACGCAGACTCCTGAA 257
    :::|||||||||||:|||:||||:|||||||||||||
 49 SerTyrIleSerSerThrIleIleTyrTyrAlaAspSerValLy 65

258 GGGCAGATTCACCATCTCCAGAGAGAACGCCAACACACTGTTTCTTC 307
    |||||||||||||||||::||||:::|||::|||||
 65 sGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeuTyrLeuG 82

308 AAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCG... 354
    |||||||||||||||||||||||||||||||||
 82 lnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArg 98

355 ...AGCTTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCAC 401
    :::     |||  :::::||||||||||||||::::||||
 99 GlyAspSerGluAlaPheAspIleTrpGlyGlnGlyThrMetValTh 115

402 CGTCTCC 408
    ||||||
115 rValSer 117

seq_name: sp_human:Q9HCC1

```
seq_documentation_block:
ID   Q9HCC1      PRELIMINARY;    PRT;   112 AA.
AC   Q9HCC1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SINGLE CHAIN FV (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT   "An antibody fragment2A3 specific for native lysozyme :Isolaion from a
RT   human synthetic phage display library and characterization.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB049915; BAB16829.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
FT   NON_TER      1     1
FT   NON_TER      112   112
SQ   SEQUENCE   112 AA;  12243 MW;  24F1A45EC3B84788 CRC64;


alignment_scores:
          Quality:   423.00              Length:  114
          Ratio:     4.273               Gaps:    1
Percent Similarity: 86.842   Percent Identity: 72.807

alignment_block:
US-09-019-441-4 x Q9HCC1

Align seg 1/1  to: Q9HCC1  from: 1  to: 112

 58 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGCAAAGCCTGGGGGGGTC 107
    ||||||||||||||||||||||||:::||||::||||||||||||
  1 GluValGlnLeuValGluSerGlyGlyGlyValGlyValArgProGlyGlySe 17

108 CCTGAGACTCTGGTCGCGAGCCTCCGGTTCAGGTTCACCTTCAATAACT 157
    ||||||::     ||||||||||||||||          ||:::::::|
 17 rLeuArgIleSerCysAlaAlaSerGly......PheThrPheAspAspT 32

158 ACTACATGGACTGGGTCCGCCCAGGCAGGGGCTGGAGTGGGTC 207
    ||  |||  ||:|||||||||||||||::|||||||||
 32 yrGlyMetSerTrpValArgGlnAlaProGlyLysGlyLeuGluTrpVal 48

208 TCACGTATTAGTAGTGGTGATCCCACATGGTACGCAGACTCCGTGAA 257
    |||  |||        :::|||||:     :::|||||||||||
 49 SerGlyIleAsnTrpAsnGlyGlySerThrGlyTyrAlaAspSerValLy 65

258 GGGCAGATTCACCATCTCCAGAGAGACGCCAACAACACACTGTTTCTTC 307
    |||||||||||||||||||||||:::||:||||||||||||||
 65 sGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeuTyrLeuG 82

308 AAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 357
    |||||||||||||||||||||||||:::||||||||||||
 82 lnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArg 98

358 TTGACTACAGGGTCGACTCCTGGGCCCAGGGAGTCCTGGTC 399
    ||       ||||||||||||||::||||||||||
 99 ArgArgTyrAlaLeuAspTyrTrpGlyGlnGlyThrLeuVal 112

seq_name: sp_human:Q9UL90

seq_documentation_block:
```

```
ID   Q9UL90      PRELIMINARY;    PRT;   113 AA.
AC   Q9UL90;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035024; AAD56260.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1     1
FT   NON_TER      113   113
SQ   SEQUENCE   113 AA;  12437 MW;  ED57FDD19086D07F CRC64;


alignment_scores:
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          Ratio:     4.132               Gaps:    2
Percent Similarity: 86.441   Percent Identity: 72.034

alignment_block:
US-09-019-441-4 x Q9UL90

Align seg 1/1  to: Q9UL90  from: 1  to: 113

 58 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGGTC 107
    ||||||||||||||||||||||||:::||||::||||||||||||
  1 GluValGlnLeuValGluSerGlyGlyGlyValGlyValGlnProGlyGlySe 17

108 CCTGAGACTCTGGTGCGCGAGCCTCCGGTTCAGGTTCACCTTCAATAACT 157
    ||||||||  |||||||||||||||||          ||||:::::|
 17 rLeuArgLeuSerCysAlaAlaSerGly......PheThrPheSerSerT 32

158 ACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTC 207
    ||  |||  ||:||||||||||||||::||||||||||||||
 32 yrGlyMetHisTrpValArgGlnAlaProGlyLysGlyLeuGluTrpVal 48

208 TCACGTATTAGTAGTGGTGATCCCACATGGTACGCAGACTCCGTGAA 257
    :::  |||        :::||||||:     :::||||||||||
 49 AlaPheIleArgTyrAspGlySerAsnLysTyrTyrAlaAspSerValLy 65

258 GGGCAGATTCACCATCTCCAGAGAGACGCCAACAACACACTGTTTCTTC 307
    ||||||||||||||||||||||||:::||:||||||||||||||
 65 sGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyrLeuG 82

308 AAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 357
    ||||||||||||||||||||||||::::|||||||||||
 82 lnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLys 98

358 TTGACTACAGGGTCGACTCCTGGGCCCAGGGAGTCCTGGTCACCGTCTC 407
    ||       |||||||||||||||||:::|||||||||||||
 99 ........AspLeuAsnTyrTrpGlyGlnGlyThrLeuValThrValSe 112

408 CTCA 411
    ||||
112 rSer 113

seq_name: sp_human:Q9UL84
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AC   Q9UL84;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035030; AAD56266.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    122    122
SQ   SEQUENCE   122 AA;  13579 MW;  36054D4136654548B8 CRC64;
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Percent Similarity:  82.258   Percent Identity:  68.548
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alignment_block:
US-09-019-441-4 x Q9UL84

Align seg 1/1  to: Q9UL84  from: 1 to: 122

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 58 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGCAAAGCCTGGGGGGTC 107
    |||||||||||||||||||||||||||::::::::|||| ||||
  1 GluValGlnLeuValGluSerGlyGlyGlyValValGlnProGlyArgSe 17

108 CCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACT 157
    |||||||||  |||||||||||    ||||||||:::::||||
 17 rLeuArgLeuSerCysAlaAlaSer......ArgPhePheSerAsnT 32

158 ACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTC 207
    || |||  ||||||||||||||||||:::|||||||||||
 32 yrGlyMetHisTrpValArgGlnAlaProGlyLysGlyLeuGluTrpVal 48

208 TCACGTATTAGTAGTGGTGATCCCACATGGTACGCAGACTCCGTGAA 257
    ::: ||||||||||::: :|||||||||||||||||||
 49 AlaAlaIleSerAsnAspGlySerAsnLysPheTyrAlaAspSerValLy 65

258 GGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTGTTTCTTC 307
    ||||||||||||  |||||||||:::::|||  :::  |||
 65 sGlyArgPheThrIleSerArgAspAsnSerLysAsnMetMetAspLeuG 82

308 AAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 357
    ||||||||||||||||||||||||:::::|||
 82 lnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLys 98

358 ..........TTGACTACAGGGTCTGACTCCTGGGGCCAGGG 389
    :::  |||  |||||||||||
 99 AspGluArgGlyArgLeuValGlyThrTyrPheAspTyrTrpGlyGlnGl 115

390 AGTCCTGGTCACCGTCTCCTCA 411
    ::|||||||||||||||
115 yThrLeuValThrValSerSer 122
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seq_name: sp_human:Q9UL93

seq_documentation_block:
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AC   Q9UL93;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035021; AAD56257.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    116    116
SQ   SEQUENCE   116 AA;  12434 MW;  0DA0348154DD6061 CRC64;
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alignment_scores:
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                   Ratio:    4.064              Gaps:    2
Percent Similarity:  85.593   Percent Identity:  71.186
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alignment_block:
US-09-019-441-4 x Q9UL93

Align seg 1/1  to: Q9UL93  from: 1 to: 116

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 61 GTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCT 110
    ||||||||||||||||||||||||||::::::::|||| |||||
  1 ValGlnLeuValGluSerGlyGlyGlyValValGlnProGlyArgSerLe 17

111 GAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACT 160
    ||||| |||||||||||||    ||||||||:::::||||
 17 uArgLeuSerCysAlaAlaSerGly......PheThrPheSerSerTyrA 32

161 ACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCA 210
    ||||  ||||||||||||||||||||:::||||||||||||||:::
 32 laMetHisTrpValArgGlnAlaProGlyLysGlyLeuGluTrpValAla 48

211 CGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACTCCGTGAAGGG 260
    ||||||||| ::||||||||::: :|||||||||||||||||||
 49 ValIleSerTyrAspGlySerAsnLysTyrTyrAlaAspSerValLysGl 65

261 CAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTGTTTCTTCAAA 310
    ||||||||||||||:::::|||  :::|||||:::|||
 65 yArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyrLeuGlnM 82

311 TGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCG...AGC 357
    ||||||||||||||||||||||:::::|||  :::
 82 etAsnSerLeuArgAlaGluAspThrAlaMetTyrTyrCysAlaGlyGly 98

358 TTGACTACAGGGTCTGACTCCTGGGGCCAGGAGTCCTGGTCACCGTCTC 407
    ||||     ::||||||||| |||||||||||:::|||
 99 GlyGlyLeuGlyLeuGlyTyrTrpGlyGlnGlyThrLeuValThrValSe 115

408 CTCA 411
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                115 rSer 116
                    ||||
399 CACCGTCCCTCA 411
    |||||||||||
114 lThrValSerSer 118
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seq_name: sp_rodent:Q920E7

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seq_documentation_block:
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DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PTERIN-MIMICKING ANTI-IDIOTOPE HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Atkin J.D. Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT   "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
RT   in Mammalian Cells.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF307937; AAL09421.1; -.
FT   NON_TER        1      1
FT   NON_TER      119    119
SQ   SEQUENCE    119 AA;   13025 MW;   F6E9040443B1CA7C CRC64;
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Percent Similarity:  85.124     Percent Identity:  66.942
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US-09-019-441-4 x Q920E7

Align seg 1/1  to: Q920E7   from: 1  to: 119

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 58 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGTC 107
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  1 GluValGlnLeuValGluSerGlyGlyGlyLeuAlaLysProGlyGlySe  17

108 CCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACT 157
    ||||||:|||       ||||||||||||     ||||||::::::|||
 17 rLeuLysLeuSerCysAlaAlaSerGly......PheThrPheSerSerT  32

158 ACTACATGGACTGGGTCCGCCAGGCTCCAGGGCTGGAGTGGGTC 207
    ||  ||||||||||||::||||    :::    ||||||||||||
 32 yrGlyMetSerTrpValArgGlnThrProAspLysArgLeuGluTrpVal  48

208 TCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACTCCGTGAA 257
    :::  ||||||||||:::|:::     |||:|||:   ||||||||||||
 49 AlaThrIleSerSerGlyGlySerTyrTyrTyrTyrProAspSerValLy  65

258 GGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTGTTCTTC 307
    ||||||||||||||||||||||::|||::|||||:|::|||:::|||||
 65 sGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyrLeuG  82

308 AAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCG... 354
    ||||||||||||||:::::||||||||||||:||||||||||||||||
 82 lnMetSerSerLeuLysSerGluAspThrAlaMetTyrTyrCysAlaArg  98

355 ......AGCTTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGT 398
    :::    |||||||||||||||||||||:||||||||||||::|||||
 99 HisGlyAspTyrArgValGlyPheAlaTyrTrpGlyGlnGlyThrLeuVa 115

399 CACCGTCTCCTCA 411
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115 lThrValSerAla 119
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seq_name: sp_human:Q9UL72

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seq_documentation_block:
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DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9877139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035042; AAD56278.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER        1      1
FT   NON_TER      118    118
SQ   SEQUENCE    118 AA;   12872 MW;   B4D1A5944B2D5CCA CRC64;
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alignment_block:
US-09-019-441-4 x Q9UL72

Align seg 1/1  to: Q9UL72   from: 1  to: 118

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    ||||||||||||||||||||||||||:::|||:::||||||||||
  1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySe  17

108 CCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACT 157
    ||||||:||||||||||       ||||||     |||||  :::::|
 17 rLeuArgLeuSerCysAlaAlaSerGly......PheThrValSerSerA  32

158 ACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTC 207
    ||  ||||||||||||::||||   :::    ||||||||||||||||||
 32 snTyrMetAsnTrpValArgGlnAlaProGlyLysGlyLeuGluSerVal  48

208 TCACGTATTAGTAGTGGTGATCCCACATGGTACCGCAGACTCCGTGAA 257
    |||  |||||||||:::|:::     |||:|||:   ||||||||||||
 49 Ser...ValThrTyrSerGlySerTyrTyrAlaAspSerValLy  64

258 GGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTGTTTCTTC 307
    ||||||||||||||||||||||::|||::||||::|||:::|||
 64 sGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyrLeuG  81

308 AAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 357
    |||||||||||||||:::|||||||||||||:||||||||||||||
 81 lnMetAsnSerLeuArgAlaGluAspThrAlaPheTyrTyrCysAlaArg  97

358 TTGACTACAGGGTCT........GACTCCTGGGGCCAGGGAGTCCTGGT 398
    |||:::        ||      ||||||||||||||||::|||||
 98 AspArgPheGlyLeuPheSerGlyTyrTrpGlyGlnGlyThrLeuVa  114
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Date: Sep 23, 2002 10:19 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US0901941/runat_23092002_095258_6321/app_query.fasta_1.1860
-DB=Pending_Patents_AA_Main - QFMT=fastan -SUFFIX=rapm
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
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-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORMext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000000
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Search information block:
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Database length: 351980561
Search time (sec): 811.400000

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seq_documentation_block:
; Sequence 8, Application US/0929053
; GENERAL INFORMATION:
;   APPLICANT: REFF, MITCHELL E.
;   APPLICANT: KLOETZER, WILLIAM S.
;   APPLICANT: NAKAMURA, TAKEHIKO
;   TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE
;   TITLE OF INVENTION: THEREOF AS THERAPEUTICS
;   FILE REFERENCE: 23522.0699
;   CURRENT APPLICATION NUMBER: US/09/292,053
;   CURRENT FILING DATE: 1999-04-14
;   PRIOR APPLICATION NUMBER: 08/803,085
;   PRIOR FILING DATE: 1997-02-20
;   NUMBER OF SEQ ID NOS: 39
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 137
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-292-053-8

alignment_scores:
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            Ratio:          5.272             Gaps:           0
Percent Similarity:        99.270    Percent identity:    99.270

alignment_block:
US-09-019-441-4 x US-09-292-053-8

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       ||||||||||||||||||||||||||||||||||||||||||||||||
    1  MetGluPheGlyLeuSerTrpValPheLeuValProLeuLeuLysGlyVa  17

   51  CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
       ||||||||||||||||||||||||||||||||||||||||||||||||||
   17  lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuAlaLysProG  34

  101  GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC  150
       ||||||||||||||||||||||||||||||||||||||||||||||||||
   34  lyGlySerLeuArgLeuSerCysAlaAlaSerGlyPheArgPheThrPhe  50

  151  AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA  200
       ||||||||||||||||||||||||||||||||||||||||||||||||||
   51  AsnAsnTyrTyrMetAspTrpValArgGlnAlaProGlyGlnGlyLeuGl  67

  201  GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT  250
       ||||||||||||||||||||||||||||||||||||||||||||||||||
   67  uTrpValSerArgIleSerSerSerGlyAspProThrTrpTyrAlaAspS  84

  251  CCGTGAAGGGCAGATTCACCATCTCCAGAGAGACGCCAACAACACACTG  300
       |||||||||||||||||||||||||||||||||||||||||||||||||
   84  erValLysGlyArgPheThrIleSerArgGluAsnAlaAsnAsnThrLeu  100

  301  TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG  350
       ||||||||||||||||||||||||||||||||||||||||||||||||||
  101  PheLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  117

  351  TGCGAGCTTGACTACAGGGTCTCACTCCTGGGGCCAGGGAGTCCTGGTCA  400
       ||||||||||||||||||||||||||||||||||||||||||||||||||
  117  sAlaSerLeuThrThrGlySerAspSerTrpGlyGlnGlyValLeuValT  134

  401  CCGTCTCCTCA  411

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134 hrValSerSer 137

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; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-50

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          Ratio:      4.411               Gaps:           2
Percent Similarity:   83.221    Percent Identity:    71.812

alignment_block:
US-09-019-441-4 x US-10-038-591-50

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    1 ATGGAGTTGGGCTGAGCTGGTTTCCTTGTTCCTCTTTTGAAAGGTGT   50
      ||||||||||||||||||||||||||| ::|||||||||||||||||
    1 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleIleLysGlyVa  17

   51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
      |||||:::::|||||||||||||||||||||||||::::||||||
   17 lGlnCysGlnValGlnLeuValGluSerGlyGlyGlyLeuValLysProG   34

  101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGTTCACCTTC   150
      ||||||||||||||||||   ||||||||   |||||||
   34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe   48

  151 AATAACTACTACATGGACTGGGTCCCCCAGGCTCCAGGGAAGGGGCTGGA   200
      :::::||||||::::|||:::|||||||||||||||||:::|||||
   49 SerAspTyrTyrMetSerTrpIleArgGlnAlaProGlyLysGlyLeuGl   65

  201 GTGGGTCTCACGTATTAGTAGTAGTGGTATCCCACATGGTACGCAGACT   250
      ||||||||||||||||||::::   ::|||||||||
   65 uTrpValSerTyrIleSerSerSerGlySerThrIleTyrTyrAlaAspS   82

  251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG  300
      ||||||||||||||||||||||:::||||||||||:::|||||
   82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu   98

  301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG  350
      :::|||||||||||||||||:::|||||||||||||||||||||
   99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  115

  351 TGCGAGCTTGACTACA...............................   366
      ||||:::
  115 sAlaSerLeuThrThr...............................   132

  367 ..GGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA   411
      :::||||::::::::            |||||||||||||
        spValTrpGlyGlnGlyThrThrValTyrTyrT  132

---

132 yrGlyMetAspValTrpGlyGlnGlyThrThrValThrValSerSer 147

seq_name: /cgn2_6/ptodata/2/paa/US100_COMB.pep:US-10-038-591-46

seq_documentation_block:
; Sequence 46, Application US/10038591
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-46

alignment_scores:
          Quality:    535.50              Length:       146
          Ratio:      4.354               Gaps:           2
Percent Similarity:   84.247    Percent Identity:    72.603

alignment_block:
US-09-019-441-4 x US-10-038-591-46

Align seg 1/1  to: US-10-038-591-46  from: 1  to: 470

    1 ATGGAGTTGGGCTGAGCTGGTTTCCTTGTTCCTCTTTTGAAAGGTGT   50
      ||||||||||||||||||||||| :::||||||||||||||||||
    1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa   17

   51 CCAGTGTGAGGTGCAGCTGGTCTGGGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
      |||||:::::|||||||||||||||::::|||
   17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG   34

  101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC   150
      ||||||||||||||||||   |||||||||   |||||||
   34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe   48

  151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA   200
      :::::|||   ||||:::||||||||||||||||:::|||||
   49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl   65

  201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT   250
      ||||||||||||||||||::::   ::|||||||||
   65 uTrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyrAlaAsps   82

  251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG  300
      ||||||||||||||||||||:::||||||||||||:::|||||
   82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu   98

  301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG  350
      :::|||||||||||||||||:::|||||||||||||||||||||
   99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  115

  351 TGCGAGC...............................TTGACTACAGGGTCTG  373
      ||||:::                               |||   |||
  115 sAlaLysGlyTyrSerSerGlyTrpTyrTyrTyrTyrTyrGlyMetA  132

  374 ACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA   411
      ||                         ||||||||||||
  132 spValTrpGlyGlnGlyThrThrValThrValSerSer  144

seq_name: /cgn2_6/ptodata/2/paa/US100_COMB.pep:US-10-038-591-49

seq_documentation_block:
; Sequence 49, Application US/10038591
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-49

alignment_scores:
        Quality:     532.50            Length:      146
           Ratio:       4.294            Gaps:        3
Percent Similarity:   84.932    Percent Identity: 73.288

alignment_block:
US-09-019-441-4 x US-10-038-591-49

Align seg 1/1  to: US-10-038-591-49  from: 1  to: 470

   1 ATGGAGTTTGGGCTGAGCTGGTTTCCTTGTTCCTTTTGAAAGGTGT  50
     ||||||||||||||||||||||||||||||    ::|||::||||
   1 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleLeuLysGlyVa  17

  51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
     ||||:|::|:||||||||||||||||||||||||||:::|||||
  17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValLysProG  34

 101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC  150
     |||||||||||||   |||::|||||||       ||||||||
  34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

 151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA  200
     ::::::||||   |||::|||||:||||||||||::||||||
  49 SerAspThrTyrMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl  65

 201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT  250
     ||||||||   |||||||:::|||||       ||||||||
  65 uTrpValSerAlaIleSerGlySerGlyThrArgAspTyrAlaAspS  82

 251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG  300
     |||||||||||||||||||||||::||:|||:::|||||||
  82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu  98

 301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTG  350
     :::||||||||||||||||||||||||||||||||||
  99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  115

 351 TGCGAGC........TTGACTACA...........GGGTCTG  373
     |::|||          ||||||
 115 sValArgAspGlyValGluThrThrPheTyrTyrTyrTyrGlyMetA  132

 374 ACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCCTCCTCA  411
     ||::|::  ||||||||||||
 132 spValTrpGlyGlnGlyThrThrValThrValSerSer  144

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seq_name: /cgn2_6/ptodata/2/paa/US100_COMB.pep:US-10-038-591-45

seq_documentation_block:
; Sequence 45, Application US/10038591
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-45

alignment_scores:
        Quality:     526.50            Length:      146
           Ratio:       4.246            Gaps:        2
Percent Similarity:   84.932    Percent Identity: 71.918

alignment_block:
US-09-019-441-4 x US-10-038-591-45

Align seg 1/1  to: US-10-038-591-45  from: 1  to: 470

   1 ATGGAGTTTGGGCTGAGCTGGTTTCCTTGTTCCTTTTGAAAGGTGT  50
     ||||||||||||||||||||||||||||||   ::|||||||||||
   1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa  17

  51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
     ||||||||||||||||||||||||||||||||::::|||||
  17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProG  34

 101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC  150
     ||||||||||||||   |||::||||||       ||||||||
  34 lyGlySerLeuArgLeuSerCysThrAlaSerGly......PheThrPhe  48

 151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA  200
     ::::::||   |||::|||||:||||||||||::||||||
  49 SerSerTyrAlaMetAsnTrpValArgGlnAlaProGlyLysGlyLeuGl  65

 201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT  250
     ||||||||   |||||||:::|||||       ||||||||
  65 uTrpValSerAlaIleSerGlySerGlyThrThrPheTyrAlaAspS  82

 251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG  300
     |||||||||||||||||||||||::||:|||:::|||||||
  82 erValLysGlyArgPheThrIleSerArgAspAsnSerArgThrThrLeu  98

 301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG  350
     :::||||||||||||||||||||||||||||||||||
  99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  115

 351 TGCGAGCTTGACTACACAGGGTCTGACTCC...........  378
     |||||::  ||||||||
 115 sAlaLysAspLeuGlyTrpSerAspSerTyrTyrTyrTyrGlyMetA  132

 379 .....TGGGGCCAGGGAGTCCTGGTCACCGTCCTCCTCA  411
     ||||||||:::::  ||||||||||
 132 spValTrpGlyGlnGlyThrThrValSerSer  144

seq_name: /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-760-479-636

seq_documentation_block:
; Sequence 636, Application US/09760479
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT253
; CURRENT APPLICATION NUMBER: US/09/760,479
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 946
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 636
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-479-636

alignment_scores:
        Quality:     519.00              Length:        145
        Ratio:        4.087              Gaps:            3
Percent Similarity:  87.586    Percent Identity:  71.724

alignment_block:
US-09-019-441-4 x US-09-760-479-636

Align seg 1/1  to: US-09-760-479-636  from: 1  to: 494

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  1 ATGGAGTTTGGCTGAGCTGGGTTTCCTTGTTCCTCTTTTGAAAGGTGT 50
    |||||||||||:||| ||||||||||||||||||:::||||||||||||
 22 MetGluPheGlyLeuSerTrpValPheLeuValAlaValLeuLysGlyVa 38

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTGTGGGGGCGGCCTTGGCAAAGCCTG 100
    ||||||||||||||:|||||||||||||:||||||||||||:::||||||||
 38 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProG 55

101 GGGGGTCCCTGAGACTCTGGTCGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    |||||||||||||||    ||||||||::    ::||:::|||
 55 lyGlySerLeuArgLeuSerCysAlaAlaAla......GluPheAlaPhe 69

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    ::||||::|||   |||||||||||||||||::||||||||||||||||||
 70 SerAsnTyrTrpMetHisTrpValArgGlnAlaProGlyLysGlyLeuLe 86

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    ||||||||::|||:::||:::|||    ||| ||||||||||
 86 uTrpValSerHisLeuAsnSerAspGlySerThrArgTyrAlaAspS 103

251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG 300
    ||||||||||||||||:||||||||:::||||||||::|||||||||||||
103 erValLysGlyArgPheThrIleSerArgAspAsnValLysAsnThrLeu 119

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACACGGCTGTCTATTACTG 350
    :::|||||::||||||||||:::|||||:::|||    ||||||||:
120 TyrLeuGlnMetSerSerLeuArgValGluAspThrAlaValTyrTyrCy 136

351 TGCG...AGCTTGACTACAGGGTCT................GACT 376
    ||||   |||:::  |||||||||                 |||
136 sAlaArgGlyValLysThrGlyLeuSerTrpPheSerProAspPheAspT 153

377 CCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
    |||||||||||||||||||||||||||||||||||
153 yrTrpGlyGlnGlyThrLeuValThrValSerSer 164
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seq_name: /cgn2_6/ptodata/2/paa/US084_COMB.pep:US-08-471-986-10

seq_documentation_block:
; Sequence 10, Application US/08471986
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION:  human monoclonal antibodies and processes and materials for MA
; NUMBER OF SEQUENCES: 48

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation, Patent Department, K-6-1, 1990
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System Software 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,986
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  PCT/US 94/03429
; FILING DATE: 06-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 93400944.0
; FILING DATE: 09-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Blasdale, John H. C.
; REGISTRATION NUMBER: 31,895
; REFERENCE/DOCKET NUMBER: SF0368KG1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-298-2902
; TELEFAX: 908-298-5388
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-471-986-10

alignment_scores:
        Quality:     518.50              Length:        140
        Ratio:        4.115              Gaps:            2
Percent Similarity:  90.000    Percent Identity:  72.143

alignment_block:
US-09-019-441-4 x US-08-471-986-10

Align seg 1/1  to: US-08-471-986-10  from: 1  to: 138

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  1 ATGGAGTTTGGCTGAGCTGGGTTTCCTTGTTCCTCTTTTGAAAGGTGT 50
    |||||||||||||||||||||||||||||||||||::||||||||||
  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaPheLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCCTTGGCAAAGCCTG 100
    |||||||||||||:::||||||||||||||:||||||||||:::||||||||
 17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProG 34

101 GGGGGTCCCTGAGACTCTGGTCGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    |||||||||||||||      |||||||||||||||||||||||||||||||
 34 lyGlySerLeuArgLeuSerCysValGlySerGly......PheThrPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    ::::|||||   ||| ||||||||||||||||||||||||||||:::||||
 49 ThrAsnTyrAlaMetThrTrpValArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    |||||||||:::||||||||||:::||||||||:::|||||||||:||||
 65 uTrpValSerAlaIleSerGlySerGlyAsnTyrTyrTyrSerAspS 82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG 300
    |||||||||||:::||||||||||:::|||||||||::||||||||||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysSerThrLeu 98
```

```
301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACGACGGCTGTCTATTACTG 350
    ::|||||||||||||||||||||||||||||||||||||||||::::|||||
 99 TyrLeuHisMetAsnSerLeuArgAlaGluAspThrAlaLeuTyrTyrCy 115

351 TGCCAGCTTGACTACAGGGTCT........GACTCCTGGGCGCAGGGAG 391
    ||||:: :::::: ::|    ||| ||||||||||
115 sAlaLysAlaAlaValHisAlaTyrPhePheAspTyrTrpGlyGlnGlyT 132

392 TCCTGGTCACCGTCTCCTCA 411
    ::|||||||||||||||||||
132 hrLeuValThrValSerSer 138
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seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-214-601-15

seq_documentation_block:
; Sequence 15, Application US/60214601
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: Yue, Henry
;  APPLICANT: Lu, Dyung Aina M.
;  APPLICANT: Lal, Preeti
;  APPLICANT: Batra, Sajeev
;  APPLICANT: Burford, Neil
;  APPLICANT: Baughn, Mariah R.
;  APPLICANT: Nguyen, Danniel B.
;  APPLICANT: Azimzai, Yalda
;  APPLICANT: Yao, Monique G.
;  APPLICANT: Walia, Narinder K.
;  TITLE OF INVENTION: SECRETED PROTEINS
;  FILE REFERENCE: PF-0789 P
;  CURRENT APPLICATION NUMBER: US/60/214,601
;  CURRENT FILING DATE: 2000-06-27
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PERL Program
; SEQ ID NO 15
;  LENGTH: 519
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  OTHER INFORMATION: Incyte ID No: 3506590CD1
US-60-214-601-15

alignment_scores:
        Quality:  517.50         Length:       144
        Ratio:      4.277        Gaps:           2
Percent Similarity:  84.028   Percent Identity:  71.528

alignment_block:
US-09-019-441-4 x US-60-214-601-15

Align seg 1/1  to: US-60-214-601-15  from: 1  to: 519

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  1 ATGGAGTTTGGCTGAGCTGGGTTTCCTTGTTCCTCTTTTGAAAGGTGT 50
    ||| |||||||||||||||||||||||||||||||||||||||::||||
  1 MetGluPheGlyLeuSerTrpValPheLeuValAlaLeuLeuArgGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGCAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
    |||||||::|||||||||||||||||||||||||::::::::||||
 17 lGlnCysGlnValGlnLeuValGlnSerGlyGlyGlyValGlnProG 34

101 GGGGGTCCCTGAGACTCTGGTGCGCCAGCCTCCGGGTTCAGGTTCACCTTC 150
    || |||||||||||||||||||||| |||||||
 34 lyArgSerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGGCTGGA 200
    ::::::|| ||| ||||||||||||||||::::||||||||
 49 SerSerTyrTyrAlaMetHisTrpValArgGlnAlaProGlyLysGlyLeuG 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTCATCCCACATGGTACCGCAGACT 250
    |||||||: ||||| ::|||||||||  ::|||||||||||
 65 uTrpValAlaValIleSerTyrAspGlySerAsnLysTyrTyrAlaAspS 82
```

```
251 CCGTGAAGGCAGATTCACCATCTCCAGAGAGACGCCAACAACACACTG 300
    |||||||||||||||||||||||||||||||::::|||::|||||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACACGGCTGTCTATTACTG 350
    ::|||||||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

351 TGCCAGCTTGACTACAGGGTCT.................GACTCCT 379
    ||||:: ::::::::|||| || ||
115 sAlaArgAlaGlyGluGlySerProAspThrLeuValAlaPheAspIleT 132

380 GGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
    ||||||||||::::::|||||||||||
132 rpGlyGlnGlyThrMetValThrValSerSer 142
```

seq_name: /cgn2_6/ptodata/2/paa/US092_COMB.pep:US-09-269-332-77

seq_documentation_block:
; Sequence 77, Application US/09269332
; GENERAL INFORMATION:
;  APPLICANT: SATO, KOH
;  APPLICANT: WAKAHARA, YUJI
;  APPLICANT: YABUTA, NAOHIRO
;  TITLE OF INVENTION: ANTIBODY AGAINST HUMAN PARATHORMONE RELATED PEPTIDES
;  FILE REFERENCE: 04853-0033
;  CURRENT APPLICATION NUMBER: US/09/269,332
;  CURRENT FILING DATE: 1999-03-25
;  PRIOR APPLICATION NUMBER: PCT/JP97/03382
;  PRIOR FILING DATE: 1997-09-24
;  PRIOR APPLICATION NUMBER: JP 255196/1996
;  PRIOR FILING DATE: 1996-09-26
;  PRIOR APPLICATION NUMBER: JP 214168/1997
;  PRIOR FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 113
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
;  LENGTH: 137
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-269-332-77

alignment_scores:
        Quality:  515.00         Length:       139
        Ratio:      4.221        Gaps:           2
Percent Similarity:  87.770   Percent Identity:  74.101

alignment_block:
US-09-019-441-4 x US-09-269-332-77

Align seg 1/1  to: US-09-269-332-77  from: 1  to: 137

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  1 ATGGAGTTTGGCTGAGCTGGGTTTCCTTGTTCCTCTTTTGAAAGGTGT 50
    ||| |||||||||||||||||||||||||||||||::||||
  1 MetGlyPheGlyLeuSerTrpValPheLeuValAlaLeuLeuArgGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
    ||||||:::|||||||||||||||||||||||||::::::::||||
 17 lGlnCysGlnValGlnLeuValGluSerGlyGlyGlyValGlnProG 34

101 GGGGGTCCCTGAGACTCTGGTGCGCCAGCCTCCGGGTTCAGGTTCACCTTC 150
    || |||||||||||||||||||||| |||||||
 34 lyArgSerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    ::::::|| ||||||||||||||||||||::::||||||||
 49 SerSerTyrGlyMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGGTGATCCCACATGGTACCGCAGACT 250
    |||||||: ||||| ::|||||||||||||
 65 uTrpValAlaThrIleSerSerGlyGlySerTyrThrTyrTyrProAspS 82
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us-09-019-441-4.rapm

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251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
    ||||||||||||||||||||||||:::||::|||::||||||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu  98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
    :::||||||||||||||||||||||||||||::||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

351 TGCGAGCTTGACTACAGGGTCT.....GACTCCTGGGCCAGGGAGTCC 394
    ||||  ||||||  ::         ||||||||||||::|
115 sAlaArgGlnThrThrMetThrTyrPheAlaTyrTrpGlyGlnGlyThrL 132

395 TGGTCACCGTCTCCTCA 411
    |||||||||||||||||
132 euValThrValSerSer 137
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seq_name: /cgn2_6/ptodata/2/paa/US094_COMB.pep:US-09-423-800-77

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alignment_scores:
          Quality: 515.00            Length:    139
            Ratio: 4.221             Gaps:        2
Percent Similarity: 87.770  Percent Identity: 74.101

alignment_block:
US-09-019-441-4 x US-09-423-800-77       ..

Align seq 1/1  to: US-09-423-800-77  from: 1  to: 137

  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTTGAAAGGTGT 50
    |||  ||||||||||||||||||||||||||||      ||||||:::||||
  1 MetGlyPheGlyLeuSerTrpValPheLeuValAlaLeuLeuArgGlyVa  17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGGGCCAAAGCCTG 100
    ||||||:::||||||||||||||||||||||||||||||||::||||
 17 lGlnCysGlnValGlnLeuValGluSerGlyGlyGlyValValGlnProG  34

101 GGGGTCCCTGAGACTCTGGTGCGCCAGCCTCCGGGTTCCAGGTTCACCTTC 150
    ||  ||||||||||||||||||||         ||||||||
 34 lyArgSerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    :::::|||  ||||:|||||||||||||||||||::|||||||
 49 SerSerTyrGlyMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl  65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTTATTCCACATGGTACGCAGACT 250
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 65 uTrpValAlaThrIleSerSerGlyGlySerTyrThrTyrTyrProAspS  82
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seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-18569-4273

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alignment_scores:
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            Ratio: 4.126             Gaps:        2
Percent Similarity: 89.130  Percent Identity: 70.290

alignment_block:
US-09-019-441-4 x PCT-US01-18569-4273        ..

Align seq 1/1  to: PCT-US01-18569-4273  from: 1  to: 193

  1 ATGGAGTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGT 50
    |||||||||||||||||||||||||||||||||||||     ::::||||
 22 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleIleLeuLysGlyVa  38

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
    |||||:::||||||||||||||||||||||||||||||::||||||
 38 lGlnCysGlnValGlnLeuValGluSerGlyGlyGlyLeuValLysProG  55

101 GGGGTCCCTGAGACTCTCGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    |||||||||||||||:||||||||||||||||||||||||||
 55 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  69

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    :::::|||:::|||::||||||||||||||||||||::||||||||
 70 SerAspPheTyrMetSerTrpIleArgGlnValProGlyLysGlyLeuGl  86

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGGTGATCCCACATGGTACGCAGACT 250
    ||||::|||| ||||| |||||:  :|||:|||
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86 uTrpIleSerTyrIleSerProSerAlaThrAsnIlePheTyrThrAspS 103

251 CCGTGAAGGGCAGATTCACCATTCCAGAGAGAACGCCAACAACACACTG 300
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103 erValGlnAspArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu 119

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
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120 TyrLeuGlnMetAsnSerLeuArgValGluAspThrAlaValTyrPheCy 136

351 TGCG...AGCTTGACTACAGGGTCTGACTCCTGGGCCCAGGAGTCCTGG 397
    |||   ::||||    |||   |||||||||||||||:::::||
136 sAlaArgGluLeuPheAspLeuPheGlyGlnGlyThrMetV 153

398 TCACCGTCTCCTCA 411
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153 alSerValSerSer 157

seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US02-04347-49

seq_documentation_block:
; Sequence 49, Application PC/TUS020347
; GENERAL INFORMATION:
; APPLICANT: diaDexus, Inc.
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Hu, Ping
; APPLICANT: Recipon, Herve
; APPLICANT: Karra, Kalpana
; APPLICANT: Cafferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
; FILE REFERENCE: DEX-0307
; CURRENT APPLICATION NUMBER: PCT/US02/04347
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/268,833
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 49
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapien
PCT-US02-04347-49

alignment_scores:
            Quality:  506.00              Length:      143
            Ratio:    4.182               Gaps:        2
Percent Similarity:   84.615   Percent Identity:   70.629

alignment_block:
US-09-019-441-4 x PCT-US02-04347-49         ..

Align seq 1/1  to: PCT-US02-04347-49  from: 1  to: 488

  1 ATGGAGTTTGGCTGAGCTGGGTTTCCTTGTTCCTCTTTTGAAAGGTGT 50
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  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGCGGCCTTGGCAAAGCCTG 100
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 17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyPheIleGlnProG 34

101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    ||||||||||    |||||||||||||      ||||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    :::::::::   ::|||||||||||||||||||::||||||
 49 SerSerPheAlaLeuIleTrpAlaArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    |||||||||     ||||||:::||||
 65 uTrpValSerGlyIleSerGlyGlySerGlyLysGlySerLysGlyTyrAlaAsps 82

251 CCGTGAAGGGCAGATTCACCATTCCAGAGAGAACGCCAACAACACACTG 300
    ||||||||||||||||||||||||||||||||::||||||:::||||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
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 99 AsnLeuGlnMetAsnSerLeuArgValGluAspThrAlaValTyrTyrCy 115

351 TGCGAGCTTGACTACAGGGTCT.............GACTCCTGGG 382
    ||||||||||||||||||:||               :::||||||
115 sAlaLysValLysGlyAsnThrTrpThrTyrTyrPheGlnSerTrpG 132

383 GCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
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132 lyGlnGlyThrLeuValIleValSerSer 141

seq_name: /cgn2_6/ptodata/2/paa/US098_COMB.pep:US-09-834-366-13609

seq_documentation_block:
; Sequence 13609, Application US/09834366
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81.US2.REG
; CURRENT APPLICATION NUMBER: US/09/834,366
; CURRENT FILING DATE:  2001-04-13
; PRIOR APPLICATION NUMBER: US 60/197,873
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 13609
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -19..-1
US-09-834-366-13609

alignment_scores:
            Quality:  504.00              Length:      137
            Ratio:    4.065               Gaps:        2
Percent Similarity:   90.511   Percent Identity:   68.613

alignment_block:
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  1 MetGluLeuGlyLeuSerTrpValPheLeuValAlaIleLeuGluGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGCGGCCGTGGCAAAGCCTG 100
    |||||||||||||||||||||||||||||||:::||:|||||
 17 lGlnCysGluValGlnValGlnLeuValLeuSerGlyGlyGlyValGlnProG 34

101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    |||||||||||||||||||||||||||||||   ||||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    :::::::::   ::|||||||||||||||||||||||||||
 49 SerAspTyrTrpMetAsnTrpValArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    ||||||:::||:::|| ::    :::||::::    ::: |||:::|||
 65 uTrpValAlaAsnIleAsnProAspGlySerGlnSerArgTyrValAspS 82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
    |||||||||||||||||:::||:::||||:::|||:::|||||:::||
 82 erValLysGlyArgPheThrValSerArgAspAsnAlaLysLysSerLeu 98

301 TTTCTTCAAATGAACAGCCTGAGGAGTCGAGGACACGGCTGTCTATTACTG 350
    :::||||||||||||||||||||||||||||:::|||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaIleTyrTyrCy 115

351 TCGCAGCTTGACTACAGGGTCTGACTCCTGGGGCCCAGGAGTCCTGGTCA 400
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115 sLeuGlyTrpSerAlaProAlaAlaProTrpGlyGlnGly.ThrTrpSer 131

401 CCGTCTCCT 409
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132 ProSerPro 134

seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-08655-218

seq_documentation_block:
; Sequence 218, Application PC/TUS0108655
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-065
; CURRENT APPLICATION NUMBER: PCT/US01/08655
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/668,317
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/695,783
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 09/728,628
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/783,066
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 09/816,828
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 584
; SOFTWARE: Custom
; SEQ ID NO 218
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-08655-218

alignment_scores:
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        Ratio: 4.564                 Gaps: 1
Percent Similarity: 93.220   Percent Identity: 82.203

alignment_block:
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  1 MetGluPheGlyLeuSerTrpValPheLeuVal.AlaIleLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCCGGCTTGGCAAAGCCTG 100
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 17 lGlnCysGluValGlnLeuValGluSerGlyGlyLeuValGlnProG 34

101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCACCTTC 150
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101

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Date: Sep 23, 2002   9:59 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

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-DB=Pending_Patents_AA_New -QFMT=fastn -SUFFIX=rapn
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09019441_@CGN1_1_60 -NCPU=6 -ICPU=3 -LONGLOG
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Search information block:
Query: US-09-019-441-4
Query length: 411
Database: Pending_Patents_AA_New:*
Database sequences: 949130
Database length: 267991220
Search time (sec): 353.570000

score_list:
Sequence                        Strd Orig   ZScore   EScore  Len  | Documentation
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/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-88895 +  524.50  818.09  3.4e-37
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-105249 +  524.50  817.49  3.4e-37
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seq_documentation_block:
; Sequence 88908, Application US/0791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
;   SEQ ID NO 88908
;   LENGTH: 143
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-88908

alignment_scores:
               Quality:    547.50                       Length:     144
               Ratio:        4.345                       Gaps:         2
  Percent Similarity:      87.500      Percent Identity:   74.306

alignment_block:
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  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa  17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGGCAAAGCCTG 100
    |||||||||||||||||||||||||||||||||||||::|||||||
 17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG  34

101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    |||||||||||| ||||||||||||||||||     ||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    ::::::|||  ||::|||||||||||||||||||||||:||||||
 49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl  65

201 GTGGGTCTCAGGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    |||||||| ||::||||||||||||||||||:|||||
 65 uTrpValSerAlaIleThrGlySerGlySerThrTyrTyrAlaAsps  82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG 300
    |||||||||||||||||||||||::||:::::::|||||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu  98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
    ::||||||||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  115

351 TGCGAGC................TTGACTACAGGGGTCTGACTCCT 379
    |||||:::                    ||| |||
115 sAlaLysAlaSerIleArgThrThrValThrProGlyPheAspTyrT  132

380 GGGGCCAGGAGTCCCTGCTCACCGTCTCCTCA 411
    ||||||||||||||::||||||||||||||
132 rpGlyGlnGlyThrLeuValThrValSerSer 142

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-19856

seq_documentation_block:
; Sequence 19856, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19856
;   LENGTH: 138
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-19856

alignment_scores:
        Quality:    546.50              Length:    140
        Ratio:      4.372               Gaps:      2
Percent Similarity: 89.286      Percent Identity: 76.429

alignment_block:
US-09-019-441-4 x US-09-791-537-19856   ..

Align seg 1/1  to: US-09-791-537-19856   from: 1  to: 138

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  1 ATGGAGTTTGGGCTGAGCTGGTTTCCTCTTTTGTTCCTCTTTTGAAAGGTGT 50
    |||||||||||||||||||||||||||||||||  ::|||||||||||
  1 MetGluPheGlyLeuSerTrpPheLeuValAlaIleLeuLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCCTTGGCAAAGCCTG 100
    |||||||||||||||::::||||||||||||||||||||||
 17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG 34

101 GGGGGTCCCTGAGACTCTGGTCGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    |||||||||||||    ||||||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    ::::::||| |||::||||||||||||||   ||||||||
 49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    ||||||||   |||||::||||   ||:::|||||||
 65 uTrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyrAlaAspS 82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAAACGCCAACAACACACTG 300
    |||||||  ||||::||||||   ||::||||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
    ::|||||||||||||||||||||||::|||::|||:::|||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

351 TGCGAGCTTGACTACAGGG.......TCTGACTCCTGGGGCCAGGGAG 391
    |||||:::   |||||||     |||   |||||::|||
115 sAlaLysAlaArgThrGlyTyrTrpTyrPheAspLeuTrpGlyArgGlyT 132

392 TCCTGGTCACCGTCTCCTCA 411
    ::|||||||||||||||||
132 hrLeuValThrValSerSer 138
```

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-19722

seq_documentation_block:
; Sequence 19722, Application US/09791537

---

; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19722
;   LENGTH: 145
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-19722

alignment_scores:
        Quality:    544.50              Length:    140
        Ratio:      4.356               Gaps:      2
Percent Similarity: 89.286      Percent Identity: 76.429

alignment_block:
US-09-019-441-4 x US-09-791-537-19722   ..

Align seg 1/1  to: US-09-791-537-19722   from: 1  to: 145

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  1 ATGGAGTTTGGGCTGAGCTGGTTTCCTCTTTTGTTCCTCTTTTGAAAGGTGT 50
    |||||||||||||||||||||||||||||||||  ::|||||||||||
  8 MetGluPheGlyLeuSerTrpPheLeuValAlaIleLeuLeuLysGlyVa 24

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCCTTGGCAAAGCCTG 100
    |||||||||||||||::::||||||||||||||||||||||
 24 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG 41

101 GGGGGTCCCTGAGACTCTGGTCGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    |||||||||||||    ||||||||||
 41 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 55

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    ::::::||| |||::||||||||||||||   ||||||||
 56 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 72

201 GTGGGTCTCACGTATTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    ||||||||   |||||::||||   ||:::|||||||
 72 uTrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyrAlaAspS 89

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAAACGCCAACAACACACTG 300
    |||||||  ||||::||||||   ||::||||||
 89 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 105

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
    ::|||||||||||||||||||||||::|||::|||:::|||||||
106 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 122

351 T.........GCGAGCTTGACTACAGGGTCTGACTCCTGGGGCCAGGGAG 391
    |  |||::::    :::|| ||| ||||||||||
122 sAlaLysAspAlaGlyTrpGlySerGlyPheAspTyrTrpGlyGlnGlyT 139

392 TCCTGGTCACCGTCTCCTCA 411
    ::|||||||||||||||||
139 hrLeuValThrValSerSer 145
```

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-102425

seq_documentation_block:
; Sequence 102425, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88984
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-88984

alignment_scores:
Quality:  542.50          Length:  142
Ratio:  4.272           Gaps:  3
Percent Similarity:  89.437   Percent Identity:  76.761

alignment_block:
US-09-019-441-4 x US-09-791-537-88984

Align seg 1/1 to: US-09-791-537-88984  from: 1  to: 141

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  1 ATGGAGTTTGGGCTGAGCTGGTTTCCTTGTTCCTTTTGAAAGGTGT 50
    ||||||||||||||||||||||||||||||||||::||||||||||
  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
    ||||||||||||||||||||::::||||||||||||||||:::::|||
 17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG 34

101 GGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    ||||||||||||  |||||||||||||    |||||  PheThrPhe 48
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48

151 AATAACTACTACATGACTGGGTCCGCCCAGGCTCCAGGGGCCAGGGGCTGGA 200
    ||||||   |||    ||||||||||||::::||||||||::||||||
 49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    ||||||||  ||:::|||||| :|||:||||||||||| :::|||||
 65 uTrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyrAlaAspS 82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACAACACTG 300
    ||||||||||||||||||||||||||||||||:::|||:::|||||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACCGCTGTCTATTACTG 350
    ::|||||||||||||||||||||:::|||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

351 TGCCGAGCTTG...ACTACAGGGTCTGCACTCC............TGGGGCC 385
    ||||::::||| :::|||||||   |||       ||||||
115 sAlaLysLeuSerThrThrValThrArgSerTyrGlyValTyrTrpGlyG 132

386 AGGGAGTCCTGTCACCGTCTCCTCA 411
    ||||:::|||||||||||||||||
132 lnGlyThrLeuValThrValSerSer 140
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-88984

seq_documentation_block:
; Sequence 102457, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT:    Debe, Derek
; APPLICANT:    Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE:  2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 102457
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens

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; TITLE OF INVENTION:  METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE:  2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 102425
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-102425

alignment_scores:
Quality:  542.50          Length:  140
Ratio:  4.375           Gaps:  2
Percent Similarity:  88.571   Percent Identity:  75.000

alignment_block:
US-09-019-441-4  to: US-09-791-537-102425

Align seg 1/1  to: US-09-791-537-102425  from: 1  to: 139

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  1 ATGGAGTTTGGGCTGAGCTGGTTTCCTTGTTCCTCTTTGAAAGGTGT 50
    ||||||||||||||||||||||||||||||||| :::::||||||||
  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleIleLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCGGCTTGGCAAAGCCTG 100
    ||||||||||||||||||||||||||||||||||||||||:::::|||
 17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValLysProG 34

101 GGGGTCCCTGAGACTCTGTGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    ||||||||||||||||||||||||||||     |||||  PheThrPhe 48
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

151 AATAACTACTACATGACTGGGTCCGCCCAGGCTCCAGGGAAGGGGCTGGA 200
    ||||||    |||   ||||||||||||:::||||||||||   |||||
 49 SerAspTyrTyrMetThrTrpIleArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    ::::||||||  :|::|||| ||||||||||||||||| :::|||||
 65 uTrpLeuSerTyrLeuSerSerSerGlyArgThrIleTyrTyrAlaAspS 82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCACATGGTACGCAGACT 300
    ||||||||||||||||||||||||||:::||:::||||||
 82 erValLysGlyArgPheThrIleSerArgAspAspAspLysSerLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACCGCTGTCTATTACTG 350
    |||||||::::|||||||||||||||||||||||||||||||||||
 99 PheLeuGlnThrAsnAsnLeuArgAlaGluAspThrAlaValTyrTyrCy 115

351 TGCCGAGCTGACTACAGGGTCT..........GACTCCTGGGCCCAGGGAG 391
    |||| :::::|||||||||||          |||   ||||||||||
115 sAlaArgValTyrSerSerSerTrpGluPheAspTyrTrpGlyGlnGlyT 132

392 TCCTGGTCACCGTCTCCTCA 411
    ::|||||||||||||||||
132 hrLeuValThrValSerSer 138
```

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-102425

seq_documentation_block:
; Sequence 88984, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT:    Debe, Derek
; APPLICANT:    Danzer, Joseph
; TITLE OF INVENTION:  THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION:  METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE:  2001-02-22
; NUMBER OF SEQ ID NOS: 153055

## Left column

US-09-791-537-102457

alignment_scores:
  Quality:    541.50              Length:    140
  Ratio:      4.332               Gaps:      2
Percent Similarity: 89.286   Percent Identity: 75.714

alignment_block:
US-09-019-441-4 x US-09-791-537-102457

Align seg 1/1  to: US-09-791-537-102457  from: 1  to: 139

```
  1 ATGGAGTTGGGCTGAGCTGGGTTTCCTTGTTCCTCTTTGAAAGGTGT   50
    |||||||||||||||||||||||| :::|||||||||||
  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa  17

 51 CCAGTGCTGAGGTGCGAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
    ||||||||||||||||||||:::|||||||||||||:::|||
 17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG  34

101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC  150
    |||||||||||         ||||||||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

151 AATAACTACTACATGACTGGGTCCGCAGGCTCCCAGGCTCAGGGGCTGGA  200
    :::::|||  |||:::|||||||||||||||||:::|||||
 49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl  65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACCATGGTACGCAGACT  250
    ::::|||  ||:::||||||||||||||  ||:::||||||
 65 uTrpValSerAlaIleSerGlySerGlyTyrThrTyrTyrAlaAspS  82

251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG  300
    |||||||||||||||| |||:::|||:::||||||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu  98

301 TTTCTTCAAATGAACAGCCTGAGAGTGAGGACACGGCTGTCTATTACTG  350
    :::|||||||||||||||:::||:::|||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  115

351 TGGGAGCTTGACTACAGGG......TCTGACTCCTGGGGCCAGGGAGGAG  391
    |||:::  |||:::|  |||||||||||||
115 sAlaLysAlaAspThrAlaMetAspProGlyAspValTrpGlyGlnGlyT  132

392 TCCTGTGTCACCGTCTCCTCA  411
    |||::  |||||||||||
132 hrThrValThrValSerSer  138
```

alignment_scores:
  Quality:    540.00              Length:    137

## Right column

Percent Similarity: 90.511   Percent Identity: 77.372
  Ratio:      4.355                                  Gaps: 2

alignment_block:
US-09-019-441-4 x US-09-791-537-89386

Align seg 1/1  to: US-09-791-537-89386  from: 1  to: 134

```
  1 ATGGAGTTGGGCTGAGCTGGGTTTCCTTGTTCCTCTTTGAAAGGTGT   50
    ||||||||||||||||||||| :::|||||||||||
  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa  17

 51 CCAGTGCTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
    |||||||||||||||||||||:::||||||||||||:::|||
 17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG  34

101 GGGGGTCCCTGAGACTCTGGTGCGCCAGCCTCCGGGTTCAGGTTCACCTTC  150
    ||||||||||||         ||||||||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

151 AATAACTACTACATGACTGGGTCCGCAGGCTCCCAGGCTCAGGGGCTGGA  200
    :::::|||  |||:::|||||||||||||||||:::|||||
 49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl  65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACCATGGTACGCAGACT  250
    ||  |||:::|||||||||
 65 uTrpValSerAlaIleSerGlySerGlyTyrThrTyrTyrAlaAspS  82

251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG  300
    |||||||||||||||||||||:::|||:::||||||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu  98

301 TTTCTTCAAATGAACAGCCTGAGAGTGAGGACACGGCTGTCTATTACTG  350
    :::|||||||||||||||:::||:::|||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  115

351 TGCGAGCTTGACTACAGGCTCCTGGGGCCAGGGAGTCCTGGTCA  400
    ||||::  ||:::
115 sAlaLys......AspGlyGlyValTyrTrpGlyGlnGlyThrLeuValT  130

401 CCGTCTCCTCA  411
    |||||||||||
130 hrValSerSer  133
```

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-72392

alignment_scores:
  Quality:    539.50              Length:    140
  Ratio:      4.316               Gaps:      2
Percent Similarity: 89.286   Percent Identity: 75.714

alignment_block:
US-09-019-441-4 x US-09-791-537-72392

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-89386

Align seg 1/1   to: US-09-791-537-72392   from: 1   to: 156

```
  1 ATGGAGTTTGGGCTGAGCTGGTTTCCTTGTTCCTCTTTGAAAGGTGT    50
    |||||||||||||||||||:::||||||||:::||||||
    CCAGTGTGAGGTGCAGCTGGTTGAGTCTGGGGGCGGCCTTGGCAAAGCCTG
 19 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa  35

 51 CCAGTGTGAGGTGCAGCTGGTTGAGTCTGGGGGCGGCCTTGGCAAAGCCTG  100
    ||||||||||||||||||||:::||||||||||||::::|||
 35 lGlnCysGlyValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG   52

101 GGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC   150
    ||||||||||||||||||||||| |||||||       |||||||
 52 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe   66

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGCTGGA   200
    :::::|||  ||||||||:::|||||||||||||::|||||||||
 67 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl   83

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT  250
    |||||||| |||||:|||||  ||:||||::||||||||||||||||
 83 uTrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyrAlaAspS  100

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGACAACGGCCAACAACACACTG 300
    ||||||||||||||||||||||:::||||||||||||||||||||||
100 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu  116

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG  350
    :::::||||||||||||||:::||||||||||||||||||||||||
117 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  133

351 TGCGAGCTTGACTACAGGGGTC.......GACTCCTGGGGCCAGGGAG    391
    |||::::             ||  ||||||||:::
133 sAlaLysLysAspTrpAsnAspAsnTrpPheAspProTrpGlyGlnGlyT  150

392 TCCTGGTCACCGTCTCCTCA    411
    ::||||||||||||||||||
150 hrLeuValThrValSerSer    156
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alignment_scores:
Quality:              538.50          Length:    146
Ratio:                4.308           Gaps:        2
Percent Similarity:   85.616          Percent Identity: 72.603

alignment_block:
US-09-019-441-4 x US-09-791-537-36911

Align seg 1/1   to: US-09-791-537-36911   from: 1   to: 160

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  1 ATGGAGTTTGGGCTGAGCTGGTTTCCTTGTTCCTCTTTGAAAGGTGT    50
    |||||||||||||||||||
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Align seg 1/1   to: US-09-791-537-51417   from: 1   to: 161

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  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa  17

 51 CCAGTGTGAGGTGCAGCTGGTTGAGTCTGGGGGCGGCCTTGGCAAAGCCTG 100
    ||||||||||||||||||||:::||||||||||||::::|||
 17 lGlnCysGlyValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG   34

101 GGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC   150
    ||||||||||||||||||||||| |||||||       ||||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe   48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGCTGGA   200
    :::::|||  ||||||||:::|||||||||||||::|||||||||
 49 SerThrTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl   65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT  250
    |||||||| |||||:|||||  ||:||||::||||||||||||||||
 65 uTrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyrAlaAspS   82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGACAACGGCCAACAACACACTG 300
    ||||||||||||||||||||||||||||||||||||||||||||||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu   98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGCGTGCTGTCTATTACTG 350
    :::||||||||||||||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  115

351 TGCGAGCTTGACTACA.............................GGGTCTG 373
    |||::: :::::::                                  |
115 sAlaLysAlaValArgGlyValIleSerTyrTyrTyrTyrGlyMetA  132

374 ACTCCTGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA  411
    ||  |||||||||||:::||||||||||||||||||
132 spValTrpGlyGlnGlyThrThrValThrValSerSer  144
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alignment_scores:
Quality:              538.50          Length:    146
Ratio:                4.308           Gaps:        2
Percent Similarity:   85.616          Percent Identity: 72.603

alignment_block:
US-09-019-441-4 x US-09-791-537-51417

Align seg 1/1   to: US-09-791-537-51417   from: 1   to: 161

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  1 ATGGAGTTTGGGCTGAGCTGGTTTCCTCTTTGTTCCTCTTTGAAAGGTGT  50
    ||||||||||||||||||||:::||||||||||||||||||
  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa  17

 51 CCAGTGTGAGGTGCAGCTGGTTGAGTCTGGGGGCGGCCTTGGCAAAGCCTG 100
    ||||||||||||||||||||:::||||||||||||::::|||
 17 lGlnCysGlyValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG   34
```

```
101 GGGGTCCCTGAGACTCTGGTGCGCCAGCCTCCGGGTTCACCTTC        150
    ||||||||||||||||||          ||||||||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe   48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGGCTGGA        200
    :::::!!!  |||:::!!!!!!!!!!!!!!!!!!!!:::!!!!!!
 49 .SerThrTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl  65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT   250
    !!!!!!!!!   !!!:::!!!!|||       !!!:::!!!!!!!!
 65 uTrpValSerGlyIleThrGlySerGlyGlySerThrTyrTyrAlaAspS   82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG   300
    !!!!!!!!!!!!!!!!!!!!!      !!!:::!!!!!!!!!!!!!
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu   98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG   350
    :::!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy   115

351 TGCGAGCT.....................GGGTCTG               373
    !!!   :::                     !!!
115 sAlaLysAlaValValArgGlyValIleSerTyrTyrTyrTyrGlyMetA   132

374 ACTCCTGGGCCCAGGGAGTCCTGGTCACCGTCTCCTCA             411
    !!   !!!!!!!!!!!!!:::       !!!!!!!!!!!!!
132 spValTrpGlyGlnGlyThrValThrValSerSer               144
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seq_name: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:PCT-US02-20181-2

seq_documentation_block:
; Sequence 2, Application PC/TUS0220181
; GENERAL INFORMATION:
;    APPLICANT: Boyle, William J
;    APPLICANT: Martin, Francis H
;    APPLICANT: Corvalan, Jose R
;    APPLICANT: Davis, C. Geoffrey
;    TITLE OF INVENTION: Antibodies to OPGL
;    FILE REFERENCE: 06843.0049-00000
;    CURRENT APPLICATION NUMBER: PCT/US02/20181
;    CURRENT FILING DATE: 2002-06-25
;    PRIOR APPLICATION NUMBER: 60/301,172
;    PRIOR FILING DATE: 2001-06-26
;    NUMBER OF SEQ ID NOS: 20
;    SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;    LENGTH: 467
;    TYPE: PRT
;    ORGANISM: Mus musculus
PCT-US02-20181-2

alignment_scores:
          Quality:    537.00                 Length:      143
          Ratio:       4.296                 Gaps:          2
Percent Similarity:   87.413       Percent Identity:   73.427

alignment_block:
US-09-019-441-4 x PCT-US02-20181-2

Align seg 1/1   to: PCT-US02-20181-2   from: 1   to: 467

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  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTTCCTCTTTTGAAAGGTGT  50
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  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
    ||||||||||||||||||||:::||||||||||||||:::||||
 17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProG   34

101 GGGGTCCCTGAGACTCTGGTGCGCCAGCCTCCGGGTTCACCTTC        150
    ||||||||||
```

```
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe   48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGGCTGGA        200
    :::::!!!  |||:::!!!!!!!!!!!!!!!!!!!!!:::!!!!!!
 49 .SerThrTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl  65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT   250
    !!!!!!!!!          !!!:::!!!!!!!!!!
 65 uTrpValSerGlyIleThrGlySerGlyGlySerThrTyrTyrAlaAspS   82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG   300
    !!!!!!!!!!!!!!!!!!!!!!      !!!:::!!!!!!!!!!!!!!
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu   98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG   350
    ::!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy   115

351 TGCGAGC.....................TTGACTACAGGGTCTGACTCCTGG  382
    !!!::::                              :::      |||   |||
115 sAlaLysAspSerProGlyTyrThrValIleMetSerTrpPheAspProTrpG 132

383 GCCAGGGAGTCCTGGTCACCGTCTCCTCA                        411
    ||||||||||||||:::||||||||||||||
132 lyGlnGlyThrValThrValSerSer                          141
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-88448

seq_documentation_block:
; Sequence 88448, Application US/09791537
; GENERAL INFORMATION:
;    APPLICANT: Bionomix, Inc.
;    APPLICANT: Debe, Derek
;    APPLICANT: Danzer, Joseph
;    TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;    TITLE OF INVENTION: METHODS OF USE THEREOF
;    FILE REFERENCE: 261/210
;    CURRENT APPLICATION NUMBER: US/09/791,537
;    CURRENT FILING DATE: 2001-02-22
;    NUMBER OF SEQ ID NOS: 153055
;    SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88448
;    LENGTH: 144
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-791-537-88448

alignment_scores:
          Quality:    536.00                 Length:      145
          Ratio:       4.323                 Gaps:          2
Percent Similarity:   85.517       Percent Identity:   73.103

alignment_block:
US-09-019-441-4  to: US-09-791-537-88448

Align seg 1/1   to: US-09-791-537-88448   from: 1   to: 144

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  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTTCCTCTTTTGAAAGGTGT  50
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  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
    ||||||||||||||||||||:::||||||||||||:::||||
 17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProG   34

101 GGGGTCCCTGAGACTCTGGTGCGCCAGCCTCCGGGTTCAGGTTCACCTTC  150
    ||||||||||||||||||        ||||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe   48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGGCTGGA        200
    :::::!!!  |||:::!!!!!!!!!!!!!!!!!!!!!:::!!!!!!
 49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl   65
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251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAACGCCAACAACACACTG 300
    |||||||||||||||||||||||||||||||||::|||||::|||:|||
82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
    :::|||||||||||||||||||||||||||||||||||||||||||||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

351 TGCGAGC...............TTGACTACAGGGTCTGACTCCTGGG 382
    ||||                  |||::|| |||::|||  ||||
115 sAlaArgAspLeuArgGlyGlnTrpLeuValGlnGlyGluAspTyrTrpG 132

383 GCCAGGAGTCCTGGTCACCGTCTCCTCA 411
    |||||||:::||||||||||||||||||
132 lyGlnGlyThrLeuValThrValSerSer 141

seq_name: /cgn2_6/ptdata/1/paa/US09_NEW_COMB.pep:US-09-791-537-16931

seq_documentation_block:
; Sequence 16931, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT:   Bionomix, Inc.
;   APPLICANT:   Debe, Derek
;   APPLICANT:   Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE:  2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16931
;   LENGTH: 141
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-16931

alignment_scores:
         Quality:    535.50                    Length:    142
         Ratio:      4.319                      Gaps:      2
Percent Similarity:  87.324      Percent Identity: 74.648

alignment_block:
US-09-019-441-4  x  US-09-791-537-16931

Align seg 1/1  to: US-09-791-537-16931  from: 1  to: 141

1 ATGGAGTTTGGGCTGAGCTGGGTTTCCTTGTTCCTCTTTTGAAAGGTGT 50
  |||||||||||||||||||||||||||||||||::|||||||  ::|||||||
1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLeuLysGlyVa 17

51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
   |||||||||||||:::|||||||||||||||||||||||||:::||||
17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG 34

101 GGGGGTCCCTGAGACTCTGGTGCCGCAGCCTCCGGGTTCACCTTC 150
    |||||||||||| |||::|||||||    |||||||||
34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCTGGA 200
    ::::::|||  ||::||||||||||||||||||::|||||||||
49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGTACGCAGACT 250
    |||||||| |||||||::||||| ||||||   |||::|||||||||||
65 uTrpValSerAlaIleSerGlySerThrTyrTyrAlaAspS 82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAACGCCAACAACACACTG 300
    |||||||||||||||||||||||||||||||::|||||::|||:|||
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350

---

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGTACGCCAGACT 250
    |||||||| |||||||::||||| |||:::|||||
65 uTrpValSerAlaIleSerGlySerGlySerThrTyrTyrAlaAspS 82

251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
    |||||||||||||||||||||||||||||||||::|||||::|||:||||
82 erValLysArgArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
    :::|||||||||||||||||||||||||||||||||||||||||||||||
82 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 98

351 TGCGAGCTTGACTACAGGG...............TCTGACT 376
    ||||::::                          ::||
115 sAlaLysAlaGlnArgGlyLeuHisThrAlaMetValProTrpGlyAspT 132

377 CCTGGGGCCCAGGAGTCCTGGTCACCGTCTCCTCA 411
    |||||||||:::|||||||||||||||||||||||
132 yrTrpGlyGlnGlyThrLeuValThrValSerSer 143

seq_name: /cgn2_6/ptdata/1/paa/US09_NEW_COMB.pep:US-09-791-537-39928

seq_documentation_block:
; Sequence 39928, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT:   Bionomix, Inc.
;   APPLICANT:   Debe, Derek
;   APPLICANT:   Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE:  2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39928
;   LENGTH: 148
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-39928

alignment_scores:
         Quality:    536.00                    Length:    143
         Ratio:      4.288                      Gaps:      2
Percent Similarity:  87.413      Percent Identity: 74.825

alignment_block:
US-09-019-441-4  x  US-09-791-537-39928

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1 MetGluLeuGlyLeuArgTrpLeuPheLeuValAlaIleLeuLeuGluGlyVa 17

51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
  |||||||||||||||||||||||||||||||||||||::||||
17 lGlnCysGluValGlnLeuValGlnSerGlyGlyGlyLeuValLysProG 34

101 GGGGGTCCCTGAGACTCTGGTGCCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
  |||||||||||||||||||||||||||||||||
34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCGGGGTTCAGGTTCACCTTC 150

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGTACGCAGACT 250
  ::::::|||  ||::|||||||||
49 SerSerTyrSerMetAsnTrpValArgGlnAlaProGlyLysGlyLeuGl 65

251 GTGGGTCTCACGTATTAGTAGTGGTGATCCCACATGTACGCAGACT 250
  |||||||||  ::||||||
65 uTrpValSerSerIleSerSerSerSerSerTyrIleTyrTyrAlaAspS 82

```
        99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

       351 TGCGAGCTTG..........ACTACAGGGTCTGACTCCTCGGGGCC 385
           |||::::                     :::      ||||||
       115 sAlaLysAlaHisTyrAspPheTrpSerGlyTyrTyrAspTyrTrpGlyG 132

       386 AGGGAGTCCTGGTCACCGTCTCCTCA 411
           |||||:::|||||||||||||||
       132 lnGlyThrLeuValThrSerSer 140
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-106513

seq_documentation_block:
; Sequence 106513, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 106513
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-106513

alignment_scores:
        Quality:    535.50              Length:     152
        Ratio:      4.250               Gaps:       3
Percent Similarity:  82.895     Percent Identity:  71.711

alignment_block:
US-09-019-441-4 x US-09-791-537-106513

Align seg 1/1   to: US-09-791-537-106513   from: 1  to: 150

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     1 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleLeuLysGlyVa 17

    51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
       |||||||||||||||||||||||||||||||||::::::|||
    17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProG 34

   101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
       |||||||||||||||||||||||||||||  ||||||||
    34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

   151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGCAGGGGCTGGA 200
       :::::||::|||  |||||||||||::||||||||::::|||||
    49 SerSerTyrTrpMetHisTrpValArgGlnAlaProGlyLysGlyLeuVa 65

   201 GTGGGTCTCACGTATTAGTAGTAGTGGTAGTGATCCCACATGGTACGCAGACT 250
       |||||||||||||||||::::||::|| |||  ||||||||||||||
    65 lTrpValSerArgIleAsnSerAspGlySerSerThrSerTyrAlaAspS 82

   251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
       ||||||||||||||||||||||||::||||||||||||||||||
    82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeu 98

   301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACACGGCTGTCTATTACTG 350
       :::|||||||||||||||||||||||||||||||||||||||
    99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

   351 TGCG.......AGCTTGACTACAGGGTCT................ 372
       |,|||      :::     ::|||||||
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   115 sAlaArgSerGlyAspTyrGlySerGlySerTyrTyrAsnProArgTyrT 132

   373 ..........GACTCCTGGGGCCAGGAGTCCTGTCACCGTC 405
             |||  ||||||::::|||:::||||||| ||||||
   132 yrTyrTyrTyrMetAspValTrpGlyLysGlyThrLeuValThrVal 148

   406 TCCTCA 411
       ||||||
   149 SerSer 150
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OM of: US-09-019-441-4 to: Issued_Patents_AA:*    out_format : pfs

Date: Sep 23, 2002 10:00 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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 -DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -GAPOP=12.000
 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
 -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=US0901941_@CGN_1_58 -NCPU=6 -ICPU=3 -LONGLOG
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Search information block:
Query: US-09-019-441-4
Query length: 411
Database: Issued_Patents_AA:*
Database sequences: 231628
Database length: 24425594
Search time (sec): 70.150000

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/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-468-671-4 +       499.00  952.92    1.0e-45  131  !
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-129-930B-96 +     496.00  946.53    2.2e-45  131  !
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-545-809A-95 +     481.00  919.39    8.5e-44  117  !
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-921-100-63 +      476.00  907.87    3.1e-43  141  !
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-416-557-51 +      476.00  907.87    3.1e-43  141  !
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-902-201-63 +      476.00  907.87    3.1e-43  141  !
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-902-201-51 +      470.00  896.31    1.4e-42  141  !
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-416-557-51 +      469.00  896.19    1.7e-42  118  !
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-545-809A-145 +    468.50  893.79    2.0e-42  136  !
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-976-183A-31 +     468.00  892.46    2.2e-42  141  !
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-902-201-65 +      468.00  892.46    2.2e-42  141  !
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-416-557-65 +      467.50  891.86    2.5e-42  136  !
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-765-783A-55 +     465.00  886.68    4.7e-42  141  !
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-921-100-55 +      465.00  886.68    4.7e-42  141  !

/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-880-142-55  +  465.00  886.68  4.7e-42  141
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-902-201-55  +  465.00  886.68  4.7e-42  141
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-416-557-55  +  465.00  886.68  4.7e-42  141
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-976-183A-34 +  464.50  886.08  5.3e-42  136
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-765-783A-59 +  464.00  884.75  6.0e-42  141

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-026-320A-2

alignment_scores:
      Quality:      516.00        Length:     141
      Ratio:        4.195         Gaps:       2
Percent Similarity:  87.234     Percent Identity:  72.340

alignment_block:
US-09-019-441-4 x US-08-026-320A-2

Align seg 1/1  to: US-08-026-320A-2    from: 1  to: 144

  1 ATGGAGTTGGCTGAGCTGGGTTTCCTTGTTCCTCTTTTGAAAGGTGT  50
    ||||||||||||||||::::|||::|||:||||||||         ||||||||||
  1 MetGluPheGlyLeuThrTrpLeuPheLeuValAlaAsnLeuLysGlyVa  17

 51 CCAGTGTGAGGTGCAGCTGGTGCAGTCTGGGGCGGCGGCTGGCAAAGCCTG  100
    |||||||||||||||::::|||||||||||||::||||||||:||||
 17 lGlnCysGluValGlnLeuLeuAspSerGlyGlyGlyLeuValGlnProG  34

101 GGGGTGCCCTGAGCACTCTGGTGCGCAGCCTCCGGTTCAGGTTCACCTTC  150
    ||||||||         |||||||||
 34 lyGlyCysLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

Percent Similarity: 94.068    Percent Identity: 81.356

alignment_block:
US-09-019-441-4 x US-08-545-809A-99

Align seg 1/1  to: US-08-545-809A-99  from: 1  to: 117

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    ||||||||||||||||||||||||||||||| :::::||||||||||
  1 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleIleLysGlyVa  17

 51 CCAGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
    |||||| ::::||||||||||||||||||||||||||::::||||||
 17 lGlnCysGlnValGlnLeuValGluSerGlyGlyGlyLeuValLysProG  34

101 GGGGTCCCTGAGACTCTGGTGCGCAGCCTTCCGGGTTCAGGTTCACCTTC  150
    |||||||||||||||||||| ||||||||||||||     ||||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA  200
    :::::||||||||||||||||||||||||::::||||||||||||||
 49 SerAspTyrTyrMetSerTrpIleArgGlnAlaProGlyLysGlyLeuGl  65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT  250
    ||||||| ||||||||||||||||||::  ::||||||||||||||
 65 uTrpValSerTyrIleSerSerSerGlySerThrIleTyrTyrAlaAspS  82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG  300
    |||||||||||||||||||||||||||||||||||::::||:::||
 82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu  98

301 TTTCTTCAAATGAACAGCCTGAGGAGCTGAGGACACGGCGTGCTATTACTG  350
    :::||||||||||||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  115

351 TGCG  354
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115 sAla  116
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seq_name: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:US-08-579-378A-20

seq_documentation_block:
; Sequence 20, Application US/08579378A
; Patent No. 6210671

GENERAL INFORMATION:
  APPLICANT: Co, Man Sung
  TITLE OF INVENTION:  Humanized Antibodies Reactive with
  TITLE OF INVENTION:  L-Selectin
  NUMBER OF SEQUENCES:  20
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  Townsend and Townsend and Crew
    STREET:  One MarketPlaza, Steuart Tower, Suite 2000,
    CITY:  San Francisco
    STATE:  California
    COUNTRY:  USA
    ZIP:  94105
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/579,378A
    FILING DATE:  27-DEC-1995
    CLASSIFICATION:  424
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 08/160,074
    FILING DATE:  30-NOV-1993
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 07/983,946
    FILING DATE:  01-DEC-1992
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  EP 95112895.8

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151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA  200
    :::::: |||:::|||||||||||||||||||::::||||||||||
 49 SerSerCysAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl  65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT  250
    |||||||| |||||||:::||||  :::||  ||::||||||||||
 65 uTrpValSerAlaIleSerGlySerGlyGlyGlySerThrTyrTyrAlaAspS  82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG  300
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 82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysSerLysAsnThrLeu  98

301 TTTCTTCAAATGAACAGCCTGAGGAGCTGAGGACACGGCGTGCTATTACTG  350
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 99 TyrLeuGlnMetAsnSerLeuArgAlaGluArgAspThrAlaValTyrTyrCy  115

351 TGCG...........AGCTTGACTACAGGGTCTGACTCCTGGGCCAGG  388
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115 sAlaLysGlyLysAsnAspIleLeuThrGlyTyrTyrAlaTrpGlyGlnG  132

389 GAGTCCTGGTCACCGTCTCCTCA  411
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132 lyThrLeuValThrValSerSer  139
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seq_name: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:US-08-545-809A-99

seq_documentation_block:
; Sequence 99, Application US/08545809A
; Patent No. 6096878

GENERAL INFORMATION:
  APPLICANT:  Honjo, Tasuku
  APPLICANT:  Matsuda, Fumihiko
  CURRENT APPLICATION DATA:
  TITLE OF INVENTION:  HUMAN IMMUNOGLOBULIN VH GENE
  TITLE OF INVENTION:  SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
  NUMBER OF SEQUENCES:  145
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  Fish & Richardson, P.C.
    STREET:  225 Franklin Street
    CITY:  Boston
    STATE:  MA
    COUNTRY:  US
    ZIP:  02110-2804
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Diskette
    COMPUTER:  IBM Compatible
    OPERATING SYSTEM:  Windows95
    SOFTWARE:  FastSEQ for Windows Version 2.0
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/545,809A
    FILING DATE:  27-MAR-1996
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  PCT/JP93/00603
    FILING DATE:  10-MAY-1993
  ATTORNEY/AGENT INFORMATION:
    NAME:  Freeman, John W.
    REGISTRATION NUMBER:  29,066
    REFERENCE/DOCKET NUMBER:  06501/004001
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  617-542-5070
    TELEFAX:  617-542-8906
    TELEX:  200154
  INFORMATION FOR SEQ ID NO: 99:
    SEQUENCE CHARACTERISTICS:
    LENGTH:  117 amino acids
    TYPE:  amino acid
    TOPOLOGY:  linear
    MOLECULE TYPE:  protein
US-08-545-809A-99

alignment_scores:
       Quality:  508.00        Length:  118
       Ratio:  4.577            Gaps:  1
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; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-579-378A-20

alignment_scores:
          Quality:   501.00              Length:    138
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  51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCCAAAGCCTG 100
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  34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

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  65 uTrpValAlaSerIleSerThrGlyGlySer...ThrTyrTyrProAspS  81

 251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACCCAACAACACTG  300
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 301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG  350
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  98 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 114

 351 TGCGAGCTTGACTACAGGG...TCTGACTCCTGGGGCCAGGGAGTCCTGG 397
     ||| ||| |||  |||||||||||||||||||||||||||||||||||
 114 sAlaArgAspTyrAspGlyTyrPheAspTyrTrpGlyGlnGlyThrLeuV 131

 398 TCACCGTCTCCTCA 411
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 131 alThrValSerSer 135

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-259-372A-2

seq_documentation_block:
; Sequence 2, Application US/08259372A
; Patent No. 5565354
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,372A
; FILING DATE: 14-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/871,426
; FILING DATE: 21-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,036
; FILING DATE: 27-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/538,796
; FILING DATE: 15-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/192,754
; FILING DATE: 11-MAY-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/925,196
; FILING DATE: 31-OCT-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/904,517
; FILING DATE: 05-SEP-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-50-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-259-372A-2

alignment_scores:
          Quality:   501.00              Length:    143
           Ratio:    4.107               Gaps:        3
Percent Similarity:  85.315      Percent Identity: 72.028

alignment_block:
US-09-019-441-4 x US-08-259-372A-2          ..

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  17 lGlnCysGlnValGlnLeuValGluSerGlyGlyGlyLeuValGlnProG  34

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 101

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201  GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT  250
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 65  uTrpValAlaValIleSerTyrAspGlySerAsnLysTrpTyrAlaAspS  82

251  CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACACACACTG  300
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 82  erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu  98

301  TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG  350
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 99  PheLeuGlnMetHisSerLeuArgAlaAlaAspThrGlyValTyrTyrCy  115

351  TGGG......AGCTTGACTACAGGGTCGACTCC...........TGGG  382
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115  sAlaLysAspGlnLeuTyrPheGlySerGlnSerProGlyHisTyrTrpV  132

383  GCCAGGGAGTCCTGGTCACCGTCTCCTCA  411
     ||||::|||||||||||||||
132  alGlnGlyThrLeuValThrValSerSer  141
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seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-468-671-2

seq_documentation_block:
; Sequence 2, Application US/08468671
; Patent No. 5648077
; GENERAL INFORMATION:
;   APPLICANT: Ostberg, Lars G.
;   TITLE OF INVENTION:  PRODUCTION OF HUMAN MONOCLONAL
;   TITLE OF INVENTION:  ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
;   NUMBER OF SEQUENCES:  16
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Townsend and Townsend and Crew LLP
;     STREET:  Two Embarcadero Center, Eighth Floor
;     CITY:  San Francisco
;     STATE:  CA
;     COUNTRY:  USA
;     ZIP:  94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/468,671
;     FILING DATE:  06-JUN-1995
;     CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/259,372
;     FILING DATE:  14-JUN-1994
;     APPLICATION NUMBER:  US 07/871,426
;     FILING DATE:  21-APR-1992
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/676,036
;     FILING DATE:  27-MAR-1991
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/538,796
;     FILING DATE:  15-JUN-1990
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/192,754
;     FILING DATE:  11-MAY-1988
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 06/925,196
;     FILING DATE:  31-OCT-1986
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 06/904,517
;     FILING DATE:  05-SEP-1986
;   ATTORNEY/AGENT INFORMATION:

;   NAME:  Smith, William M.
;   REGISTRATION NUMBER:  30,223
;   REFERENCE/DOCKET NUMBER:  11823-50-7
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (415) 326-2400
;     TELEFAX:  (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  141 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-468-671-2

alignment_scores:
       Quality:   501.00              Length:    143
       Ratio:       4.107             Gaps:        3
Percent Similarity:  85.315    Percent Identity:  72.028

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US-09-019-441-4 x US-08-468-671-2

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  1  MetGluPheGlyLeuSerTrpValPheLeuValAlaLeuArgGlyVa  17

 51  CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
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 17  lGlnCysGlnValGlnLeuValGluSerGlyGlyGlyValValGlnProG  34

101  GGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC  150
     ||  |||||||||||||||||||||||||||||      |||||||
 34  lyArgSerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

151  AATAACTACTACATGACTGGGTCCCGCCAGGCTCCAGGGCAGGGGCTGGA  200
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 49  SerArgTyrGlyMetHisTrpValArgGlnAlaProGlyLysGlyLeuGl  65

201  GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT  250
     ||||||::|  |||||  ::|||||  |||||||||||||||||||
 65  uTrpValAlaValIleSerTyrAspGlySerAsnLysTrpTyrAlaAspS  82

251  CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACACACACTG  300
     ||||||||||||||||||||::||::|||||||||||||::|||||
 82  erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu  98

301  TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG  350
     |||||||||||||||||||||  ||||||::||||||||||||
 99  PheLeuGlnMetHisSerLeuArgAlaAlaAspThrGlyValTyrTyrCy  115

351  TGGG......AGCTTGACTACAGGGTCGACTCC...........TGGG  382
     ||||  :::|||     |||||:::|||      |||
115  sAlaLysAspGlnLeuTyrPheGlySerGlnSerProGlyHisTyrTrpV  132

383  GCCAGGGAGTCCTGGTCACCGTCTCCTCA  411
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132  alGlnGlyThrLeuValThrValSerSer  141
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seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-259-372A-4

seq_documentation_block:
; Sequence 4, Application US/08259372A
; Patent No. 5565354
; GENERAL INFORMATION:
;   APPLICANT:  Ostberg, Lars G.
;   TITLE OF INVENTION:  PRODUCTION OF HUMAN MONOCLONAL
;   TITLE OF INVENTION:  ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
;   NUMBER OF SEQUENCES:  16
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Townsend and Townsend and Crew LLP

```
    STREET:   Two Embarcadero Center, Eighth Floor
    CITY:     San Francisco
    STATE:    CA
    COUNTRY:  USA
    ZIP:      94111-3834
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER:    IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE:   PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/259,372A
    FILING DATE:  14-JUN-1994
    CLASSIFICATION:  424
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 07/871,426
    FILING DATE:  21-APR-1992
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 07/676,036
    FILING DATE:  27-MAR-1991
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 07/538,796
    FILING DATE:  15-JUN-1990
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 07/192,754
    FILING DATE:  11-MAY-1988
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 06/925,196
    FILING DATE:  31-OCT-1986
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 06/904,517
    FILING DATE:  05-SEP-1986
  ATTORNEY/AGENT INFORMATION:
    NAME: Smith, William M.
    REGISTRATION NUMBER:  30,223
    REFERENCE/DOCKET NUMBER: 11823-50-7
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  (415) 326-2400
    TELEFAX:   (415) 576-0300
  INFORMATION FOR SEQ ID NO: 4:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  131 amino acids
      TYPE:  amino acid
      TOPOLOGY: linear
    MOLECULE TYPE: protein
US-08-259-372A-4
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alignment_scores:
         Quality:       499.00          Length:        137
         Ratio:         4.229           Gaps:            3
Percent Similarity:    86.131    Percent Identity:  74.453

alignment_block:
US-09-019-441-4 x US-08-259-372A-4

Align seq 1/1  to: US-08-259-372A-4   from: 1  to: 131

  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGT  50
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  1 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleLeuGluGlyVa  17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
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 17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProG  34

101 GGGGTCCCTGAGACTCTGCTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    |||||||||||||  ||||||||||||||||||        |||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe  48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
    :::::||| ||| ||||||||||||||||||| |||:::||||||
 49 SerArgTyrAspMetTyrTrpValArgGlnAlaThrGlyLysGlyLeuGl  65
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201 GTGGGTCTCACGTATTAGTAGTAGTAGTGGTGATCCCACATGTACCGAGACT 250
    |||||||||  |||::: :::||||| |||:::||||||||||
 65 uTrpValSerAlaIleGlyProThrGlyAsp...ThrTyrTyrAlaAspS  81

251 CCGTGAAGGCAGATTCACCATCTCCAGAGACAACGCCAACAACAACACTG 300
    ||||||||||||||||||||||||||||||:::|||:::||:||
 81 erValLysGlyArgPheThrIleSerArgGluAsnAlaLysAsnSerLeu  97

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
    :::||  |||||||:::|||||||||||||  |||||||||||||
 98 TyrLeuThrMetAsnGlyLeuArgAlaGlyAspThrAlaValTyrTyrCy 114

351 TGCGAGCTTGACTACAGGGGTCCTGACTCCTGGGGCCAGGGAGTCCTGGTCA 400
    ||||  ||||||||||:::||||||||||:::|||||
114 sAla........ArgAspLeuGluTrpGlyGlnGlyThrLeuValT 128

401 CCGTCTCCTCA 411
    |||||||||||
128 hrValSerSer 131
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;       TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  4:
;       SEQUENCE CHARACTERISTICS:
;       LENGTH:   131 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;       MOLECULE TYPE:  protein
US-08-468-671-4

alignment_scores:
        Quality:   499.00              Length:   137
        Ratio:    4.229                Gaps:      3
Percent Similarity:  86.131    Percent Identity: 74.453

alignment_block:
US-09-019-441-4 x US-08-468-671-4

Align seq 1/1  to: US-08-468-671-4  from: 1  to: 131

   1 ATGGAGTTTGGCTGAGCTGGGTTTCCTTGTTCCTCTTTTGAAAGGTGT  50
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   1 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleLeuGluGlyVa  17

  51 CCAGTGTGAGGTGCAGCTGGTGAGTCTGGGGCGGCCGGTTGGGCAAAGCCTG 100
     |||||||||||||||||||||||||||||||||||||:::||||||||
  17 IGlnCysGluValGlnLeuValGlyGlyGlyGlyLeuValGlnProG  34

 101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
     |||||||||||||| ||||||||||||    ||||||||
  34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

 151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
     :::||| ||| |||||||||||||:||||||||   ||||||||||||||
  49 SerArgTyrAspMetTyrTrpValArgGlnAlaThrGlyLyrGlyLeuGl  65

 201 GTGGGGTCACGTATTAGTAGTAGTGGTGATCCCACCATGGTACGCCAGACT 250
     ||||||||| ||::|   ::||||| ||::|||||||
  65 uTrpValSerAlaIleGlyProThrGlyAsp...ThrTyrTyrAlaAspS  81

 251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACACACACTG 300
     |||||||||||||||||||||||||:::||:::::||::||||
  81 erValLysGlyArgPheThrIleSerArgGluAsnAlaLysAsnSerLeu  97

 301 TTTCTTCAAATGAACAGCCTGAGGAGTGAGGACCACCGGCTGTTCTATTACTG 350
     :::||| ||||||:::|||| |||||||||||||
  98 TyrLeuThrMetAsnGlyLeuArgAlaGlyAlaGluAspThrArgLeuValT 114

 351 TGCGAGCTTGACTACAGGGTCTGACTCCTGGGCCAGGAGTCCTGGTCA 400
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 114 sAla........ArgAspLeuGluLeuTrpGlyGlnGlyThrLeuValT 128

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 128 hrValSerSer 131
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;       TELEFAX:  (510) 521-3541
;       TELEX:  n.a.
INFORMATION FOR SEQ ID NO:  96:
;       SEQUENCE CHARACTERISTICS:
;       LENGTH:  139 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;       MOLECULE TYPE:  peptide
US-08-129-930B-96

alignment_scores:
        Quality:   496.00              Length:   141
        Ratio:    4.066                Gaps:      2
Percent Similarity:  86.525    Percent Identity: 70.213

alignment_block:
US-09-019-441-4 x US-08-129-930B-96

Align seq 1/1  to: US-08-129-930B-96  from: 1  to: 139

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   1 MetAspPheGlyLeuSerLeuValPheLeuValLeuIleLeuLysGlyVa  17

  51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGCGGCGGCTTGGCAAAGCCTG 100
     |||||||||||||||||||||||||||||||||||::::||||||
  17 lGlnCysGluValGlnMetValGluSerGlyGlyGlyLeuValGlnProG  34

 101 GGGGGTCCCTGAGACTCTGGTGCGCCAGCCAGCCTCCGGGTTCAGGTTCACCTTC 150
     |||||||||||| |||||||||||     ||:::::||
  34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheAlaPhe  48

 151 AATAACTACTACATGGACTGGGTCCGGCAGGCTCCAGGCAGGGGCTGGA 200
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  49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl  65

 201 GTGGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACCATGGTACGCAGACT 250
     ||||||||||   ||||:||::||::||::||| :::||||
  65 uTrpValAlaGluIleSerSerGlyGlyAsnTyrAlaTyrTyrGlnAspT  82

 251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACACACACTG 300
     :::||  ||||||||||||||||||||||||||::||:::::|||
  82 hrValThrGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu  98

 301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACGACACGGCTGTTATTACTG 350
     ::::||||||:::|||||||||||||||||||||
  99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

 351 TGCGAGCTTGACTACAGGGTCTGACTCC...........TGGGGCCAGG 388
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 115 sAlaArgGluAspTyrGlyIleProAlaTrpPheAlaTyrTrpGlyGlnG 132
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;       STREET:  2055 No. 5804187th Broadway, Suite 201
;       CITY:  Walnut Creek
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94596
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS 5.0
;       SOFTWARE:  Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/129,930B
;       FILING DATE:  September 30, 1993
;       CLASSIFICATION:  424
;   ATTORNEY/AGENT INFORMATION:
;       NAME:  Amzel Ph.D., Viviana
;       REGISTRATION NUMBER:  30,930
;       REFERENCE/DOCKET NUMBER:  CRFCC-008A
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (510) 521-1333
;       TELEFAX:  (510) 521-3541
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seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-129-930B-96

seq_documentation_block:
; Sequence 96, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
;   APPLICANT:  do Couto Dr., Fernando J.R.
;   APPLICANT:  Ceriani Dr., Roberto L.
;   APPLICANT:  Peterson Dr., Jerry A.
;   APPLICANT:  Padlan Dr., Eduardo A.
;   TITLE OF INVENTION:  Analogue Peptides With Broad
;   TITLE OF INVENTION:  Carcinoma Specificity, and Kit and
;   TITLE OF INVENTION:  Diagnostic Vaccination and
;   TITLE OF INVENTION:  Therapeutic Methods
;   NUMBER OF SEQUENCES:  96
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  V. AMZEL & ASSOC.
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389 GAGTCCTGGTCACCGTCTCCTCA 411
    ||:::||||||||||||||||
132 lyThrLeuValThrValSerSer 139
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seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-134-346A-51

seq_documentation_block:
; Sequence 51, Application US/08134346A
; Patent NO. 6281335
; GENERAL INFORMATION:
; APPLICANT:    do Couto, F.J.R.
; APPLICANT:    Ceriani, R.L.C.
; APPLICANT:    Petersen, J.A.
; TITLE OF INVENTION:    HYBRIDOMA AND ANTI-KC-4 HUMANIZED
; TITLE OF INVENTION:    MONOCLONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND
; TITLE OF INVENTION:    DIAGNOSTIC AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES:    51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:    Ostrager, Chong & Flaherty
; STREET:    300 Park Avenue
; CITY:    New York
; STATE:    NY
; COUNTRY:    US
; ZIP:    10022-7499
; COMPUTER READABLE FORM:
; MEDIUM TYPE:    Diskette-3.50 inch, 1.44 Mb storage
; COMPUTER:    IBM PC compatible
; OPERATING SYSTEM:    PC-DOS/MS-DOS
; SOFTWARE:    PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:    US/08/134,346A
; FILING DATE:    08-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME:    Onofrio, Dara L.
; REGISTRATION NUMBER:    34,889
; REFERENCE/DOCKET NUMBER:    CLT 149,608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:    212-826-6565
; TELEFAX:    212-826-5909
; INFORMATION FOR SEQ ID NO:    51:
; SEQUENCE CHARACTERISTICS:
; LENGTH:    139 amino acids
; TYPE:    amino acid
; STRANDEDNESS:
; TOPOLOGY:    linear
; MOLECULE TYPE:    peptide
US-08-134-346A-51

alignment_scores:
    Quality:    496.00         Length:    141
    Ratio:    4.066            Gaps:    2
Percent Similarity:    86.525    Percent Identity:    70.213

alignment_block:
US-09-019-441-4 x US-08-134-346A-51

Align seq 1/1  to: US-08-134-346A-51  from: 1  to: 139

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  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGT 50
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  1 MetAspPheGlyLeuSerLeuValPheLeuValLeuIleLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
    |||||||||||||||||:::|||||||||||||||||:::||||
 17 lGlnCysGluValGlnMetValGluSerGlyGlyGlyLeuValGlnProG 34

101 GGGGGTCCCTGAGACTCTGTCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    |||||||||||  |||||||||| ||:::|||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheAlaPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
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(right column)

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 49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG1 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    ||||||:::||||||||::::|||||||::::  ::::::||| |||:
 65 uTrpValAlaGluIleSerSerGlyGlyAsnTyrAlaTyrTyrGlnAspT 82

251 CCGTGAAGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
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 82 hrValThrGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
    :::|||||||||||||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

351 TGCGAGTTGACTACAGGTCTGACTCC...........TGGGGCCAGG 388
    |||                            :::||||||||
115 sAlaArgGluAspTyrGlyIleProAlaTyrTrpGlyGlyGlnG 132

389 GAGTCCTGGTCACCGTCCCTCA 411
    ||:::||||||||||||||||
132 lyThrLeuValThrValSerSer 139
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seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-976-288A-96

seq_documentation_block:
; Sequence 96, Application US/08976288A
; Patent No. 6315997
; GENERAL INFORMATION:
; APPLICANT:    do Couto Dr., Fernando J.R.
; APPLICANT:    Ceriani Dr., Roberto L.
; APPLICANT:    Peterson Dr., Jerry A.
; APPLICANT:    Padlan Dr., Eduardo A.
; TITLE OF INVENTION:    Analogue Peptides With Broad
; TITLE OF INVENTION:    Carcinoma Specificity, and Kit and
; TITLE OF INVENTION:    Diagnostic Vaccination and
; TITLE OF INVENTION:    Therapeutic Methods
; NUMBER OF SEQUENCES:    96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:    Pretty, Schroeder & Poplawski
; STREET:    444 South Flower St., 19th Floor
; CITY:    Los Angeles
; STATE:    California
; COUNTRY:    USA
; ZIP:    90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE:    Floppy disk
; COMPUTER:    IBM PC compatible
; OPERATING SYSTEM:    PC-DOS/MS-DOS 5.0
; SOFTWARE:    PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:    US/08/976,288A
; FILING DATE:    No. 6315997ember 21, 1997
; CLASSIFICATION:    424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:    08/129,930
; FILING DATE:    September 30, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:    07/977,696
; FILING DATE:    No. 6315997ember 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME:    Viviana Amzel Ph.D.
; REGISTRATION NUMBER:    30,930
; REFERENCE/DOCKET NUMBER:    P6639938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:    (213) 622-7700
; TELEFAX:    (213) 489-4210
; TELEX:    n.a.
; INFORMATION FOR SEQ ID NO:    96:
; SEQUENCE CHARACTERISTICS:
; LENGTH:    139 amino acids
; TYPE:    amino acid
; TOPOLOGY:    linear

; MOLECULE TYPE: peptide
US-08-976-288A-96

alignment_scores:
      Quality:      496.00          Length:      141
      Ratio:        4.066           Gaps:        2
Percent Similarity: 86.525    Percent Identity: 70.213

alignment_block:
US-09-019-441-4 x US-08-976-288A-96

Align seg 1/1  to: US-08-976-288A-96  from: 1  to: 139

  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGT 50
    |||::::|||||||||||  ||||||||||   ::||||||||||
  1 MetAspPheGlyLeuSerLeuValPheLeuValLeuLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
    |||||||||||||||||::|||:::||::||||||||||||||::||||
 17 lGlnCysGluValGlnMetValGluSerGlyGlyGlyLeuValGlnProG 34

101 GGGGGTCCCTGAGACTCTGGTCGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    ||||||||||||||||||||   ||||||||||::|||:::||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheAlaPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCCAGGCTCCAGGGCAGGGGCTGGA 200
    ::::::|||  |||::|||||||||||||||||::|||||||
 49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    ||||||||||::::::||||||||:::||||   |||
 65 uTrpValAlaGluIleSerSerGlyGlyAsnTyrAlaTyrTyrGlnAspT 82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACACACTG 300
    :::||  ||||||||||||||||::|||::|||||||
 82 hrValThrGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACCGGCTGTCTATTACTG 350
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 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

351 TGCGAGCTTGACTACAGGGTCTGACTCC..........TGGGGCCAGG 388
    |||   |||||||||||||   |||   |||
115 sAlaArgGluAspTyrGlyIleProAlaTrpPheAlaTyrTrpGlyGlnG 132

389 GAGTCCTGGTCACCGTCTCCTCA 411
    ||::|||||||||||||||||
132 lyThrLeuValThrValSerSer 139

seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-545-809A-109

seq_documentation_block:
; Sequence 109, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
;    APPLICANT: Honjo, Tasuku
;    APPLICANT: Matsuda, Fumihiko
;    TITLE OF INVENTION:  HUMAN IMMUNOGLOBULIN VH GENE
;    TITLE OF INVENTION:  SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;    NUMBER OF SEQUENCES:  145
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fish & Richardson, P.C.
;       STREET:  225 Franklin Street
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  US
;       ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  Windows95
;       SOFTWARE:  FastSEQ for Windows Version 2.0

;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/545,809A
;       FILING DATE:  27-MAR-1996
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP93/00603
;       FILING DATE:  10-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;       NAME:  Freeman, John W.
;       REGISTRATION NUMBER:  29,066
;       REFERENCE/DOCKET NUMBER:  06501/004001
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-542-5070
;       TELEFAX:  617-542-8906
;       TELEX:  200154
; INFORMATION FOR SEQ ID NO:  109:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  117 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-545-809A-109

alignment_scores:
      Quality:      492.00          Length:      118
      Ratio:        4.514           Gaps:        1
Percent Similarity: 92.373    Percent Identity: 79.661

alignment_block:
US-09-019-441-4 x US-08-545-809A-109

Align seg 1/1  to: US-08-545-809A-109  from: 1  to: 117

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  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaLysIleLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
    |||||||||||||||||||||||||||||||||||||||||::||||
 17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG 34

101 GGGGGTCCCTGAGACTCTGGTCGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    ||||||||||||||||||||||||||||||   |||:::||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCCAGGCTCCAGGGCAGGGGCTGA 200
    ::||   ||::|:||||||||||||||||::|||||||
 49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
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 65 uTrpValSerAlaIleSerGlySerGlySerGlyGlySerThrTyrTyrAlaAspS 82

251 CCCTGAAGGGCAGATTCACCATCTCCAGAGAGACGCCAACACACTG 300
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 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
    ::||||||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAlaAspThrAlaValTyrTyrCy 115

351 TGCG 354
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115 sAla 116

seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-545-809A-107

seq_documentation_block:
; Sequence 107, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
;    APPLICANT:  Honjo, Tasuku
;    APPLICANT:  Matsuda, Fumihiko

; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson, P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: US
;   ZIP: 02110-2804
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows95
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/545,809A
;   FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/JP93/00603
;   FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
;   NAME: Freeman, John W.
;   REGISTRATION NUMBER: 29,066
;   REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-542-5070
;   TELEFAX: 617-542-8906
;   TELEX: 200154
; INFORMATION FOR SEQ ID NO: 107:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 117 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-08-545-809A-107

alignment_scores:
          Quality:      484.00            Length:      118
          Ratio:         4.440            Gaps:          1
Percent Similarity:     92.373    Percent Identity:    79.661

alignment_block:
US-09-019-441-4 x US-08-545-809A-107

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   1 MetGluLeuGlyLeuArgTrpValPheLeuValAlaIleLeuLeuGlyVa  17

  51 CCAGTGTGAGGTGCAGCTGCTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
     |||||||||||||||||||||||||||||||||||||||::::|||||||
  17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuGlyLeuProG  34

 101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
     ||||||||||  ||:||||||||  ||||||||
  34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

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  49 SerSerTyrTyrMetAspTrpValArgGlnAlaProGlyLysGlyLeuGl  65

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  65 uTrpValSerIleSerSerSerSerSerTyrIleTyrTyrAlaAspS    82

 251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG    300
     |||||||||||||||||||||||:::||||||:::||||||||
  82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu  98

 301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTG  350


;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;
  99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115
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 351 TGCG 354
     ||||
 115 sAla 116

seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-545-809A-130

seq_documentation_block:
; Sequence 130, Application US/0854809A
; Patent No. 6096878
; GENERAL INFORMATION:
;   APPLICANT: Honjo, Tasuku
;   APPLICANT: Matsuda, Fumihiko
;   TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
;   TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;   NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson, P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: US
;   ZIP: 02110-2804
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows95
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/545,809A
;   FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/JP93/00603
;   FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
;   NAME: Freeman, John W.
;   REGISTRATION NUMBER: 29,066
;   REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-542-5070
;   TELEFAX: 617-542-8906
;   TELEX: 200154
; INFORMATION FOR SEQ ID NO: 130:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 117 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-08-545-809A-130

alignment_scores:
          Quality:      481.00            Length:      118
          Ratio:         4.413            Gaps:          1
Percent Similarity:     92.373    Percent Identity:    78.814

alignment_block:
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   1 MetGluLeuGlyLeuCysTrpValPheLeuValAlaIleLeuLeuGlyVa  17

  51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
     ||||||||||||||||||||||||||||||||||||||::||||||||||
  17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuGlyLeuGlnProG  34

 101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
     ||||||||||  |||||||||||

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Align seg 1/1   to: US-08-545-809A-95   from: 1   to: 117

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 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
    ||||||||||||||||||||||||||||||||:::||||||||
 17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProG  34

101 GGGGGTCCCTGAGACTCTGGTGCCAGCCTCCGGGTTCCACCTTC  150
    |||||||||||||||      |||||||||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA  200
    :::::||:::|||||||||||||||||||:::|||||||
 49 SerSerTyrSerMetAsnTrpValArgGlnAlaProGlyLysGlyLeuGl  65

201 GTGGGTCTCACGTATTAGTAGTGGTGATCCCACATGGTACGCAGACT  250
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 65 uTrpValSerTyrIleSerSerSerSerThrIleTyrTyrAlaAspS  82

251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACACACTG  300
    ||||||||||||||||:::|||||:::|||||:||:::|||
 82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu  98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG  350
    :::||||||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  115

351 TGCG  354
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115 sAla  116
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seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-545-809A-95

seq_documentation_block:
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; Patent No. 6096878
; GENERAL INFORMATION:
;   APPLICANT:  Honjo, Tasuku
;   APPLICANT:  Matsuda, Fumihiko
;   TITLE OF INVENTION:  HUMAN IMMUNOGLOBULIN VH GENE
;   TITLE OF INVENTION:  SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;   NUMBER OF SEQUENCES:  145
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Fish & Richardson, P.C.
;     STREET:  225 Franklin Street
;     CITY:  Boston
;     STATE:  MA
;     COUNTRY:  US
;     ZIP:  02110-2804
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  Windows95
;     SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/545,809A
;     FILING DATE:  27-MAR-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/JP93/00603
;     FILING DATE:  10-MAY-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Freeman, John W.
;     REGISTRATION NUMBER:  29,066
;     REFERENCE/DOCKET NUMBER:  06501/004001
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  617-542-5070
;     TELEFAX:  617-542-8906
; INFORMATION FOR SEQ ID NO:  95:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  117 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-545-809A-95

alignment_scores:
       Quality:   478.00          Length:  118
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Percent Similarity:  94.915   Percent Identity:  76.271

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;   TELEX:   200154
;  INFORMATION FOR SEQ ID NO:   106:
;  SEQUENCE CHARACTERISTICS:
;     LENGTH:   117 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;  MOLECULE TYPE:  protein
US-08-545-809A-106


alignment_scores:
         Quality:   478.00           Length:    118
         Ratio:     4.426            Gaps:       1
Percent Similarity:   91.525     Percent Identity: 77.966

alignment_block:
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 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCCGGCTTGGCAAAGCCTG 100
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 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGCTGGA 200
    ::::::|||    |||:::||||||||||||||:::||||||
 49 AspAspTyrGlyMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
    |||||||||   :::||||   |||  ||||||||||
 65 uTrpValSerGlyIleAsnTrpAsnGlyGlySerThrGlyTyrAlaAspS 82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
    ||||||||||||||||||||||:::||||||:::|||
 82 erValLysGlyArgPheThrIleSerArgAsnAlaLysAsnSerLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACCGGCTGTCTATTACTG 350
    :::|||||||||||||||||||||||||||||:::|||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaLeuTyrHisCy 115

351 TGCG 354
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115 sAla 116
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Date: Sep 23, 2002 10:06 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

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-DB=A_Genseq_032802 -QFMT=fastan -SUFFIX=rag -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0901941_@CGN_1_175 -NCPU=6 -ICPU=3 -LONGLOG
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Search information block:
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Query length: 411
Database: A_Geneseq_032802:*
Database sequences: 747574
Database length: 111073796
Search time (sec): 193.710000
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DT   18-NOV-1998  (first entry)
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XX
KW   Anti-human CD23 5E8 monoclonal antibody; heavy chain variable region;
KW   human CD23; IgE; FceRii/CD23; gamma-1 constant region;
KW   gamma-3 constant region; allergy; inflammation; autoimmune disease;
KW   allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia.
XX
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XX
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FT   Protein         20..137
FT                   /note= "anti-human CD23  5E8 heavy chain variable
FT                   region"
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PD   27-AUG-1998.
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PF   17-FEB-1998;   98WO-US02253.
XX
PR   05-FEB-1998;   98US-0803085.
PR   20-FEB-1997;   97US-0803085.
XX
PA   (IDEC-) IDEC PHARM CORP.
PA   (SEGK ) SEIKAGAKU CORP.
XX
PI   Kloetzer WS,  Nakamura T,   Reff ME;
XX
DR   WPI; 1998-467495/40.
DR   N-PSDB; AAV33310.
XX
PT   New anti-human CD23 monoclonal antibody - used for inhibiting IgE
PT   expression to treat or prevent allergic, inflammatory and
PT   auto:immune conditions
XX
PS   Example 1; Pages 108-110; 146pp; English.
XX
CC   The present sequence represents the heavy chain variable region of
CC   primate monoclonal antibody anti-human CD23 5E8. The invention
CC   provides primate monoclonal antibodies which specifically bind human
CC   CD23, the low affinity receptor for IgE (FceRii/CD23), and comprise
CC   either of a human gamma-1 or human gamma-3 constant region that binds
CC   to human Fc gamma receptors and inhibits IgE expression. The monoclonal
CC   antibodies of the invention are claimed to be useful for inhibiting
CC   induced IgE production for treating or preventing allergic, inflammatory
CC   and autoimmune conditions e.g. allergic rhinitis conjunctivitis,
CC   autoimmune haemolytic anaemia, etc.
XX
SQ   Sequence    137 AA;
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alignment_scores:
              Quality:    731.00              Length:    137
              Ratio:        5.336              Gaps:        0
Percent Similarity:     100.000     Percent Identity:  100.000

alignment_block:
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   51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
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   51 AsnAsnTyrTyrMetSerTrpValArgGlnAlaProGlyGlnGlyLeuGl  67

  201 GTGGGTCTCAGTATTAGTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT  250
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   67 uTrpValSerArgIleSerSerSerGlyAspProThrTrpTyrAlaAspS  84

  251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG  300
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   84 erValLysGlyArgPheThrIleSerArgGluAsnAlaAsnAsnThrLeu  100

  301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACCGCTGTCTATTACTG  350
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  101 PheLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  117

  351 TGCGAGCTTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCA  400
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  117 sAlaSerLeuThrThrGlySerAspSerTrpGlyGlnGlyValLeuValT  134

  401 CCGTCTCCTCA 411
      |||||||||||
  134 hrValSerSer 137

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:AAM23924

seq_documentation_block:
ID  AAM23924 standard; Protein; 596 AA.
XX
AC  AAM23924;
XX
DT  12-OCT-2001  (first entry)
XX
DE  Human EST encoded protein SEQ ID NO: 1449.
XX
KW  Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW  tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW  diagnostics; forensic test; gene mapping; genetic disorder;
KW  biodiversity; gene therapy; nutrition.
XX
OS  Homo sapiens.
XX
PN  WO200154477-A2.
XX
PD  02-AUG-2001.
XX
PF  25-JAN-2001; 2001WO-US02687.
XX
PR  25-JAN-2000; 2000US-0491404.
PR  17-JUL-2000; 2000US-0617746.

PR  03-AUG-2000; 2000US-0631451.
PR  15-SEP-2000; 2000US-0663870.
XX
PA  (HYSE-) HYSEQ INC.
XX
PI  Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI  Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR  WPI; 2001-476164/51.
DR  N-PSDB; AAH98583.
XX
PT  Isolated polypeptide for treatment of diseases, diagnostics, raising
PT  antibodies and research use -
XX
PS  Claim 20; Page 1011-1012; 1275pp; English.
XX
CC  The present invention provides the protein and coding sequences of novel
CC  proteins from a variety of organisms, including human, dog, cat, horse,
CC  cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC  urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC  from the organism of interest. They can be used in diagnostics,
CC  forensics, gene mapping, identification of mutations, to assess
CC  biodiversity and for nutritional purposes. The present sequence is a
CC  protein of the invention.
XX
SQ  Sequence   596 AA;

alignment_scores:
              Quality:    540.00              Length:    145
              Ratio:        4.355              Gaps:        2
Percent Similarity:     85.517     Percent Identity:  74.483

alignment_block:
US-09-019-441-4 x AAM23924

Align seg 1/1  to: AAM23924   from: 1  to: 596

    1 ATGGAGTTTGGGCTGAGCTGGGTTTCCTTGTTCCTCTTTGAAAGGTGT  50
      |||||||||||||||||||||||||||    :::||||||||||||||
    1 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleLeuLysGlyVa  17

   51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
      ||||||||||||||||||||||||||||||||||||||||||:::::|||
   17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProG  34

  101 GGGGGTCCCTGAGACTCTGGTGCCGCAGCCTCCGGTTCAGGTTCACCTTC  150
      |||||||||||||  ||||||||||||||||||||||||||||||||||
   34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

  151 AATAACTACTACATGAGCTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA  200
      :::::|||:::||  |||||||||||||||||||||||||||::::||||
   49 SerSerTyrTrpMetHisTrpValArgGlnAlaProGlyLysGlyLeuVa  65

  201 GTGGGTCTCAGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT  250
      |||||||||||||||||||:::::    ||| |||||||||||||||||
   65 lTrpValSerArgIleAsnThrAspGlySerSerThrSerTyrAlaAspS  82

  251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG  300
      ||||||||||||||||||||||||||| || |||||||||||||||||
   82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeu  98

  301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACCGCTGTCTATTACTG  350
      :::||||||||||||||||||||||||||||||||||||||||||||||
   99 TyrLeuGlnMetAsnSerLeuArgLeuAlaGluAspThrAlaValTyrTyrCy  115

  351 TGCGAGCTTGACTACAGGGTCT...................GACT  376
      |||            :::              |||
  115 sAlaArgAlaAspAsnCysSerSerThrSerCysTyrLysCysPheAspT  132

  377 CCTGGGCCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
      ||||||||:::||||||||||||||||||||||||
  132 yrTrpGlyGlnGlyThrLeuValThrValSerSer 143

us-09-019-441-4.rag

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2001.DAT:AAU14320

seq_documentation_block:
ID   AAU14320 standard; Protein; 313 AA.
XX
AC   AAU14320;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human novel protein #191.
XX
KW   Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW   immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW   anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW   antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW   thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW   Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW   tissue regeneration; immune disorder.
XX
OS   Homo sapiens.
XX
PN   WO20015437-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US02623.
XX
PR   25-JAN-2000; 2000US-0491404.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Drmanac RT;
XX
DR   WPI; 2001-451939/48.
DR   N-PSDB; AAS22625.
XX
PT   Isolated polypeptides useful for treating anti-inflammatory diseases,
PT   nervous system disorders, and for regenerating bone and cartilage -
XX
PS   Example 4; Page 630-631; 894pp; English.
XX
CC   The invention relates to polynucleotides encoding novel human
CC   proteins or their active domains. The polypeptides, polynucleotides and
CC   antibodies raised against the polypeptides are used in a method of
CC   treatment of a mammal and prevention of disorders caused by the aberrant
CC   protein expression or activity.  The polypeptides can be used as
CC   molecular weight markers, food supplements, and in antibody production.
CC   The polypeptides are used to identify compounds which bind to the
CC   polypeptides. Polynucleotides of the invention are used as probes and
CC   primers, for sequencing, for chromosome or gene mapping, in the
CC   production of recombinant proteins, and in generating anti-sense DNA or
CC   RNA and in gene therapy.  Polypeptides of the invention can be used to
CC   target drugs to a tumour, in assays to determine biological activity, to
CC   raise antibodies/elicit an immune response, to determine quantitative
CC   protein levels, as tissue markers, and to isolate receptors or ligands.
CC   Polypeptides of the invention may also be useful in treating platelet
CC   disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC   ligament and/or nerve tissue, wound healing, treating burns, promoting
CC   the proliferation, differentiation and survival of stem cells, as a
CC   contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC   Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral
CC   sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC   fungal infection or from autoimmunity, cancer, allergy, asthma,
CC   graft-versus-host disease, eczema, haemophilia, thrombosis,
CC   anti-inflammatory diseases, nervous system disorders, and infection.
CC   The present sequence represents a protein of the invention.
XX
SQ   Sequence  313 AA;

alignment_scores:
       Quality:  538.50          Length:     148

                                 Ratio:    4.343
Percent Similarity:    83.784     Percent Identity:   83.784     Gaps:     2
                                                                          72.297

alignment_block:
US-09-019-441-4 x AAU14320

Align seq 1/1 to: AAU14320  from: 1  to: 313

     1 ATGGAGTTGGGCTGAGCTGGGTTTCCTTGTTCCTCTTTTGAAAGGTGT 50
       |||||||||||||||||||||||||||||||||  ::||||||||||||
    42 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 58

    51 CCAGTGAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAAGCCTG 100
       |||||||||||||||||||||| ||||||||||||::|||||:::||||
    58 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG 75

   101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
       ||||||||||||||||  ||||||||||||||||||  |||||
    75 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 89

   151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGCTGGA 200
       :::::|||  |||:::|||||||||||||||||||||::|||:||||||
    90 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 106

   201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
       |||||||||||:||||||  :||||||||||||||||||||||||||||
   106 uTrpValSerAlaIleSerGlySerGlySerThrTyrTyrAlaAspS 123

   251 CCGTGAAGGGCAGATTCACCATTCCAGAGAGAACGGCCAACAACACACTG 300
       ||||||||||||||||||||||||||||||:||::::::||||||||
   123 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 139

   301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
       ::|||||||||||||||||||||||||||||||||||||||||||||||
   140 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 156

   351 TGCGAGCTTGACTACAGGG.................................. 369
       ||||::|    |||
   156 sAlaLysSerHisProGlyTyrTyrTyrTyrAspSerSerGlyTyrSerTyrT 173

   370 ..TCTGACTCCTGGGCACCAGGGAGTCCTGGTCACCGTCCTCCTCA 411
         |||  |||||||||||||||::||||||||||||||||||||||
   173 yrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 187

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2001.DAT:AAU14225

seq_documentation_block:
ID   AAU14225 standard; Protein; 307 AA.
XX
AC   AAU14225;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human novel protein #96.
XX
KW   Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW   immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW   anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW   antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW   thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW   Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW   tissue regeneration; immune disorder.
XX
OS   Homo sapiens.
XX
PN   WO20015437-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US02623.
XX
PR   25-JAN-2000; 2000US-0491404.
XX

PA    (HYSE-) HYSEQ INC.
XX
PI    Tang YT, Liu C, Drmanac RT;
XX
DR    WPI; 2001-451939/48.
DR    N-PSDB; AAS22530.
XX
PT    Isolated polypeptides useful for treating anti-inflammatory diseases,
PT    nervous system disorders, and for regenerating bone and cartilage -
XX
PS    Example 4; Page 575; 894pp; English.
XX
CC    The invention relates to polynucleotides encoding novel human
CC    proteins or their active domains. The polypeptides, polynucleotides and
CC    antibodies raised against the polypeptides are used in a method of
CC    treatment of a mammal and prevention of disorders caused by the aberrant
CC    protein expression or activity. The polypeptides can be used as
CC    molecular weight markers, food supplements, and in antibody production.
CC    The polypeptides are used to identify compounds which bind to the
CC    polypeptides. Polynucleotides of the invention are used as probes and
CC    primers, for sequencing, for chromosome or gene mapping, in the
CC    production of recombinant proteins, and in generating anti-sense DNA or
CC    RNA and in gene therapy.  Polypeptides of the invention can be used to
CC    target drugs to a tumour, in assays to determine biological activity, to
CC    raise antibodies/elicit an immune response, to determine quantitative
CC    protein levels, as tissue markers, and to isolate receptors or ligands.
CC    Polypeptides of the invention may also be useful in treating platelet
CC    disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC    ligament and/or nerve tissue, wound healing, treating burns, promoting
CC    the proliferation, differentiation and survival of stem cells, as a
CC    contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC    Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC    sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC    fungal infection or from autoimmunity, cancer, allergy, asthma,
CC    graft-versus-host disease, eczema, haemophilia, thrombosis,
CC    anti-inflammatory diseases, nervous system disorders, and infection.
CC    The present sequence represents a protein of the invention.
XX
SQ    Sequence  307 AA;

alignment_scores:
          Quality:      534.00            Length:     137
          Ratio:          4.341            Gaps:          1
Percent Similarity:  89.781    Percent Identity:  75.912

alignment_block:
US-09-019-441-4 x AAU14225       ..

Align seg 1/1  to: AAU14225   from: 1  to: 307

  1 ATGGAGTTTGGGCTGAGCTGGTTTCCTTGTTGTTCCTTCTTTTGAAAGGTGT 50
    |||||||||||||||||||||||||||||||| :::||||||||||||||
  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCCGCCTTGCCAAAGCCTG 100
    ||||||||||||||||::||||||||||||||||||||||||||::::||||
 17 lGlnCysGluValGlnLeuLeuLeuGluSerGlyGlyGlyLeuAlaGlnProG 34

101 GGGGGTCCCTGAGACTCTGCCGCCAGCCTCCGGGTTCACCTTC 150
    ||||||||| |||||||||||||||||||||   |||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

151 AATAACTACTACCATGGACTGGGTCCGCCCAGGCTCCAGGGCAGGGGCTGGA 200
    :::::::::  |||::|||||||||||||||||||||||||||||||||
 49 SerSerPheSerMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGTACCGCAGACT 250
    ||||||||  |||||||||||::: |||:||||||||||||||||||
 65 uTrpValSerIleSerGlySerSerGlyThrThrTyrTyrTyrAlaAspS 82

251 -CCGTGAAGGGCAGATTCACCATCTCCAGAGAGACGCCAACAACACACTG 300
    ||||||||||||||||||:||::||||||||::::||||||||||||||

 82 ervalLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACGACACGGCTGTCTATTACTG 350
    ::|||||||||||||||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

351 TGCGAGCTTGACTACAGGGTCTGCACTCCTGGGCCCAGGAGTCCTGGTCA 400
    ||| ||||||||||||  ||||||||:::|||||||
115 sAlaLysProPheProTyrPheAspTyrTrpGlyGlnGlyThrLeuValT 132

401 CCGTCTCCTCA 411
    |||||||||
132 hrValSerSer 135

seq_name: /SIDS1/scgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:AAU14228

seq_documentation_block:
ID    AAU14228 standard; Protein; 363 AA.
XX
AC    AAU14228;
XX
DT    24-OCT-2001  (first entry)
XX
DE    Human novel protein #99.
XX
KW    Human; novel protein; Antianaemic; osteopathic; antinflammatory;
KW    immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW    anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW    antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW    thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW    Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW    tissue regeneration; immune disorder.
XX
OS    Homo sapiens.
XX
PN    WO200155437-A2.
XX
PD    02-AUG-2001.
XX
PF    25-JAN-2001; 2001WO-US02623.
XX
PR    25-JAN-2000; 2000US-0491404.
XX
PA    (HYSE-) HYSEQ INC.
XX
PI    Tang YT, Liu C, Drmanac RT;
XX
DR    WPI; 2001-451939/48.
DR    N-PSDB; AAS22533.
XX
PT    Isolated polypeptides useful for treating anti-inflammatory diseases,
PT    nervous system disorders, and for regenerating bone and cartilage -
XX
PS    Example 4; Page 577; 894pp; English.
XX
CC    The invention relates to polynucleotides encoding novel human
CC    proteins or their active domains. The polypeptides, polynucleotides and
CC    antibodies raised against the polypeptides are used in a method of
CC    treatment of a mammal and prevention of disorders caused by the aberrant
CC    protein expression or activity.  The polypeptides can be used as
CC    molecular weight markers, food supplements, and in antibody production.
CC    The polypeptides are used to identify compounds which bind to the
CC    polypeptides. Polynucleotides of the invention are used as probes and
CC    primers, for sequencing, for chromosome or gene mapping, in the
CC    production of recombinant proteins, and in generating anti-sense DNA or
CC    RNA and in gene therapy.  Polypeptides of the invention can be used to
CC    target drugs to a tumour, in assays to determine biological activity, to
CC    raise antibodies/elicit an immune response, to determine quantitative
CC    protein levels, as tissue markers, and to isolate receptors or ligands.
CC    Polypeptides of the invention may also be useful in treating platelet
CC    disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC    ligament and/or nerve tissue, wound healing, treating burns, promoting
CC    the proliferation, differentiation and survival of stem cells, as a

CC   contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC   Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC   sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC   fungal infection or from autoimmunity, cancer, allergy, asthma,
CC   graft-versus-host disease, eczema, haemophilia, thrombosis,
CC   anti-inflammatory diseases, nervous system disorders, and infection.
CC   The present sequence represents a protein of the invention.
XX
SQ   Sequence   363 AA;

alignment_scores:
        Quality:   534.00          Length:      137
        Ratio:     4.341           Gaps:          1
Percent Similarity:  89.781     Percent Identity:  75.912

alignment_block:
US-09-019-441-4 x AAU14228          ..

Align seg 1/1   to: AAU14228   from: 1   to: 363

    1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTGAAAGGTGT 50
      ||||||||||||||||||||||||::|||||||||||||:::||||||||
    1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17

   51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGCCAAAGCCTG 100
      ||||||||||||||||||||:::|||||||||||||||||::::||||||
   17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG 34

  101 GGGGGTCCCTGAGACTCTGGTCGCCAGCCTCCGGGTTCAGGTTCACCTTC 150
      ||||||||||||||||||||||||||||:||||| ||||||
   34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

  151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
      :::::::||||:::|||::|||||||||||||||||::|||||||||||
   49 SerSerPheSerMetSerTrpValArgGlnAlaProGlyLyLysGlyLeuGl 65

  201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACACATGGTACGCAGACT 250
      |||||||||||||||||:::|||::::|||   |||:::||||||||||
   65 uTrpValSerSerIleSerGlySerSerGlyThrThrTyrTyrAlaAspS 82

  251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
      |||||||||||||||||||||||||:::::||::::::||||||||||
   82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98

  301 TTTCTTCAAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
      ::||||||||||||||||||||||||||::|:|||||||||||||||||
   99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

  351 TGCGAGCTTGACTACACAGGGTCTGACTCCTGGGGCCAGGAGTCCTGGTCA 400
      ||::: ||| |||||||||::::|||||::::||||
  115 sAlaLysProPheProTyrPheAspTyrTrpGlyGlnGlyThrLeuValT 132

  401 CCGTCCTCCTCA 411
      ||||||||||
  132 hrValSerSer 135

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:AAM24101

OS   Homo sapiens.
XX
PN   WO200154477-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US02687.
XX
PR   25-JAN-2000; 2000US-0491404.
PR   17-JUL-2000; 2000US-0617746.
PR   03-AUG-2000; 2000US-0631451.
PR   15-SEP-2000; 2000US-0663870.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI   Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
PS   Claim 20; Page 1102-1103; 1275pp; English.
XX
CC   The present invention provides the protein and coding sequences of novel
CC   proteins from a variety of organisms, including human, dog, cat, horse,
CC   cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC   urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC   from the organism of interest. They can be used in diagnostics,
CC   forensics, gene mapping, identification of mutations, to assess
CC   biodiversity and for nutritional purposes. The present sequence is a
CC   protein of the invention.
XX
SQ   Sequence   384 AA;

alignment_scores:
        Quality:   530.50          Length:      154
        Ratio:     4.278           Gaps:          2
Percent Similarity:  80.519     Percent Identity:  68.831

alignment_block:
US-09-019-441-4 x AAM24101          ..

Align seg 1/1   to: AAM24101   from: 1   to: 384

    1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTGAAAGGTGT 50
      |||||||||||||||||||||||||:::||||||||   ::|||||||||
    1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17

   51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGCCAAAGCCTG 100
      |||||||||||||||||||||||||||||:::|||||| :|:|||||||||
   17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG 34

  101 GGGGGTCCCTGAGACTCTGGTGCGCCAGCCTCCGGGTTCAGGTTCACCTTC 150
      |||||||||||||||| ||||||||||||||||||||| ||||||
   34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48

  151 AATAACTACTACATGAGCTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
      :::::||| |||:::||||::||||||||||||||||||||||||||||
   49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65

  201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACACATGGTACGCAGACT 250
      ||||||||||||||||||::::|||||:::||:::||::||||||||||
   65 uTrpValSerGlyIleGlyGlySerGlySerThrThrTyrTyrAlaAsps 82

  251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
      |||||||||||||||||||||||||::::::|||::::::||||||||||
   82 erValLysGlyArgPheThrIleSerArgAspAsnSerGlnAsnThrLeu 98

  301 TTTCTTCAAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350

Align seg 1/1   to: AAB99111   from: 1 to: 152

```
   1 ATGGAGTTGGCTGAGCTGGGTTTCCTTGTTCCTCTTTGAAAGGTGT 50
     |||||::!|||||   ||||||||||||   ::!||::!||||
   1 MetGluLeuGlyLeuArgTrpValPheLeuValAlaIleLeuGluGlyVa 17

  51 CCAGTGTGAGGTGCAGTCTGGTGGAGTCTGGGGCGGCTTGGCAAAGCCTG 100
     ||||||||||||||||||||||||||||||||||||::!||||
  17 1GlnCysGluValGlnLeuValGluSerGlyGlyLeuVallysProG 34

 101 GGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
     ||||||||||||||||||||||   |||||||
  34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

 151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
     ::::::::  |||::!||||||||||||||||::!||||||
  49 SerSerPheSerMetAsnTrpValArgGlnAlaProGlyLysGlyLeuGl 65

 201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
     ||||||||||  ||||||||||||||||||||||||
  65 uTrpValSerSerIleSerSerSerSerTyrIleTeyrTyrThrAspS 82

 251 CCGTGAAGGGCAGATTCACCATCTCCAGAGACGCCAACAACACACTG 300
     |||||||||||||||||||||||::!||||||||||::!|||
  82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu 98

 301 TTTCTTCAAATGAACAGCCTGAGAGTGGAGGACACGGCTGTCTATTACTG 350
     ::!|||||||||||||||||||||||||||||||||||||||||
  99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

 351 TGCGAGCTTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCA 400
     |||   |||   |||||||||||||||::!|||||
 115 sAlaArgGlyTyrTrpGlyPheAspTyrTrpGlyGlnGlyThrLeuValT 132

 401 CCGTCTCCTCA 411
     |||||||||||
 132 hrValSerSer 135
```

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:AAU14227

seq_documentation_block:
ID  AAU14227 standard; Protein; 312 AA.
XX
AC  AAU14227;
XX
DT  24-OCT-2001  (first entry)
XX
DE  Human novel protein #98.
XX
KW  Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW  immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW  anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW  antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW  thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW  Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW  tissue regeneration; immune disorder.
XX
OS  Homo sapiens.
XX
PN  WO200155437-A2.
XX
PD  02-AUG-2001.
XX
PF  25-JAN-2001; 2001WO-US02623.
XX
PR  25-JAN-2000; 2000US-0491404.
XX
PA  (HYSE-) HYSEQ INC.
XX
PI  Tang YT, Liu C, Drmanac RT;
XX
DR  WPI; 2001-451939/48.

---

```
  99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115
     ::!||||||||||||||||||||||||||||||||
 351 TGCGAGC.................................... 357

 115 sAlaLysSerHisProAlaTyrTyrTyrGlySerGlySerTyrSerSerH 132
     ||::!|||   |||
 358 .....TTGACTACAGGGTCTGACTCCTGGGCCAGGAGTCCTGGTC 399

 132 isTyrTyrTyrTyrGlyMetAspValTrpGlyGlnGlyThrThrVal 148
     ||||||||||:::::   |||
 400 ACCGTCTCCTCA 411
     ||||||||||
 149 ThrValSerSer 152
```

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:AAB99111

seq_documentation_block:
ID  AAB99111 standard; Protein; 152 AA.
XX
AC  AAB99111;
XX
DT  22-AUG-2001  (first entry)
XX
DE  Human protein SEQ ID 4.
XX
KW  Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis;
KW  Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;
KW  signal transduction inhibition; tissue fibrosis; atherosclerosis.
XX
OS  Homo sapiens.
XX
PN  WO200136642-A1.
XX
PD  25-MAY-2001.
XX
PF  17-NOV-2000; 2000WO-JP08129.
XX
PR  18-NOV-1999;  99JP-0328681.
PR  08-NOV-2000;  2000JP-0340216.
XX
PA  (NISB ) JAPAN TOBACCO INC.
XX
PI  Sakamoto S, Kamada M;
XX
DR  WPI; 2001-343825/36.
DR  N-PSDB; AAH41153.
XX
PT  Human monoclonal antibodies recognizing human TGF-beta II receptor,
PT  useful for treating TGF-beta associated diseases such as tissue
PT  fibrosis -
XX
PS  Claim 10; Page 94-95; 118pp; Japanese.
XX
CC  The present invention relates to novel human monoclonal antibodies. The
CC  antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II
CC  receptor, resulting in the inhibition of the signal transduction of human
CC  TGF-beta into cells. The antibodies can be used for the prevention and
CC  treatment of diseases associated with the production of TGF-beta, such as
CC  tissue fibrosis in the lung, liver, skin, kidney or other tissues,
CC  atherosclerosis, atopy, keloid and arthritis. The present sequence was
CC  used in the present invention.
XX
SQ  Sequence  152 AA;

alignment_scores:
         Quality:   528.00        Length:     137
            Ratio:    4.328          Gaps:        1
Percent Similarity:  89.051    Percent Identity: 75.912

alignment_block:
US-09-019-441-4 x AAB99111

DR   N-PSDB; AAS22532.
XX
PT   Isolated polypeptides useful for treating anti-inflammatory diseases,
PT   nervous system disorders, and for regenerating bone and cartilage -
XX
PS   Example 4; Page 576-577; 894pp; English.
XX
CC   The invention relates to polynucleotides encoding novel human
CC   proteins or their active domains. The polypeptides, polynucleotides and
CC   antibodies raised against the polypeptides are used in a method of
CC   treatment of a mammal and prevention of disorders caused by the aberrant
CC   protein expression or activity.  The polypeptides can be used as
CC   molecular weight markers, food supplements, and in antibody production.
CC   The polypeptides are used to identify compounds which bind to the
CC   polypeptides. Polynucleotides of the invention are used as probes and
CC   primers, for sequencing, for chromosome or gene mapping, in the
CC   production of recombinant proteins, and in generating anti-sense DNA or
CC   RNA and in gene therapy.  Polypeptides of the invention can be used to
CC   target drugs to a tumour, in assays to determine biological activity, to
CC   raise antibodies/elicit an immune response, to determine quantitative
CC   protein levels, as tissue markers, and to isolate receptors or ligands.
CC   Polypeptides of the invention may also be useful in treating platelet
CC   disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC   ligament and/or nerve tissue, wound healing, treating burns, promoting
CC   the proliferation, differentiation and survival of stem cells, as a
CC   contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC   Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC   sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC   fungal infection or from autoimmunity, cancer, allergy, asthma,
CC   anti-inflammatory diseases, nervous system disorders, and infection.
CC   The present sequence represents a protein of the invention.
XX
SQ   Sequence   312 AA;

alignment_scores:
          Quality:   526.50           Length:       142
          Ratio:       4.179          Gaps:           3
Percent Similarity:   88.732    Percent Identity:   72.535

alignment_block:
US-09-019-441-4 x AAU14227

Align seq 1/1 to: AAU14227   from: 1 to: 312

    1 ATGGAGTTGGGCTGCAGCTGGGTTTCCTTGTCCTCTTTTGAAAGGTGT  50
      |||||||||||||||||||||||:::||||||      ::|||||||||
    1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLlysGlyVa  17

   51 CCAGTGTGAGGTGCAGCTGGTGCAGTCTGGGGCGGCTGGCAAAGCCTG  100
      |||||||||||||||||||:::||||||||||||||||::::::|||
   17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG  34

  101 GGGGGTCCCTGAGACTCTGTCGCCAGCCTCCGGTTCAGGTTCACCTTC  150
      |||||||||||||||  ||||||||      ||||||||||||||||
   34 lyGlySerLeuArgLeuSerCysAlaAlaThrGly.....PheThrPhe  48

  151 AATAACTACTACATGGACATGGTTCCGCCAGGCTCCAGGGCAGGGCTGGA  200
      :::::||| ||:||||||||||||||||||||||::::||||||
   49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl  65

  201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT  250
      ||||||::||  ||||||||       ||:::|||||||||
   65 uTrpValSerGluIleIleSerSerGlyGlyThrThrTyrTyrAlaAsp5  82

  251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG  300
      ||||||||||||||||||||||::::|||||:::::||||||||
   82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu  98

  301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG  350
      ::|||||||::::||||||||||||||||||||:::||||||||
   99 TyrLeuGlnMetAsnGlyMetArgAlaGluAspThrAlaIleTyrTyrCy  115

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2001.DAT:AAU14226

seq_documentation_block:
ID   AAU14226 standard; Protein; 159 AA.
XX
AC   AAU14226;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human novel protein #97.
XX
KW   Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW   immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW   anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW   antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW   thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW   Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW   tissue regeneration; immune disorder.
XX
OS   Homo sapiens.
XX
PN   WO20015437-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US02623.
XX
PR   25-JAN-2000; 2000US-0491404.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-451939/48.
DR   N-PSDB; AAS22531.
XX
PT   Isolated polypeptides useful for treating anti-inflammatory diseases,
PT   nervous system disorders, and for regenerating bone and cartilage -
XX
PS   Example 4; Page 576; 894pp; English.
XX
CC   The invention relates to polynucleotides encoding novel human
CC   proteins or their active domains. The polypeptides, polynucleotides and
CC   antibodies raised against the polypeptides are used in a method of
CC   treatment of a mammal and prevention of disorders caused by the aberrant
CC   protein expression or activity.  The polypeptides can be used as
CC   molecular weight markers, food supplements, and in antibody production.
CC   The polypeptides are used to identify compounds which bind to the
CC   polypeptides. Polynucleotides of the invention are used as probes and
CC   primers, for sequencing, for chromosome or gene mapping, in the
CC   production of recombinant proteins, and in generating anti-sense DNA or
CC   RNA and in gene therapy.  Polypeptides of the invention can be used to
CC   target drugs to a tumour, in assays to determine biological activity, to
CC   raise antibodies/elicit an immune response, to determine quantitative
CC   protein levels, as tissue markers, and to isolate receptors or ligands.
CC   Polypeptides of the invention may also be useful in treating platelet
CC   disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC   ligament and/or nerve tissue, wound healing, treating burns, promoting
CC   the proliferation, differentiation and survival of stem cells, as a
CC   contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC   Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral
CC   sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC   fungal infection or from autoimmunity, cancer, allergy, asthma,
CC   graft-versus-host disease, eczema, haemophilia, thrombosis,

  351 TGCG..AGCTTGACTACAGGGTCT..........GACTCCTGGGGCC  385
      |||  ::::||  :::  ::||        |||  ||||||
  115 sAlaLysAspIleIleSerAspSerTrpArgTyrPheAspTyrTrpGlyG  132

  386 AGGGAGTCCTGTCACCGTCCTCA  411
      ||||::||||||||||||||||||
  132 lnGlyAlaLeuValThrValSerSer  140

CC   anti-inflammatory diseases, nervous system disorders, and infection.
CC   The present sequence represents a protein of the invention.
XX
SQ   Sequence   159 AA;

alignment_scores:
        Quality:    523.50            Length:      142
        Ratio:        4.122             Gaps:          3
Percent Similarity:  89.437    Percent Identity: 71.831

alignment_block:
US-09-019-441-4 x AAU14226       ..

Align seg 1/1  to: AAU14226   from: 1  to: 159

  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGTTGTCCTCTTTGAAAGGTGT 50
    ||||||||||||||||||||||||||||||||  :::||||||||||||
  1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyLVa 17

 51 CCAGTGTGAGGTGCAGCTGGTCGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
    |||||||||||||||:::|||||||||||||||||:::::|||:::|||
 17 lGlnCysGluValGlnLeuLeuLeuGluSerGlyGlyGlyLeuValGlnProG 34

101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    |||||||||||||||||||||||||||||||||||||
 34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

151 AATAACTACTACATGGACTGGTCTCCCCAGCTCCAGGGCAGGGGCTGGA 200
    ::::::|||   |||||||::|||||||||||||::|||:::|||||||
 49 AspSerTyrArgAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuAs 65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCACCATGGTACGCAGACT 250
    :||||||||   :::||||:::|||   |||:::||||||||||
 65 pTrpValSerAlaValSerGlyGlyGlyGlySerThrTyrTyrAlaAspS 82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAAGAACGGCCAACAACACACTG 300
    :||||||||||||||||||||||||:::||||||||||||||||
 82 erValLysGlyArgPheThrIleSerArgAspAspAsnAlaLysSerThrMet 98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
    ::|||||||||||||||||||||||||||:::||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaMetTyrTyrCy 115

351 TGCG..........AGCTTGACTACAGGTCT..GACTCCTGGGGCC 385
    ||||           :::|||::|||   ||| |||||||
115 sAlaLysAspAsnTyrAspPheTrpSerGlyThrPheAspTyrTrpGlyG 132

386 AGGGAGTCCTGGTCACCGTCTCCTCA 411
    ||||||||||||||||||||||||||
132 lnGlyThrLeuValThrValSerSer 140

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1996.DAT:AAW03726

seq_documentation_block:
ID  AAW03726 standard; Protein: 184 AA.
XX
AC  AAW03726;
XX
DT  02-APR-1997  (first entry)
XX
DE  Humanised MAb 39-1.106 heavy chain variable region.
XX
KW  Heavy chain; variable region; murine; mouse; anti-human; disease;
KW  glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma;
KW  diagnosis; inhibition; B-cell; activation; treatment; disorder;
KW  immune; autoimmune; allergic response; organ rejection; drug;
KW  graft versus host; cell imaging; tumour; targetted; delivery;
KW  targetted; humanised.
XX
OS  Mus musculus.
XX
FH  Key              Location/Qualifiers

---

FT  Misc-difference 13
FT                   /note= "corresponding codon TGA"
FT  Misc-difference 23
FT                   /note= "corresponding codon TAA"
XX
PN  WO9623071-A2.
XX
PD  01-AUG-1996.
XX
PF  26-JAN-1996;  96WO-US01119.
XX
PR  26-JAN-1995;  95US-0379057.
XX
PA  (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI  Aruffo AA,  Bajorath J,  Gilliland LK,  Gordon ML;
PI  Harris LJ,  Hollenbaugh D, Sladak AW;
XX
DR  WPI; 1996-362694/36.
DR  N-PSDB; AAT36025.
XX
PT  Monoclonal antibodies specific for different epitope(s) on human
PT  gp39 - used for inhibiting B cell activation and for the diagnosis
PT  of various disorders, e.g. cancer, psoriasis etc..
XX
PS  Example 13; Fig 18; 167pp; English.
XX
CC  The present sequence is the heavy chain variable region of the
CC  humanised murine anti-human glycoprotein (gp) 39 monoclonal
CC  antibody (MAb) 39-1.106. The MAb may be useful for diagnosing
CC  disease states, inhibiting B-cell activation and for treating
CC  immunological disorders, e.g. autoimmune disorders, allergic
CC  responses, organ rejection and graft versus host disease. It may
CC  also be used for imaging cells which express gp39 on their surface,
CC  e.g. tumour cells, and to target therapeutic agents to such cells.
CC  The MAb inhibits the CD40/gp39 interaction, therefore limiting both
CC  prim. and sec. responses to T-cell dependent antigens and Ab prodn.
CC  specific to these antigens. A typical compsn. for intramuscular
CC  injection pref. contains 50 mg of MAb in 1 ml of sterile buffered
CC  water.
XX
SQ  Sequence  184 AA;

alignment_scores:
        Quality:    522.50            Length:      141
        Ratio:        4.318             Gaps:          3
Percent Similarity:  85.816    Percent Identity: 75.177

alignment_block:
US-09-019-441-4 x AAW03726       ..

Align seg 1/1  to: AAW03726   from: 1  to: 184

  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGTTGTCCTCTTTGAAAGGTGT 50
    |||||||||||||||||||||||||||||||  :::||||||||||:::||
 38 MetGluGlyLeuArgTrpValPheLeuValAlaIleLeuLeuGluGlyLyVa 54

 51 CCAGTGTGAGGTGCAGCTGGTCGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
    |||||||||||||||||||||||||||||||||||||||||||||||||
 54 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValLysProG 71

101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
    ||||||||||||  ||||::|||||||  ||||||||  ||||||||
 71 lyGlySerLeuArgLeuSerCysAlaThrSerGly......PheThrPhe 85

151 AATAACTACTACATGGACTGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA 200
    |||||||||||||||||||::||||||||||||||||::|||||||
 86 AsnAsnTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 102

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCACCATGGTACGCAGACT 250
    :::||||||||         :::|||||||||||||||||||||||
102 uTrpValAlaSerIle...SerSerGlyAspSerIleTyrTyrAlaAspS 118

```
CC  disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC  ligament and/or nerve tissue, wound healing, treating burns, promoting
CC  the proliferation, differentiation and survival of stem cells, as a
CC  contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC  Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral
CC  sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC  fungal infection or from autoimmunity, cancer, allergy, asthma,
CC  graft-versus-host disease, eczema, haemophilia, thrombosis,
CC  anti-inflammatory diseases, nervous system disorders, and infection.
CC  The present sequence represents a protein of the invention.
XX
SQ  Sequence   367 AA;

alignment_scores:
          Quality:   516.50              Length:      154
          Ratio:       4.099              Gaps:          4
  Percent Similarity:  81.818    Percent Identity:  69.481

alignment_block:
US-09-019-441-4 x AAU14556            ..

Align seg 1/1  to: AAU14556   from: 1   to: 367

    1 ATGGAGTTGGGCTGAGCTGGGTTTCCTTGGTTCCTTCTTTTGAAAGGTGT 50
      ||||||||||||||||||||||||||||||||||||   :::|||||||||
    1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17

   51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG 100
      |||||||||||||||||||||||||||||||||||||||:::::||:||||
   17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProG 34

  101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC 150
      ||||||||||||||   ||||||||||||||      ||||||||
   34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

  151 AATAACTACTACATGACTGGGTCCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
      ::::::||   |||::||||||||||||||||||||||::::|||||||||
   49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65

  201 GTGGGTCTCACGTATTAGT.......AGTAGTGTGATCCCACATGGT 241
      ||||||||||   :::::::           :::|||:|||    |||::|
   65 uTrpValSerGlyPheThrGlySerGlyGlySerGlyGlySerThrTyrT 82

  242 ACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAAC 291
      |||||||||||||||||||||||||||||||||||||:::||::::||:::
   82 yrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLys 98

  292 AACACACTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGT 341
      ||||||||||||||||||||||||||||||||||||||::::|||||||||
   99 AsnThrLeuPheLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaVa 115

  342 CTATTACTGTGCG.................AGCTTGACTACAG 367
      |||||||||||||               :::  ||||||||||
  115 lTyrTyrCysAlaLysGlyLeuLeuProProArgTrpAlaTyrArgValT 132

  368 GGTCTGACTCC.............TGGGGCCAGGGAGTCCTGGTC 399
      :::|||||||                 ||||||||||:::||||||
  132 yrGluAspSerGlyIlePhePheAspTyrTrpGlyGlnGlyThrLeuVal 148

  400 ACCGTCTCCTCA 411
      ||||||||||||
  149 ThrValSerSer 152
```

seq_name: /SIDS1/gcgdata/hold-geneseqp/geneseqp-embl/AA1998.DAT:AAW57603

```
seq_documentation_block:
ID  AAW57603 standard; Protein; 137 AA.
XX
AC  AAW57603;
XX
DT  03-SEP-1998  (first entry)
XX
```

```
  251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACACCACTG 300
      ||||||||||||||||||||||||||||||||||   |||::::|||  |||
  118 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnIleLeu 134

  301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
      ::|||||||||||||||||||||||||||||||||||||||||||||||||
  135 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 151

  351 TGCGAGCTTG..........ACTACAGGGTCTGACTCCTGGGGCCAGG 388
      ||||          ::   |||   |||||||||||||
  151 sAlaArgHisTyrAspTyrAspSerTyrAlaMetAspTyrTrpGlyGlnG 168

  389 GAGTCCTGGTCACCGTCTCCTCA 411
      ||::||||||||||||||||||||
  168 lyThrLeuValThrValSerSer 175
```

seq_name: /SIDS1/gcgdata/hold-geneseqp/geneseqp-embl/AA2001.DAT:AAU14556

```
seq_documentation_block:
ID  AAU14556 standard; Protein; 367 AA.
XX
AC  AAU14556;
XX
DT  24-OCT-2001  (first entry)
XX
DE  Human novel protein #427.
XX
KW  Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW  immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW  anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;
KW  antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW  thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW  Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW  tissue regeneration; immune disorder.
XX
OS  Homo sapiens.
XX
PN  WO200155437-A2.
XX
PD  02-AUG-2001.
XX
PF  25-JAN-2001; 2001WO-US02623.
XX
PR  25-JAN-2000; 2000US-0491404.
XX
PA  (HYSE-) HYSEQ INC.
XX
PI  Tang YT, Liu C, Drmanac RT;
XX
DR  WPI; 2001-451939/48.
DR  N-PSDB; AAS22861.
XX
PT  Isolated polypeptides useful for treating anti-inflammatory diseases,
PT  nervous system disorders, and for regenerating bone and cartilage -
XX
PS  Example 4; Page 872-873; 894pp; English.
XX
CC  The invention relates to polynucleotides encoding novel human
CC  proteins or their active domains. The polypeptides, polynucleotides and
CC  antibodies raised against the polypeptides are used in a method of
CC  treatment of a mammal and prevention of disorders caused by the aberrant
CC  protein expression or activity. The polypeptides can be used as
CC  molecular weight markers, food supplements, and in antibody production.
CC  The polypeptides are used to identify compounds which bind to the
CC  polypeptides. Polynucleotides of the invention are used as probes and
CC  primers, for sequencing, for chromosome or gene mapping, in the
CC  production of recombinant proteins, and in generating anti-sense DNA or
CC  RNA and in gene therapy. Polypeptides of the invention can be used to
CC  target drugs to a tumour, in assays to determine biological activity, to
CC  raise antibodies/elicit an immune response, to determine quantitative
CC  protein levels, as tissue markers, and to isolate receptors or ligands.
CC  Polypeptides of the invention may also be useful in treating platelet
```

```
DE   Chimeric antibody fragment against hPTRP SEQ ID NO:58.
XX
KW   Chimeric; antibody; human parathormone related peptide; hPTRP; mouse;
KW   L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;
KW   hypophosphaemia; pathogen; vitamin D resistance; V region; C region;
KW   humanised.
XX
OS   Synthetic.
OS   Chimeric - Mus sp.
OS   Chimeric - Homo sapiens.
XX
FH            Key              Location/Qualifiers
FT   Peptide          1..19
FT                    /label- signal
XX
PN   WO9813388-A1.
XX
PD   02-APR-1998.
XX
PF   24-SEP-1997;      97WO-JP03382.
XX
PR   24-JUL-1997;      97JP-0214168.
PR   26-SEP-1996;      96JP-0255196.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Sato K,  Wakahara Y,  Yabuta N;
XX
DR   WPI; 1998-230640/20.
DR   N-PSDB; AAV24243.
XX
PT   New chimeric antibodies against human parathormone related
PT   peptide(s) - useful for, e.g. treatment of hypercalcaemia and other
PT   disorders caused by malignant neoplasm(s)
XX
PS   Claim 60; Page 122-123; 182pp; Japanese.
XX
CC   New antibodies have been developed which are specific for human
CC   parathormone related peptides (hPTRP). The antibodies comprise chimeric
CC   L and/or H chains, where the C region is of human and L region of mouse,
CC   origin. The present sequence represents a specifically claimed region of
CC   an antibody of the invention. Host cells, transformed with vectors
CC   containing DNA encoding antibodies of the invention, can be used to
CC   produce the antibodies. The antibodies may be used to treat
CC   hypercalcaemia, especially that due to a malignancy, e.g. cancers of
CC   pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,
CC   breast, kidney, bladder, womb or prostate or malignant lymphoma. They
CC   may also be used for treatment of hypophosphaemia such as that due to
CC   pathogens or to vitamin D resistance.
XX
SQ   Sequence   137 AA;

alignment_scores:
          Quality:   515.00              Length:   139
          Ratio:     4.221               Gaps:       2
Percent Similarity:  87.770   Percent Identity: 74.101

alignment_block:
US-09-019-441-4 x AAW57603              ..

Align seg 1/1  to: AAW57603   from: 1  to: 137

  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTGCCCTCTTTTGAAAGGTGT  50
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  1 MetGlyPheGlyLeuSerTrpValPheLeuValAlaLeuLeuArgGlyVa   17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG  100
    |||||::||||||||||||||||||||||||||||||||||::::::|||
 17 lGlnCysGlnValGlnLeuValGluSerGlyGlyGlyLeuAlaLysProG   34

101 GGGGGTCCCTGAGACTCTGGTGCGCAGCTCCGGGTTCACCTTCACCTTC  150
    || |||||||||||  |||||||||||||||| |||||  |||||||||
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 34 lyArgSerLeuArgLeuSerCysAlaAlaSerGly.......PheThrPhe  48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGCTGGA  200
    :::::::|||  ||:|||||||||||||||||||||::::||||||||
 49 SerSerTyrGlyMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl   65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGTACGCAGACT  250
    |||||::: |||||||: ||||||::||||::  ||::|||  |||
 65 uTrpValAlaThrIleSerGlyGlySerTyrThrTyrTyrProAspS   82

251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG  300
    |||||||||||||||||||||||||||:: ||:::||||||||||||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu  98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG  350
    :::||||||||||||||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  115

351 TGCGAGCTTGACTACAGGGTCT......GACTCCTGGGCCAGGGAGTCC  394
    ||||  ||||||  ||:::      |||||||||||||||:::|||
115 sAlaArgGlnThrThrMetThrTyrPheAlaTyrTrpGlyGlnGlyThrL  132

395 TGGTCACCGTCTCCTCA  411
    |||||||||||||||||
132 euValThrValSerSer  137

seq_name:  /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1999.DAT:AAW89635

seq_documentation_block:
ID   AAW89635 standard; Protein; 137 AA.
XX
AC   AAW89635;
XX
DT   14-APR-1999  (first entry)
XX
DE   Human antibody heavy chain protein.
XX
KW   Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;
KW   inhibitor; humanised.
XX
OS   Homo sapiens.
XX
FH            Key              Location/Qualifiers
FT   Peptide          1..19
FT                    /label- signal
FT   Protein          20..137
XX
PN   WO9851329-A1.
XX
PD   19-NOV-1998.
XX
PF   13-MAY-1998;      98WO-JP02116.
XX
PR   18-JUL-1997;      97JP-0194445.
PR   15-MAY-1997;      97JP-0125505.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Ishii K,  Sato K,  Tunenari T;
XX
DR   WPI; 1999-070101/06.
DR   N-PSDB; AAX00116.
XX
PT   Inhibitors of binding of parathyroid hormone related peptide to its
PT   receptor - useful for, e.g. treatment of cachexia arising from
PT   cancer or other diseases
XX
PS   Example 4; Page 83-84; 125pp; Japanese.
XX
CC   The present invention describes compositions for the treatment of
CC   cachexia containing a substance which inhibits the binding of a
CC   parathyroid hormone related peptide (PTHrP) to its receptor, as an
CC   active component. This substance may be an antagonist to the receptor,
```

PN  WO20000219-A1.
XX
PD  06-JAN-2000.
XX
PF  25-JUN-1999;    99WO-JP03433.
XX
PR  26-JUN-1998;    98JP-0180143.
XX
PA  (CHUS ) CHUGAI SEIYAKU KK.
XX
PI  Sato K, Tsunenari T;
XX
DR  WPI; 2000-117115/10.
DR  N-PSDB; AAZ58914.
XX
PT  Treatment of hypercalcemic crisis with a substance inhibiting binding
PT  of parathyroid hormone related peptide to its receptor  -
XX
PS  Example 4; Page 98-99; 120pp; Japanese.
XX
CC  The invention relates to a method of treatment of hypercalcemic crisis.
CC  A composition for the treatment of hypercalcemic crisis contains as
CC  active component a substance which inhibits the binding of parathyroid
CC  hormone related peptide (PTHrP) to its receptor. The inhibitor is used
CC  for the treatment of hypercalcemic crisis, such as that associated with
CC  a malignant tumour.
XX
SQ  Sequence  137 AA;

alignment_scores:
      Quality:  515.00                Length:       139
      Ratio:    4.221                 Gaps:           2
Percent Similarity:  87.770     Percent Identity:  74.101

alignment_block:
US-09-019-441-4 x AAY77514

Align seq 1/1  to: AAY77514   from: 1  to: 137

  1 ATGGAGTTGGCTGAGCTGGGTTTTCCTTGTCCTCTTTGAAAGGTGT    50
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  1 MetGlyPheGlyLeuSerTrpValPheLeuValAlaLeuLeuArgGlyVa  17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG   100
    ||||||:::|||||||||||||||||||||||||||||||:::||||
 17 lGlnCysGlnValGlnLeuValGluSerGlyGlyGlyValGlnProG     34

101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC   150
    || |||||||||||  ||||||||||||||||||||||||    |||||||||
 34 lyArgSerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA   200
    ::::::|||  ||::|||||||||||||||||||||:::|||||||
 49 SerSerTyrGlyMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl  65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT   250
    |||||||::: |||||||::|||::: ||::||| |||::|||  |||
 65 uTrpValAlaThrIleSerSerGlyGlySerTyrThrTyrTyrProAspS  82

251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG  300
    ||||||||:::|||||||||||||||:::|||::|||:::||||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu  98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG  350
    ::::||||||||||||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  115

351 TGCGAGCTTGACTACAGGGTCT......GACTCCTGGGGCCAGGGAGTCC  394
    |||| ::: ||||||       |||||||||||::::|
115 sAlaArgGlnThrThrMetThrTyrPheAlaTyrTrpGlyGlnGlyThrL  132

395 TGGTCACCGTCTCCTCA  411
    ||||||||||||||||
132 euValThrValSerSer  137

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CC  or an antibody (preferably monoclonal) or antibody fragment,
CC  recognising PTHrP. The antibody is preferably humanised or chimeric.
CC  The present invention also describes a humanised antibody prepared
CC  by hybridoma 23-57-137-1 (FERM BP-5631). The composition is used for
CC  the treatment of cachexia arising in connection with diseases such as
CC  cancer, thereby improving the quality of life of the patient. The
CC  present sequence represents a human antibody heavy chain from the
CC  present invention.
XX
SQ  Sequence  137 AA;

alignment_scores:
      Quality:  515.00                Length:       139
      Ratio:    4.221                 Gaps:           2
Percent Similarity:  87.770     Percent Identity:  74.101

alignment_block:
US-09-019-441-4 x AAW89635

Align seq 1/1  to: AAW89635   from: 1  to: 137

  1 ATGGAGTTGGCTGAGCTGGGTTTTCCTTGTCCTCTTTGAAAGGTGT    50
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  1 MetGlyPheGlyLeuSerTrpValPheLeuValAlaLeuLeuArgGlyVa  17

 51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTG   100
    ||||||:::|||||||||||||||||||||||||||||||:::||||
 17 lGlnCysGlnValGlnLeuValGluSerGlyGlyGlyValGlnProG     34

101 GGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTC   150
    || |||||||||||  ||||||||||||||||||||||||    |||||||||
 34 lyArgSerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe  48

151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA   200
    ::::::|||  ||::|||||||||||||||||||||:::|||||||
 49 SerSerTyrGlyMetSerTrpValArgGlnAlaProGlyLyLysGlyLeuGl  65

201 GTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT   250
    |||||||::: |||||||::|||::: ||::||| |||::|||  |||
 65 uTrpValAlaThrIleSerSerGlyGlySerTyrThrTyrTyrProAspS  82

251 CCGTGAAGGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG  300
    ||||||||:::|||||||||||||||:::|||::|||:::||||||
 82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu  98

301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG  350
    ::::||||||||||||||||||||||||||||||||||||||||||||
 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy  115

351 TGCGAGCTTGACTACAGGGTCT......GACTCCTGGGGCCAGGGAGTCC  394
    |||| ::: ||||||       |||||||||||::::|
115 sAlaArgGlnThrThrMetThrTyrPheAlaTyrTrpGlyGlnGlyThrL  132

395 TGGTCACCGTCTCCTCA  411
    ||||||||||||||||
132 euValThrValSerSer  137

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seq_documentation_block:
ID  AAY77514 standard; Protein; 137 AA.
XX
AC  AAY77514;
XX
DT  26-APR-2000  (first entry)
XX
DE  Peptide encoded by DNA seq ID NO: 58.
XX
KW  Hypercalcemic crisis; parathyroid hormone related peptide; PTHrP; tumour.
XX
OS  Homo sapiens.
XX

```
            |||||||||||||||||||
        132 euValThrValSerSer 137

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:AAG67112

seq_documentation_block:
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XX
AC  AAG67112;
XX
DT  13-NOV-2001  (first entry)
XX
DE  Amino acid sequence of a human protein.
XX
KW  Tissue decomposition inhibitor; parathyroid hormone; cancer cachexia;
KW  septicemia; injury; muscular dystrophy; cytokine; interleukin-6;
KW  granulocyte colony stimulating factor; interleukin-11;
KW  leukemia inhibitory factor; weight loss.
XX
OS  Homo sapiens.
XX
FH  Key             Location/Qualifiers
FT  Peptide         1..19
FT                  /note= "signal peptide"
FT  Protein         20..137
FT                  /note= "mature protein; this sequence given as sequence
FT                  number 56 in the specification"
XX
PN  WO200016249-A1.
XX
PD  07-SEP-2001.
XX
PF  30-AUG-2000; 2000WO-JP05886.
XX
PR  28-FEB-2000; 2000JP-0052414.
XX
PA  (CHUS ) CHUGAI SEIYAKU KK.
XX
PI  Saito H, Tsunenari T, Onuma E, Sato K;
XX
DR  WPI; 2001-550131/61.
DR  N-PSDB; AAH75115.
XX
PT  Tissue decomposition inhibitor that prevents parathyroid hormone
PT  associated proteins from binding to its receptor -
XX
PS  Example 1; Page 107-108; 132pp; Japanese.
XX
CC  The specification describes a tissue decomposition inhibitor, which
CC  comprises a substance that inhibits peptides associated with
CC  parathyroid hormone (PTH) from binding with their receptor. The method
CC  is used to inhibit tissue decomposition caused by cancer cachexia,
CC  septicemia, heavy external injury or muscular dystrophy, and for
CC  treating patients with elevated cytokine (interleukin-6, Granulocyte
CC  colony stimulating factor, Interleukin-11 and Leukemia inhibitory
CC  factor) levels. It may also be used for preventing weight loss caused
CC  by cancer cachexia. The present sequence represents a protein, which is
CC  used in the course of the invention.
XX
SQ  Sequence   137 AA;

alignment_scores:
     Quality:  515.00        Length:        139
     Ratio:      4.221       Gaps:            2
Percent Similarity:  87.770    Percent Identity: 74.101

alignment_block:
US-09-019-441-4 x AAG67112 ...

Align seg 1/1  to: AAG67112  from: 1  to: 137

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    1 MetGlyPheGlyLeuSerTrpValPheLeuValAlaLeuLeuArgGlyVa 17

   51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGCCGGCTTGGCAAAGCCTG 100
      |||||||::::||||||||||||||||||||:::||:::::||||
   17 lGlnCysGlnValGlnLeuValGluSerGlyGlyGlyValValGlnProG 34

  101 GGGGGTCCCTGAGACTCTGGTGCCAGCCTCCGGGTTCAGGTTCACCTTC 150
      ||  |||||||||||  ||||||||||||||||        |||||||||
   34 lyArgSerLeuArgLeuSerCysAlaAlaSerGly......PheThrPhe 48

  151 AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGA 200
      :::::::|||   |||::::||||||||||||||||||||||::||||||
   49 SerSerTyrGlyMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65

  201 GTGGGTCTCCACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACT 250
      ||||||:: ||||||||||::::||:::  ||:::||   ||||  ||||
   65 uTrpValAlaThrIleSerSerGlyGlySerTyrThrTyrTyrProAspS 82

  251 CCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
      |||||||||||||||||||||||||||||||||:::||||||||||||||
   82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98

  301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
      :::|||||||||||||||||||||||||||||||||||||||||||||||
   99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

  351 TGCGAGCTTGACTACAGGGTCT......GACTCCTGGGCCCAGGGAGTCC 394
      |||| |||||| :::|      ||||||||||||||:::||
  115 sAlaArgGlnThrThrMetThrTyrPheAlaTyrTrpGlyGlnGlyThrL 132

  395 TGGTCACCGTCTCCTCA 411
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  132 euValThrValSerSer 137
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OM of: US-09-019-441-1 to: A_Geneseq_032802:*     out_format : pfs

Date: Sep 23, 2002 10:06 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
 -DELOP=6.000 -DELEXT=7.000 -START=-1 -MATRIX=blosum62
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 -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=US0901941 @CGN_1_175 -NCPU=6 -ICPU=3 -LONGLOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
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Query length: 390
Database: A_Geneseq_032802:*
Database sequences: 747574
Database length: 111073796
Search time (sec): 193.710000

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| /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:AAW78424 | + | 485.00 | 908.45 | 1.7e-42 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:AAW78425 | + | 485.00 | 908.45 | 1.7e-42 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:AAW78426 | + | 485.00 | 908.45 | 1.7e-42 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:AAW78430 | + | 485.00 | 908.45 | 1.7e-42 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:AAW78431 | + | 485.00 | 908.45 | 1.7e-42 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:AAW78428 | + | 480.00 | 899.04 | 5.7e-42 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:AAW78429 | + | 477.00 | 893.39 | 1.2e-41 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:AAR89148 | + | 473.89 | 473.89 | 4.3e-41 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:ABG15261 | + | 472.00 | 879.56 | 4.3e-41 | | |
| /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:AAG65591 | + | 472.00 | 876.52 | 4.6e-41 | | |

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:AAW70377

seq_documentation_block:
ID   AAW70377 standard; Protein; 130 AA.
XX
AC   AAW70377;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Anti-human CD23 6G5 monoclonal antibody light chain variable region.
XX
KW   Anti-human CD23 6G5 monoclonal antibody; light chain variable region;
KW   human CD23; IgE; FceRii/CD23; gamma-1 constant region;
KW   gamma-3 constant region; allergy; inflammation; autoimmune disease;
KW   allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia.
XX
OS   Macaca fascicularis
XX
FH   Key             Location/Qualifiers
FT   Protein         1..19
FT                   /note= "Signal peptide"
FT   Protein         20..130
FT                   /note= "anti-human CD23  6G5 light chain variable
FT                   region"
FT
FT   Binding-site    42..55
FT                   /note= "CDR 1"
FT   Binding-site    71..77
FT                   /note= "CDR 2"
FT   Binding-site    110..119
FT                   /note= "CDR 3"
XX
PN   WO9837099-A1.
XX
PD   27-AUG-1998.
XX
PF   17-FEB-1998;   98WO-US02253.
XX
PR   05-FEB-1998;   98US-0803085.
PR   20-FEB-1997;   97US-0803085.
XX
PA   (IDEC-) IDEC PHARM CORP.
PA   (SEGK ) SEIKAGAKU CORP.
XX
PI   Kloetzer WS, Nakamura T,   Reff ME;
XX
DR   WPI; 1998-467495/40.
DR   N-PSDB; AAV33307.
XX
PT   New anti-human CD23 monoclonal antibody - used for inhibiting IgE
PT   expression to treat or prevent allergic, inflammatory and
PT   auto:immune conditions
XX
PS   Example 1; Pages 102-104; 146pp; English.
XX
CC   The present sequence represents the light chain variable region of
CC   primate monoclonal antibody anti-human CD23 6G5. The invention
CC   provides primate monoclonal antibodies which specifically bind human
CC   CD23, the low affinity receptor for IgE (FceRii/CD23), and comprise
CC   either of a human gamma-1 or human gamma-3 constant region that binds
CC   to human Fc gamma receptors and inhibits IgE expression. The monoclonal
CC   antibodies of the invention are claimed to be useful for inhibiting
CC   induced IgE production for treating or preventing allergic, inflammatory
CC   and autoimmune conditions e.g. allergic rhinitis conjunctivitis,
CC   autoimmune haemolytic anaemia, etc.
XX
SQ   Sequence    130 AA;

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:AAU02620 +   468.00   876.45   1.0e
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:AAU02577 +   466.00   872.68   1.7e
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:AAY43257 +   466.00   872.60   1.7e
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:AAB85908 +   466.00   865.00   2.0e
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:AAR45606 +   463.00   866.95   3.5e

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alignment_scores:
           Quality:    686.00         Length:       130
           Ratio:        5.277         Gaps:           0
Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-019-441-1 x AAW70377

Align seg 1/1  to: AAW70377   from: 1  to: 130

     1 ATGGCCTGGACTCGTCCTCCTCGTCACCCTCCTCACTCAGGGCACAGGATC  50
       ||||||||||||||||||||||||||||||||||||||||||||||||||
     1 MetAlaTrpThrLeuLeuLeuValThrLeuLeuThrGlnGlyThrGlySe  17

    51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCTGGTGTCTGGTCTCCTG  100
       ||||||||||||||||||||||||||||||||||||||||||||||||||
    17 rTrpAlaGlnSerAlaProThrGlnProSerValSerGlySerProG   34

   101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT  150
       ||||||||||||||||||||||||||||||||||||||||||||||||||
    34 lyGlnSerValThrIleSerCysThrGlyThrSerAspValGlyGly  50

   151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCCAAACT  200
       ||||||||||||||||||||||||||||||||||||||||||||||||||
    51 TyrAsnTyrValSerTrpTyrGlnHisHisProGlyLysAlaProLysLe  67

   201 CATGATTTATGATGTCGCTAAGGCGGCCTCAGGGGTCTCTGATCGCTTCT  250
       ||||||||||||||||||||||||||||||||||||||||||||||||||
    67 uMetIleTyrAspValAlaLysAlaSerGlyValSerAspArgPheS  84

   251 CTGGGTCCAAGTCTGGCAACACGGCCTCCTCCTGACCATCTCTGGGCTCCAG  300
       ||||||||||||||||||||||||||||||||||||||||||||||||||
    84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln  100

   301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC  350
       ||||||||||||||||||||||||||||||||||||||||||||||||||
   101 AlaGluAspGluAlaAspTyrTyrCysCysSerTyrThrThrSerSerTh  117

   351 TTTGTTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT  390
       ||||||||||||||||||||||||||||||||||||||||
   117 rLeuLeuPheGlyArgGlyThrArgLeuThrValLeuGly  130
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:AAR31024

```
FH  Key             Location/Qualifiers
FT  Peptide         1..19
FT                  /note= "signal peptide"
FT  Region          20..42
FT                  /label= FR1
FT  Region          43..53
FT                  /label= CDR1
FT  Region          54..68
FT                  /label= FR2
FT  Region          69..75
FT                  /label= CDR2
FT  Region          76..107
FT                  /label= FR3
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FT  Region          108..116
FT                  /label= CDR3
FT  Region          117..126
FT                  /label= FR4
FT  Domain          127..234
FT                  /label= C lambda
XX
PN  EP523949-A.
XX
PD  20-JAN-1993.
XX
PF  14-JUL-1992;    92EP-0306420.
XX
PR  15-JUL-1991;    91GB-0015284.
PR  01-AUG-1991;    91GB-0016594.
PR  23-MAR-1992;    92GB-0006284.
XX
PA  (WELL ) WELLCOME FOUND LTD.
XX
PI  Crowe JS,  Lewis AP;
XX
DR  WPI; 1993-019951/03.
DR  N-PSDB; AAQ35100.
XX
PT  Prodn. of recombinant primate antibodies - useful for treating
PT  infections caused by hepatitis A, B and C, herpes,
PT  cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,
PT  arthritis etc.
XX
PS  Disclosure; Fig 3; 35pp; English.
XX
CC  The sequences given in AAR31023-24 represent the heavy and light chains
CC  of Antibody D respectively.  Antibody D is a monoclonal antibody which
CC  was derived from peripheral blood lymphocytes from a hepatitis A virus
CC  (HAV) sero positive patient.  Antibody D is closely related in nature
CC  to murine antibody B5B3.  Total RNA was isolated from antibody D
CC  expressing cells and polyadenylated RNA was extracted.  These polyA
CC  RNA's were used to prepare a cDNA library which was screened for human
CC  kappa light (L) chains and two positive clones were detected.
CC  Further heavy (H) chain clones were also isolated.
XX
SQ  Sequence     235 AA;
```

```
alignment_scores:
           Quality:    569.00         Length:       130
           Ratio:        4.664         Gaps:           0
Percent Similarity:  93.846    Percent Identity:  82.308

alignment_block:
US-09-019-441-1 x AAR31024

Align seg 1/1  to: AAR31024   from: 1  to: 235

     1 ATGGCCTGGACTCGTCCTCCTCGTCACCCTCCTCACTCAGGGCACAGGATC  50
       |||||||||||::|||||||||::||||||||||||||||||||||||||
     1 MetAlaTrpAlaLeuLeuLeuLeuThrLeuLeuThrGlnAspThrGlySe  17

    51 CTGGGCTCAGTCGCCGCACTCAGCCTCCCTCTGTCTGGGCTCCTG  100
       ||||||||||:||:::||||||||||:|||||||::||||||||||
    17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG  34

   101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCCAGCAGCCATGACGTTGGTGGT  150
       ||||||||::||||||||||:::|||||||||||::||||||||||:::
    34 lyGlnSerIleThrIleSerCysThrGlyThrAsnAsnAspValGlySer  50

   151 TATAACTATGTCTCCTGGTACCAACACCACCAACCAGGCAAAGCCCCCAAACT  200
       |||||| |||||||:::|||||||||||||:||||||||||:|||||||||
    51 TyrAsnTyrTyrTyrGlnHisProGlyLysAlaProLysIl  67

   201 CATGATTTATGATGTCGCTAAGGCGGCCCTCAGGGGTCTCTGATCGCTTCT  250
       :||||||||||:|||||||||:::||||||||||||||||||||||||||
    67 eMetIleTyrGluValSerLysProSerGlyValSerAsnArgPheS  84
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251 CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCAATCTCTGGGCTCCAG 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100

301 GCTGAGGACGAGGCTGATTATTACTGTTGTCATATACAACCAGTAGCAC 350
    ||||||||||||||||||||||||||||||||:::   ||| ||
101 AlaGluAspGluAlaAspTyrTyrCysCysSerTyrAlaGlySerTyrTh 117

351 TTTGTTATTCGGAGAGGGACCCGGTTGACCGTCCTAGGT 390
    |:::|||||||  ||||||:|||||||||||||||||||
117 rValValPheGlyGlyGlyThrLysLeuThrValLeuGly 130
```

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:ABG19293

seq_documentation_block:
ID  ABG19293 standard; Protein; 236 AA.
XX
AC  ABG19293;
XX
DT  18-FEB-2002 (first entry)
XX
DE  Novel human diagnostic protein #19284.
XX
KW  Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW  food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS  Homo sapiens.
XX
PN  WO200175067-A2.
XX
PD  11-OCT-2001.
XX
PF  30-MAR-2001; 2001WO-US08631.
XX
PR  31-MAR-2000; 2000US-0540217.
PR  23-AUG-2000; 2000US-0649167.
XX
PA  (HYSE-) HYSEQ INC.
XX
PI  Drmanac RT, Liu C, Tang YT;
XX
DR  WPI; 2001-639362/73.
DR  N-PSDB; AAS83480.
XX
PT  New isolated polynucleotide and encoded polypeptides, useful in
PT  diagnostics, forensics, gene mapping, identification of mutations
PT  responsible for genetic disorders or other traits and to assess
PT  biodiversity -
XX
PS  Claim 20; SEQ ID No 49652; 103pp; English.
XX
CC  The invention relates to isolated polynucleotide (I) and
CC  polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC  polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC  and gene mapping, and in recombinant production of (II). The
CC  polynucleotides are also used in diagnostics as expressed sequence tags
CC  for identifying expressed genes. (I) is useful in gene therapy techniques
CC  to restore normal activity of (II) or to treat disease states involving
CC  (II). (II) is useful for generating antibodies against it, detecting or
CC  quantitating a polypeptide in tissue, as molecular weight markers and as
CC  a food supplement. (II) and its binding partners are useful in medical
CC  imaging of sites expressing (II). (I) and (II) are useful for treating
CC  disorders involving aberrant protein expression or biological activity.
CC  The polypeptide and polynucleotide sequences have applications in
CC  diagnostics, forensics, gene mapping, identification of mutations
CC  responsible for genetic disorders or other traits to assess biodiversity
CC  and to produce other types of data and products dependent on DNA and
CC  amino acid sequences. ABG00010-ABG30377 represent novel human
CC  diagnostic amino acid sequences of the invention.
CC  Note: The sequence data for this patent did not appear in the printed
CC  specification, but was obtained in electronic format directly from WIPO
CC  at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ  Sequence    236 AA;

alignment_scores:
        Quality:  561.50              Length:    131
          Ratio:    4.602              Gaps:       1
Percent Similarity:  93.130   Percent Identity:  81.679

alignment_block:
US-09-019-441-1 x ABG19293        ..
Align seg 1/1 to: ABG19293   from: 1   to: 236

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  1 ATGGCCTGGACTCTGCCTCCTGTCACCCTCCTCACTCAGGCACACGGATC 50
    ||||||||||:::||||||||||::||||||||||||||  ||||||||
  1 MetAlaTrpAlaLeuLeuLeuLeuThrLeuLeuThrGlnAspThrGlySe 17

 51 CTGGCTCAGTCTGCCCGACTCAGCCTCCCTGTGTGTCTGGGTCTCCTG 100
    ||||||||||||||||||||  ||||||||  ||||||||||||||||
 17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 34

101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCCATGACGTTGGTGGT 150
    |||||||||::||||||||||||||||||||||:::::|||||||||:::
 34 lyGlnSerIleThrIleSerCysThrGlyThrAsnAsnAspValGlySer 50

151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACT 200
    |||||  ||||||||||||:::||||||||||||||||||||||||:::
 51 TyrAsnLeuValSerTrpTyrGlnHisProGlyLysAlaProLysIl 67

201 CATGATTTATGATGTCGCTAAGCGGCCTCAAGGGGTCTCTGATCGCTTCT 250
    :||||||||:::::||||:::||||||  ||||||||||::::||||||||
 67 eMetIleTyrGluValSerLysArgProSerGlyValSerAsnArgPhes 84

251 CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
    |||||||||||||||||||||||||||||||||||||||||||||||||
 84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100

301 GCTGAGGACGAGGCTGATTATTACTGTTGTCATATACAACCAGT...AG 347
    |||||||||||||||||||||||||||||||||||||||||::::||
101 AlaGluAspGluAlaAspTyrTyrCysCysSerTyrSerSerArgPr 117

348 CACTTTGTTATTCGGAGAGGGACCCGGTTGACCGTCCTAGGT 390
    ::::|||||||||||||||||||||||||||||||||||||
117 oAspValValPheGlyGlyGlyThrLysLeuThrValLeuGly 131
```

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:ABG12883

seq_documentation_block:
ID  ABG12883 standard; Protein; 148 AA.
XX
AC  ABG12883;
XX
DT  13-FEB-2002 (first entry)
XX
DE  Novel human diagnostic protein #12874.
XX
KW  Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW  food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS  Homo sapiens.
XX
PN  WO200175067-A2.
XX
PD  11-OCT-2001.
XX
PF  30-MAR-2001; 2001WO-US08631.
XX
PR  31-MAR-2000; 2000US-0540217.
PR  23-AUG-2000; 2000US-0649167.
XX
PA  (HYSE-) HYSEQ INC.
XX

PI    Drmanac RT,  Liu C,  Tang YT;
XX
DR    WPI; 2001-639362/73.
DR    N-PSDB: AAS77070.
XX
PT    New isolated polynucleotide and encoded polypeptides, useful in
PT    diagnostics, forensics, gene mapping, identification of mutations
PT    responsible for genetic disorders or other traits and to assess
PT    biodiversity -
XX
PS    Claim 20; SEQ ID No 43242; 103pp; English.
XX
CC    The invention relates to isolated polynucleotide (I) and
CC    polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC    polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC    and gene mapping, and in recombinant production of (II). The
CC    polynucleotides are also used in diagnostics as expressed sequence tags
CC    for identifying expressed genes. (I) is useful in gene therapy techniques
CC    to restore normal activity of (II) or to treat disease states involving
CC    (II). (II) is useful for generating antibodies against it, detecting or
CC    quantitating a polypeptide in tissue, as molecular weight markers and as
CC    a food supplement. (II) and its binding partners are useful in medical
CC    imaging of sites expressing (II). (I) and (II) are useful for treating
CC    disorders involving aberrant protein expression or biological activity.
CC    The polypeptide and polynucleotide sequences have applications in
CC    diagnostics, forensics, gene mapping, identification of mutations
CC    responsible for genetic disorders or other traits to assess biodiversity
CC    and to produce other types of data and products dependent on DNA and
CC    amino acid sequences. ABG00010-ABG30377 represent novel human
CC    diagnostic amino acid sequences of the invention.
CC    Note: The sequence data for this patent did not appear in the printed
CC    specification, but was obtained in electronic format directly from WIPO
CC    at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ    Sequence    148 AA;

alignment_scores:
        Quality:   559.00              Length:     130
        Ratio:       4.620             Gaps:         0
Percent Similarity:    93.077      Percent Identity:  81.538

alignment_block:
US-09-019-441-1 x ABG12883

Align seg 1/1   to: ABG12883    from: 1  to: 148

   1 ATGGGCTGGACTCGTCCCTCGTCACCCTCCTCACTCAGGGCACAGGATC 50
     |||||||||:||||||||||::||||||||||||||||  ||||||
  16 MetAlaTrpAlaLeuLeuLeuLeuThrLeuLeuThrGlnAspThrGlySe 32

  51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCGTGTCTGGGTCTCCTG 100
     ||||||||:||||  ||||||||  |||||||||||::|||||||
  32 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 49

 101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT 150
     ||||||:||:||||||||||||||||:|||||||::|||||||||||||
  49 lyGlnSerIleThrIleSerCysThrGlyThrSerAspValGlyAsn 65

 151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACT 200
     ||||| ||||||||||||||||||||||||::|||||||||||||
  66 TyrAsnLeuValSerTrpTyrGlnHisProGlyLysAlaProLysSLe 82

 201 CATGATTTATGATGTCGCTAAGCGGCCTCAGGGGTCTCTGATCGGTTCT 250
     |:::||:||||:  ::||||| |||||||||||::|||||
  82 uIleIleTyrGluGlySerLysArgProSerGlyValSerSerArgPheS 99

 251 CTGGCTCCAAGTCATGGCAACACCGGCCTCCCTGACCATCTCTGGGCTCCAG 300
     ||||||||||||||||||||||||||||||||||::||||||||
  99 erGlySerLysSerGlyAsnThrAlaSerLeuThrMetSerGlyLeuGln 115

 301 GCTGAGGAGGCTGATTATTACTGTGTTCATATACAACCAGTAGCAC 350
     |||||||||||||||||||||||||||:::  ||||||
116 AlaGluAspGluAlaAspTyrTyrCysCysSerTyrAlaGlySerSerTh 132

351 TTTGTTATTCGGAAGAGGACCGGTTGACCGTCCTAGGT 390
    |:::|||||| |||||::::||||||||||||||
132 rTyrValPheGlyProGlyThrLysValThrValLeuGly 145

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:ABG12886

seq_documentation_block:
ID    ABG12886 standard; Protein; 249 AA.
XX
AC    ABG12886;
XX
DT    13-FEB-2002  (first entry)
XX
DE    Novel human diagnostic protein #12877.
XX
KW    Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW    food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS    Homo sapiens.
XX
PN    WO200175067-A2.
XX
PD    11-OCT-2001.
XX
PF    30-MAR-2001; 2001WO-US08631.
XX
PR    31-MAR-2000; 2000US-0540217.
PR    23-AUG-2000; 2000US-0649167.
XX
PA    (HYSE-) HYSEQ INC.
XX
PI    Drmanac RT,  Liu C,  Tang YT;
XX
DR    WPI; 2001-639362/73.
DR    N-PSDB: AAS77073.
XX
PT    New isolated polynucleotide and encoded polypeptides, useful in
PT    diagnostics, forensics, gene mapping, identification of mutations
PT    responsible for genetic disorders or other traits and to assess
PT    biodiversity -
XX
PS    Claim 20; SEQ ID No 43245; 103pp; English.
XX
CC    The invention relates to isolated polynucleotide (I) and
CC    polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC    polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC    and gene mapping, and in recombinant production of (II). The
CC    polynucleotides are also used in diagnostics as expressed sequence tags
CC    for identifying expressed genes. (I) is useful in gene therapy techniques
CC    to restore normal activity of (II) or to treat disease states involving
CC    (II). (II) is useful for generating antibodies against it, detecting or
CC    quantitating a polypeptide in tissue, as molecular weight markers and as
CC    a food supplement. (II) and its binding partners are useful in medical
CC    imaging of sites expressing (II). (I) and (II) are useful for treating
CC    disorders involving aberrant protein expression or biological activity.
CC    The polypeptide and polynucleotide sequences have applications in
CC    diagnostics, forensics, gene mapping, identification of mutations
CC    responsible for genetic disorders or other traits to assess biodiversity
CC    and to produce other types of data and products dependent on DNA and
CC    amino acid sequences. ABG00010-ABG30377 represent novel human
CC    diagnostic amino acid sequences of the invention.
CC    Note: The sequence data for this patent did not appear in the printed
CC    specification, but was obtained in electronic format directly from WIPO
CC    at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ    Sequence    249 AA;

alignment_scores:
        Quality:   557.00              Length:     130
        Ratio:       4.528             Gaps:         0

Percent Similarity:  94.615    Percent Identity: 80.000

alignment_block:
US-09-019-441-1 x ABG12886

Align seg 1/1  to: ABG12886  from: 1  to: 249

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  1 ATGGCCTGGACTCTGCCTCCTGTCACCCTCCTCACTCAGGGCACAGGATC  50
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 15 MetAlaTrpAlaLeuLeuIleLeuThrLeuLeuThrGlnGlyThrGlySe  31

 51 CTGGGCCTCAGTCTGCCCGACTCCCCTCCCTGTGTCTGGGTCTCCTG  100
    |||||||||||||||  |||||||||||||||::||||||||  |
 31 rTrpAlaGlnSerAlaLeuThrGlnProProSerAlaSerGlySerLeuG  48

101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGTTGGTGGT  150
    |||||||||||||||||||::||:||||||||||||||||||||::::
 48 lyGlnSerValThrProSerCysSerGlyThrSerSerAspIleGlyAsn  64

151 TATAACTATGTCTCCTGTACCAACACCACCCAGGCAAAGCCCCCAAACT  200
    ||||||||||||||||::||::||||||||||||||||||||||||||
 65 TyrAsnTyrValSerTrpTyrArgGlnHisProGlyLysAlaProLysSe  81

201 CATGATTTATGATGTCGCTAAGCGGCCTCAGGGGTCTCGATCGCTTCT  250
    ||||||||||||::|||||||   ::||||||||||  :||||||||
 81 uMetIleTyrGluValThrLysArgProSerGlyValProSerGlyValPhes  98

251 CTGGCTCCAAGTCTGGCAACACGGCCTCCTGACCATCTCTGGGCTCCAG  300
    ||||||||||||||||||||||||||||||||||||||||||||||||
 98 erGlySerLysSerGlyAsnThrAlaSerLeuThrValSerGlyLeuGln  114

301 GCTGAGGACGAGGCTGATTATTACTGTGTTCATATACAACCAGTAGCAC  350
    ||||||||||||||||||||||::  |||:::||
115 AlaGluAspGluAlaAspTyrTyrCysSerSerTyrArgAlaGlySerAsnSe  131

351 TTTGTTATTCGGAAGAGGAGGACCCGGTTGACCGTCCTAGGT  390
    :|||::||||| ||||||||||||||||||
131 rLeuIlePheGlyLysGlyGlyThrArgLeuThrValLeuGly  144
```

seq_name: /SIDS1/gcgdata/hold-geneseqp-embl/AA2001.DAT:AAB36212

seq_documentation_block:
ID  AAB36212 standard; protein; 235 AA.
XX
AC  AAB36212;
XX
DT  15-FEB-2001  (first entry)
XX
DE  Human immune system associated protein HISAP-10.
XX
KW  Human; immune system associated protein; HISAP-10; immune disorder;
KW  infection; autoimmune disease; cancer.
XX
OS  Homo sapiens.
XX
PN  US6135941-A.
XX
PD  24-OCT-2000.
XX
PF  27-MAR-1998;    98US-0049672.
XX
PR  27-MAR-1998;    98US-0049672.
XX
PA  (INCY-) INCYTE PHARM INC.
XX
PI  Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
PI  Hillman JL, Au-Young J;
XX
DR  WPI; 2001-030926/04.
DR  N-PSDB; AAC66528.
XX
PT  New human immune system associated proteins (HISAP) and polynucleotides
PT  encoding the HISAP, useful for diagnosing, treating or preventing

---

PT  immune or cell proliferative disorders or infections  -
XX
PS  Claim 1; Column 65-68; 54pp; English.
XX
CC  The present invention provides the coding and protein sequences for a
CC  number of human immune system associated proteins (HISAPs). These can be
CC  used in the diagnosis and treatment of various autoimmune disorders,
CC  infections and cell proliferation diseases. The diseases include AIDS,
CC  adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC  Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC  gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC  erythematosus, arteriosclerosis, cirrhosis and cancer.
XX
SQ  Sequence   235 AA;

alignment_scores:
     Quality:     554.00            Length:      130
     Ratio:         4.579           Gaps:          0
Percent Similarity:  93.077    Percent Identity: 80.769

alignment_block:
US-09-019-441-1 x AAB36212

Align seg 1/1  to: AAB36212  from: 1  to: 235

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  1 ATGGCCTGGACTCTGCCTCCTGTCACCCTCCTCACTCAGGGCACAGGATC  50
    |||||||||||||||||||:::||||:||||||||||||||||||||||
  1 MetAlaTrpAlaLeuPheLeuThrLeuLeuThrGlnGlyThrGlySe  17

 51 CTGGGCCTCAGTCTGCCCCGACTCCAGCCTCCCTCTGTGTCTGGGTCTCCTG  100
    ||||||||||||||||:::|||||||||||:::||||||||||||||
 17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG  34

101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGT  150
    ||||||:|::|||||||||||||||||||||:::||||||||
 34 lyGlnSerIleThrIleSerCysThrGlyThrSerSerAspValGlyGly  50

151 TATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCCAAACT  200
    ||||||||||||||||||||:::  |||||   :||||||||||||||
 51 TyrAsnTyrValSerTrpTyrGlnGlnSerProGlyThrAlaProLysSe  67

201 CATGATTTATGATGTCGCTAAGCGGCCTCAGGGGTCTCTGATCGCTTCT  250
    |||||||||||||:::||||||||   ||||||||  :||||||||||
 67 uMetIleTyrGluValSerAsnArgProSerGlyValSerArgAsnArgPheS  84

251 CTGGCTCCAAGTCTGGCAACACGGCCTCCTGACCATCTCTGGGCTCCAG  300
    ||||||||||||||||||||||||||||||||||||||||||||||||
 84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln  100

301 GCTGAGGACGAGGCTGATTATTACTGTGTTCATATACAACCAGTAGCAC  350
    |||||||||||||| ||||||||  :::::
101 AlaGluAspGluAlaAspTyrTyrCysSerSerTyrValGlyAsnAsnIl  117

351 TTTGTTATTCGGAAGAGGAGGACCCGGTTGACCGTCCTAGGT  390
    :|::||||||||||||||||||||||||||
117 eValValPheGlyGlyGlyThrLysLeuThrValLeuGly  130
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seq_name: /SIDS1/gcgdata/hold-geneseqp-embl/AA2001.DAT:ABG12884

seq_documentation_block:
ID  ABG12884 standard; Protein; 151 AA.
XX
AC  ABG12884;
XX
DT  13-FEB-2002  (first entry)
XX
DE  Novel human diagnostic protein #12875.
XX
KW  Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW  food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS  Homo sapiens.

```
59 TyrAsnTyrValSerTrpTyrGlnGlnHisProGlyLysAlaProGluLe   75

201 CATGATTTATGATGTCGCTAAGCGGCCTCCAGGGGTCTCGATCGCTTCT   250
    |::::||::::||||:::||||                |||||||     ||||||
 75 uIlellePheAspValSerAsnArgProLeuGlyValSerThrArgPheS   92

251 CTGGCTCCAAGTCTGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG   300
    ||||||||||||||               |||||||||||||||||||||||
 92 erGlySerLysSerGlyIleMetAlaSerLeuThrIleSerGlyLeuGln  108

301 GCTGAGGACGAGGCTGATTATTACTGTGTTCATATACACCAGTAGCAC    350
    ||||||||||||||||||||||||||              :::::      ::::::
109 AlaGluAspGluAlaAspTyrTyrCysSerPheThrSerArgAsnSe    125

351 TTTGTTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT          390
    :::||||||       |||||:::::::||||||||||||
125 rArgValPheGlySerGlyThrLysValThrValLeuGly           138
```

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:ABG19291

seq_documentation_block:
```
ID  ABG19291 standard; Protein; 251 AA.
XX
AC  ABG19291;
XX
DT  18-FEB-2002 (first entry)
XX
DE  Novel human diagnostic protein #19282.
XX
KW  Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW  food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS  Homo sapiens.
XX
PN  WO200175067-A2.
XX
PD  11-OCT-2001.
XX
PF  30-MAR-2001; 2001WO-US08631.
XX
PR  31-MAR-2000; 2000US-0540217.
PR  23-AUG-2000; 2000US-0649167.
XX
PA  (HYSE-) HYSEQ INC.
XX
PI  Drmanac RT, Liu C, Tang YT;
XX
DR  WPI; 2001-639362/73.
DR  N-PSDB; AAS83478.
XX
PT  New isolated polynucleotide and encoded polypeptides, useful in
PT  diagnostics, forensics, gene mapping, identification of mutations
PT  responsible for genetic disorders or other traits and to assess
PT  biodiversity -
XX
PS  Claim 20; SEQ ID NO 49650; 103pp; English.
XX
CC  The invention relates to isolated polynucleotide (I) and
CC  polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC  polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC  and gene mapping, and in recombinant production of (II). The
CC  polynucleotides are also used in diagnostics as expressed sequence tags
CC  for identifying expressed genes. (I) is useful in gene therapy techniques
CC  to restore normal activity of (II) or to treat disease states involving
CC  (II). (II) is useful for generating antibodies against it, detecting or
CC  quantitating a polypeptide in tissue, as molecular weight markers and as
CC  a food supplement. (II) and its binding partners are useful in medical
CC  imaging of sites expressing (II). (I) and (II) are useful for treating
CC  disorders involving aberrant protein expression or biological activity.
CC  The polypeptide and polynucleotide sequences have applications in
CC  diagnostics, forensics, gene mapping, identification of mutations
CC  responsible for genetic disorders or other traits to assess biodiversity
CC  and to produce other types of data and products dependent on DNA and
```

---

```
XX
PN  WO200175067-A2.
XX
PD  11-OCT-2001.
XX
PF  30-MAR-2001; 2001WO-US08631.
XX
PR  31-MAR-2000; 2000US-0540217.
PR  23-AUG-2000; 2000US-0649167.
XX
PA  (HYSE-) HYSEQ INC.
XX
PI  Drmanac RT, Liu C, Tang YT;
XX
DR  WPI; 2001-639362/73.
DR  N-PSDB; AAS77071.
XX
PT  New isolated polynucleotide and encoded polypeptides, useful in
PT  diagnostics, forensics, gene mapping, identification of mutations
PT  responsible for genetic disorders or other traits and to assess
PT  biodiversity -
XX
PS  Claim 20; SEQ ID NO 43243; 103pp; English.
XX
CC  The invention relates to isolated polynucleotide (I) and
CC  polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC  polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC  and gene mapping, and in recombinant production of (II). The
CC  polynucleotides are also used in diagnostics as expressed sequence tags
CC  for identifying expressed genes. (I) is useful in gene therapy techniques
CC  to restore normal activity of (II) or to treat disease states involving
CC  (II). (II) is useful for generating antibodies against it, detecting or
CC  quantitating a polypeptide in tissue, as molecular weight markers and as
CC  a food supplement. (II) and its binding partners are useful in medical
CC  imaging of sites expressing (II). (I) and (II) are useful for treating
CC  disorders involving aberrant protein expression or biological activity.
CC  The polypeptide and polynucleotide sequences have applications in
CC  diagnostics, forensics, gene mapping, identification of mutations
CC  responsible for genetic disorders or other traits to assess biodiversity
CC  and to produce other types of data and products dependent on DNA and
CC  amino acid sequences. ABG00010-ABG30377 represent novel human
CC  diagnostic amino acid sequences of the invention.
CC  Note: The sequence data for this patent did not appear in the printed
CC  specification, but was obtained in electronic format directly from WIPO
CC  at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ  Sequence  151 AA;
```

alignment_scores:
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       Quality:  548.00           Length:   130
         Ratio:    4.567            Gaps:     0
Percent Similarity:  92.308    Percent Identity: 78.462
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alignment_block:
US-09-019-441-1 x ABG12884

Align seg 1/1 to: ABG12884  from: 1 to: 151

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  1 ATGGCCTGGACTCGTCCTCGTCACCCTCCTCACTCAGGGCACAGGATC   50
    ||:||||::||||:::||||::::::||||||||||||||||||||||||||||
  9 MetAlaTrpAlaLeuPheLeuThrLeuLeuThrGlnGlyThrGlySe    25

 51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTG  100
    |||||||||||||     |||||||      |||||:::||||||||||||
 25 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG   42

101 GACAGTCCGGTCACCATCTCCTGACTGGAACCAGCAGCGTTGGTGGT    150
    |||||||:::|||||||||||||||||||:::||||||||||||||||
 42 lyGlnSerIleThrIleSerCysThrGlyThrSerAsnAspValGlyGly   58

151 TATAACTATGTCTCCTGGTACCAACACCACCCCAGGCAAAGCCCCCAAACT  200
    ||||||||||||||||:::||||||||||||||||||||||||||||::||
```

```
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note:The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   251 AA;

alignment_scores:
     Quality:    546.00              Length:    132
     Ratio:    4.439                 Gaps:      1
Percent Similarity:   93.182    Percent Identity:   78.030

alignment_block:
US-09-019-441-1  x ABG19291

Align seg 1/1  to: ABG19291  from: 1  to: 251   ..

    1 ATGGCCTGGACTCGTCCCTCGTCACCCTCCTCACTCAGGGCACAGGATC  50
      ||||||::::|||||:|||||||||||||||||||||||||||||
   15 MetAlaTrpAlaLeuLeuIleLeuThrLeuLeuThrGlnGlyThrGlySe  31

   51 CTGGGCTCAGTCGCCCGACTCAGCCTCCTCCTCGTGTCGGGTCTCCTG  100
      ||||||||||||  ||||||||||||||::|||||||      |
   31 rTrpAlaGlnSerAlaLeuThrGlnProSerAlaSerGlySerLeuG  48

  101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT  150
      |||||||||:::|||||||||||||||:||||::|||:::|
   48 lyGlnSerValThrPheSerCysSerGlyThrSerSerAspIleGlyAsn  64

  151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCCAAACT  200
      ||||||||||||||:::||||||||||||||||||||||||||
   65 TyrAsnTyrValSerTrpTyrArgGlnHisProGlyLysAlaProLysSe  81

  201 CATGATTTATGATGTCGCTAAGCGGGTCTCCTGATCGCTTCT  250
      ||||||||::|||||  :::||||||
   81 uMetIleTyrGluValThrLysArgProSerGlyValProAsnArgPheS  98

  251 CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCGGCTCCAG  300
      |||||||||||||||||||:::||||||
   98 erGlySerLysSerGlyAsnThrAlaSerLeuThrValSerGlyLeuGln  114

  301 GCTGAGGACGAGCGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC  350
      ||||||||||||||||||:::||||:::  :::|
  115 AlaGluAspGluAlaAspTyrTyrCysSerTyrAlaGlyAspTyrTh  131

  351 T......TTGTTATTCGGAAGAGGGACCCCGTTGACCGTCCTAGGT  390
      :::::||||  |||||::||||||||||||||
  131 rProGlyValValPheGlyGlyGlyThrLysLeuThrValLeuGly  146
```

seq_name: /SIDS1/gcgdata/hold-geneseqp-embl/AA2001.DAT:ABG19290

```
seq_documentation_block:
ID   ABG19290 standard; Protein; 235 AA.
XX
AC   ABG19290;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #19281.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000;  2000US-0540217.
PR   23-AUG-2000;  2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS83477.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 20; SEQ ID No 49649; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note:The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   235 AA;

alignment_scores:
     Quality:    544.00              Length:    130
     Ratio:    4.496                 Gaps:      0
Percent Similarity:   78.462    Percent Identity:   93.077

alignment_block:
US-09-019-441-1  x ABG19290

Align seg 1/1  to: ABG19290  from: 1  to: 235   ..

    1 ATGGCCTGGACTCGTCCCTCGTCACCCTCCTCACTCAGGGCACAGGATC  50
      |||||||||||||||||:::::||||||||||||||||||||||||||
    1 MetAlaTrpThrLeuLeuPheLeuThrLeuLeuThrGlnGlyThrGlySe  17

   51 CTGGGCTCAGTCGCCCGACTCAGCCTCCTCCTCGTGTCGGGTCTCCTG  100
      |||||||||||||  |||||||| :::||||  |||||||||||||||
   17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG  34

  101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT  150
      ||||||||:::|||||||::||||||||:||||::|||:::||:::
   34 lyGlnSerIleThrIleSerCysSerGlyThrSerSerAspIleGlyAla  50

  151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCCAAACT  200
      ||||||||||||||:::|||||||||||::::|||||||||||||||
   51 TyrTyrPheValSerTrpTyrGlnGlnTyrProGlyLysAlaProLysLe  67

  201 CATGATTTATGATGTCGCTAAGCGGCCTCAGGGGTCTCGATCGCTTCT  250
      :::::||||||::: |||  ||||||:::::||:::||||:::
   67 uLeuIlePheAspValSerGlyArgProSerGlyIleSerSerArgPheS  84

  251 CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGCTCCAG  300
```

```
            |||||||||||||||||||||||||||||||||||||||
        84  erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100

       301  GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC 350
            ||||||||||||||||||||||||||:::||||::||||| ||||||||
       101  AlaGluAspGluAlaAspTyrTyrCysAlaSerTyrAlaArgSerSerTh 117

       351  TTTGTTATTCGGAAGAGGACCCGGTTGACCGTCCTAGGT 390
            |::::||||||| |||||| ::|||||||||||||
       117  rValValPheGlyGlyGlyThrSerValThrValLeuGly 130
```

seq_name: /SIDS1/gcgdata/hold-geneseqp-embl/AA2001.DAT:ABG22850

seq_documentation_block:
ID   ABG22850 standard; Protein; 236 AA.
XX
AC   ABG22850;
XX
DT   18-FEB-2002 (first entry)
XX
DE   Novel human diagnostic protein #22841.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS87037.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 20; SEQ ID No 53209; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence, 236 AA;
```

alignment_scores:
```
              Quality:   544.00           Length:    130
              Ratio:       4.496          Gaps:        0
  Percent Similarity:  93.077   Percent Identity:  78.462
```

alignment_block:
US-09-019-441-1 x ABG22850

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  Align seg 1/1  to: ABG22850    from: 1  to: 236

    1  ATGGCCTGGACTCTGCTCCTCGTCACCCTCCTCACTCAGGCACAGGATC  50
       ||||||||||||||||||:::::||||||||||||||||||||||||||
    1  MetAlaTrpThrLeuLeuPheLeuValThrLeuLeuThrGlnThrGlyLySe  17

   51  CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCGTCGTCTGGGTCTCCTG  100
       |||||||||||  |||||||||||||||||||||  |||||||||||||||
   17  rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG  34

  101  GACAGTCGGTCACCATCCTCGCACTGCGAACCAGCAGGATGACGTTGGTGGT  150
       ||||||||||::|||||||||||  |||||||||::::||::::||:::
   34  lyGlnSerIleThrIleSerCysIleGlyThrSerSerAspIleGlyAla  50

  151  TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACT  200
       ||| :::||||||||||||:::::||||||||||||||||||||||||
   51  TyrTyrPheValSerTrpTyrGlnGlnTyrProGlyLysAlaProLysLe  67

  201  CATGATTTATGATGTCGCTAAGCGGGGCCTCAGGGGTCTTCGATCGCTTCT  250
       |:::::||||::::|||  ||| |||||||||||||||:::||||||||
   67  uLeuIlePheAspValSerGlyArgProSerGlyIleSerSerSerArgPhes  84

  251  CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGCTCCAG  300
       ||||||||||||||||||||||||||||||||||||||||||||||||
   84  erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln  100

  301  GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC  350
       ||||||||||||||||||||||::::||||::::||||| ||||||||
  101  AlaGluAspGluAlaAspTyrTyrCysAlaSerTyrAlaArgSerSerTh  117

  351  TTTGTTATTCGGAAGAGGACCCGGTTGACCGTCCTAGGT  390
       |::::||||||| |||||| ::|||||||||||||||
  117  rValValPheGlyGlyGlyThrSerValThrValLeuGly  130
```

seq_name: /SIDS1/gcgdata/hold-geneseqp-embl/AA2001.DAT:ABG12887

seq_documentation_block:
ID   ABG12887 standard; Protein; 161 AA.
XX
AC   ABG12887;
XX
DT   13-FEB-2002 (first entry)
XX
DE   Novel human diagnostic protein #12878.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX

DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS77074.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 20; SEQ ID No 43246; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   161 AA;

alignment_scores:
        Quality:  543.00          Length:     130
          Ratio:    4.415           Gaps:       0
Percent Similarity:  94.615   Percent Identity:  79.231

alignment_block:
US-09-019-441-1 x ABG12887

Align seg 1/1  to: ABG12887   from: 1  to: 161

  1 ATGGCCTGGACTCTGCTCCCTGCGTCCCTCCACTCAGGGCACAGGATC  50
    |||||||||||||::||||||||:::||||||||||||||||||||||
 22 MetAlaTrpAlaLeuLeuLeuProAlaSerLeuThrLeuGlnGlyThrGlySe  38

 51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCCTGTCTGTGGGTCCTG  100
    ||||||||||||  |||||||||||:::||||||||||||||||
 38 rTrpAlaGlnSerAlaLeuThrGlnProProSerAlaSerGlySerProG  55

101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGT  150
    ||||||||||||||||||:::|||:::||||
 55 lyGlnSerValThrIleSerCysThrGlyThrSerSerAspIleGlyTyr  71

151 TATAACCATGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCAAACT  200
    |||:||||||||||:::||||||:::|||||||||||||||||||
 72 TyrAspPheValSerTrpTyrGlnGlnArgProGlyLysAlaProLysLe  88

201 CATGATTTATGATGTCGCTAAGCGGCCTCAGGGGTCTCTGATCGCTTCT  250
    |:::||::::|||   |||||||   ||||||||||||
 88 uIleIlePheGluValAsnLysArgProSerGlyValProAspArgPheS  105

251 CTGGGCTCCAAGTCTGGCAACACGCGCCTCCCTGACCATCTGGGCTCCAG  300
    |||||||||||||||||||||||||||:::||||||||||
105 erGlySerLysSerAlaAsnThrAlaSerLeuThrValSerGlyLeuGln  121

301 GCTGAGGACGAGGCTGATTATTACTGTTGTCATATACAACCAGTAGCAC  350
    ||||||||||||||||||||||||||||
122 AlaGluAspGluAlaAspTyrTyrCysGlySerTyrAlaLeuAsnAspAs  138

---

351 TTTGTTATTCGGAAGAGGAGGACCCGGTTGACCGTCCTAGGT  390
    : |||||||||||||||||:::||||||||||||||||
138 nGlyLeuPheGlyArgGlyThrLysLeuThrValLeuGly  151

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:AAR31535

seq_documentation_block:
ID   AAR31535 standard; Protein; 131 AA.
XX
AC   AAR31535;
XX
DT   25-MAY-1993  (first entry)
XX
DE   MH4H7 MAb light chain.
XX
KW   Human; recombinant; light chain; monoclonal; antibody; MAb; MH4H7;
KW   Namalwa; microbial infection.
XX
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   Domain         43..56
FT                  /label= CDR1
FT   Domain         72..78
FT                  /label= CDR2
FT   Domain         111..120
FT                  /label= CDR3
XX
PN   JP04360696-A.
XX
PD   14-DEC-1992.
XX
PF   06-JUN-1991;  91JP-0163886.
XX
PR   06-JUN-1991;  91JP-0163886.
XX
PA   (SUMO ) SUMITOMO CHEM CO LTD.
PA   (SUMU ) SUMITOMO SEIYAKU KK.
XX
DR   WPI; 1993-032623/04.
DR   N-PSDB; AAQ36134.
XX
PT   Recombinant human antibody - produced using new human B
PT   lymphocyte strain as the host
XX
PS   Claim 5; Fig 9; 27pp; Japanese.
XX
CC   This sequence represents the light chain of a recombinant human
CC   monoclonal antibody (MAb) designated MH4H7. This sequence was
CC   introduced in to a Namalwa cell strain which was cultured. The
CC   MAb may be used in a drug for the prevention and treatment of
CC   diseases caused by microbial infection.
XX
SQ   Sequence   131 AA;

alignment_scores:
        Quality:  538.50          Length:     131
          Ratio:    4.487           Gaps:       1
Percent Similarity:  91.603   Percent Identity:  80.153

alignment_block:
US-09-019-441-1 x AAR31535

Align seg 1/1  to: AAR31535   from: 1  to: 131

  1 ATGGCCTGGACTCTGCTCCCTGCGTCCCTCCACTCAGGGCACA...GG  47
    ||||||||||||||||:::||||||||||||||||||||   ||
  1 MetAlaTrpAlaLeuLeuLeuProAlaSerLeuThrLeuGlnGlyGlyGl  17

 48 ATCCTGGGCTCAGTCTGCCCCGACTCCCCTCAGCCTCCCTGTCTGTGGGTCC  97
    |||||||||||||  ||||||||  ||||||||||||||||
 17 ySerTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerP  34

CC      a food supplement. (II) and its binding partners are useful in medical
CC      imaging of sites expressing (II). (I) and (II) are useful for treating
CC      disorders involving aberrant protein expression or biological activity.
CC      The polypeptide and polynucleotide sequences have applications in
CC      diagnostics, forensics, gene mapping, identification of mutations
CC      responsible for genetic disorders or other traits to assess biodiversity
CC      and to produce other types of data and products dependent on DNA and
CC      amino acid sequences. ABG00010-ABG30377 represent novel human
CC      diagnostic amino acid sequences of the invention.
CC      Note: The sequence data for this patent did not appear in the printed
CC      specification, but was obtained in electronic format directly from WIPO
CC      at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ      Sequence    236 AA;

alignment_scores:
        Quality:      527.50              Length:      131
          Ratio:        4.433               Gaps:        1
Percent Similarity:    90.840       Percent Identity:  77.099

alignment_block:
US-09-019-441-1 x ABG19298

Align seg 1/1  to: ABG19298  from:  1  to: 236

     1 ATGGCCTGGACTCGCTCCTGCACTGGAACCAGCAGCCGATGACGTTGGT  50
       |||||||||||||||||:::||||||||||||||||||::||:::||:||
     1 MetAlaTrpAlaLeuLeuProLeuHisThrGlnGlyThrGlySe       17

    51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGCTCCTG  100
       ||||||||||||||    ||||||||  |||:||||||||||||||||||
    17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG  34

   101 GACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGCGATGACGTTGGTGGT  150
       ||||||||:::||||||||||||||||||||:||::||||||||||||||||
    34 lyGlnSerIleThrIleSerCysThrGlySerSerSerAspValGlyGly    50

   151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACT  200
       ||||||||||||||||||||:::||||||||||||||||||||||||||
    51 TyrAsnTyrValSerTrpTyrGlnHisHisProGlyLysAlaProLysLe  67

   201 CATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGATCGCTTCT  250
       |||::::|||::    :::||||||    :::||||||||||||||||:||
    67 uIleHisTyrGluGlySerLysArgProSerArgValTyrArgAspArgPheS  84

   251 CTGGCTCCAGTCTGCAACACGGCCTCCTGACCATTCTGGGCTCCAG  300
       |||||||    ||||||||||||||||||||||||||||||||||||
    84 erGlySerMetSerAlaAsnThrAlaSerLeuThrIleSerGlyLeuGln  100

   301 GCTGAGGACGAGGCTGATTATTACTGTGTCATATACAACCAGTAGCAC  350
       ||||:::||||||||||||||||||||||||:::    |||:::|||||
   101 AlaAspAspGluAlaAspTyrTyrCysSerPheAlaGlySerSerAl  117

   351 TTTG...TTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT  390
       ::::||    :::||||||||||||||||||||||||| |||:::|||
   117 aLeuArgIlePheGlySerGlyThrArgValIleValLleGly  131

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:ABG19296

seq_documentation_block:
ID      ABG19296 standard;  Protein;  244 AA.
XX
AC      ABG19296;
XX
DT      18-FEB-2002  (first entry)
XX
DE      Novel human diagnostic protein #19287.
XX
KW      Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW      food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS      Homo sapiens.

---

    98 CTGGACAGTCGGTCACCATCTCCTGCACTGGAACCAGCAGCCGATGACGTTGGT  147
       ||||||||||:::||||||||||||||||||||||||::||:::||::::||
    34 roGlyGlnSerIleThrIleSerCysThrGlyThrSerAspIleGly        50

   148 GGTATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCCAA  197
       ||||||||||||||||||||||||||::||||||||||||||||||||||
    51 GlyTyrAsnTyrValSerTrpTyrGlnGlnHisProGlyLysAlaProLy  67

   198 ACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGATCGCT  247
       |||:::||||| |||::::::|||    |||||||||||  |||||||| |||
    67 sLeuValIleTyrAlaValSerAsnArgProSerGlyValSerHisArgP  84

   248 TCTCTGGCTCCAAGTCTGGCAACACGGCCTCCTGACCATCTCTGGGGCTC  297
       ||||||||||||||||||||||||||||||||||||||||||||||||||
    84 heSerGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeu  100

   298 CAGGCTGAGGACGAGGCTGATTATTACTGTGTTCATATACAACCAGTAG  347
       ||||||||||||||||||||||||||||||  |||   ::::::::|
   101 GlnAlaGluGluAspGluAlaAspTyrTyrCysAsnSerAspAlaSerThrSe  117

   348 CACTTTGTTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT  390
       :::||||| ||||::::||||||||||||||
   117 rLysTrpValPheGlyGlyGlyThrLysLeuThrValLeuGly  131

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:ABG19298

seq_documentation_block:
ID      ABG19298 standard;  Protein;  236 AA.
XX
AC      ABG19298;
XX
DT      18-FEB-2002  (first entry)
XX
DE      Novel human diagnostic protein #19289.
XX
KW      Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW      food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS      Homo sapiens.
XX
PN      WO200175067-A2.
XX
PD      11-OCT-2001.
XX
PF      30-MAR-2001; 2001WO-US08631.
XX
PR      31-MAR-2000; 2000US-0540217.
PR      23-AUG-2000; 2000US-0649167.
XX
PA      (HYSE-) HYSEQ INC.
XX
PI      Drmanac RT,  Liu C,  Tang YT;
XX
DR      WPI; 2001-639362/73.
DR      N-PSDB; AAS83485.
XX
PT      New isolated polynucleotide and encoded polypeptides, useful in
PT      diagnostics, forensics, gene mapping, identification of mutations
PT      responsible for genetic disorders or other traits and to assess
PT      biodiversity -
XX
PS      Claim 20; SEQ ID No 49657; 103pp; English.
XX
CC      The invention relates to isolated polynucleotide (I) and
CC      polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC      polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC      and gene mapping, and in recombinant production of (II). The
CC      polynucleotides are also used in diagnostics as expressed sequence tags
CC      for identifying expressed genes. (I) is useful in gene therapy techniques
CC      to restore normal activity of (II) or to treat disease states involving
CC      (II). (II) is useful for generating antibodies against it, detecting or
CC      quantitating a polypeptide in tissue, as molecular weight markers and as

```
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS83483.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 20; SEQ ID No 49655; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   244 AA;

alignment_scores:
     Quality:    527.00           Length:     131
     Ratio:        4.504          Gaps:         1
Percent Similarity:  89.313       Percent Identity:  77.099

alignment_block:
US-09-019-441-1 x ABG19296

Align seg 1/1  to: ABG19296  from: 1  to: 244

  1 ATGGGCTGGACTCTGCCCCTGCTCCTCCTCACCCTCCTCACTCAGGGCACAGGATC 50
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  8 MetAlaTrpAlaLeuLeuLeuLeuThrLeuLeuThrGlnGlyThrGlySe 24

 51 CTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCTGTCTGTCTGGGTCTCCTG 100
    |||||||||||| |||||||| |||||||||||||||||||||||||||||||
 24 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValAsnGlySerProG 41

101 GACAGTCGGTCACCATCTCCTGCACTGGGAACCAGCCAGCGATGACGTTGGTGGT 150
    |||| ::||||||||||||||||||  |||::||:::|||:||||||
 41 lyGlnLeuIleIleSerCysThrGlyProSerAspIleGlyThrLysGlyAsp 57

151 TATAACTATGTCTCCTGGTACCAACACCACCAGGCAAAGCCCCAAACT 200
    |||::|||||::||||||||||||||||  ||||||||||||||||||
```

```
 58 TyrGlnTyrIleSerTrpTyrTyrGlnGlnHisProGlyLysAlaProLysLe 74

201 CATGATTATGATGTCGCTAAGCGGCCTCAGGGGTCTCTGATCGCTTCT 250
    |:::|||||||||||  |||||  ||||||||||||||||||::||||||
 74 uIleIleTyrAspValAspLysArgProSerGlyValSerAsnArgPheS 91

251 CTGGCTCCAAGTCTGGCAACACGGCCTCCTGACCATCTCTGGGCTCCAG 300
    |||||||||||||||||||||||||||||||||||||||||||||||||
 91 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 107

301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC 350
    ||||||||||||||||||||||||| ||||||  |||:::|||
108 AlaGluAspGluAlaAspTyrTyrCysSerTyrArgGlySerAlaTh 124

351 T......TTGTTATTCGGAAGAGGGAGCCCGTTGACCGTCCTA 387
    |  :::::||||||  ||||:|:::|||||||||
124 rPheGluValPheGlyGlyGlyThrLysValThrValLeu 138

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:AAG80206

seq_documentation_block:
ID   AAG80206 standard; Protein; 117 AA.
XX
AC   AAG80206;
XX
DT   22-JAN-2002  (first entry)
XX
DE   Human autoantibody MICA-1 variable region heavy chain.
XX
KW   Autoantigen; fusion protein; islet cell antigen; MICA autoantibody;
KW   glutamate decarboxylase; diabetes mellitus type I; stiff-man syndrome;
KW   polyglandular autoimmune syndrome; autoimmune disorder; IA2; GAD65;
KW   variable region; heavy chain; MICA-1.
XX
OS   Homo sapiens.
XX
XX
PN   EP1149914-A2.
XX
PD   31-OCT-2001.
XX
PF   29-MAR-2001; 2001EP-0107702.
XX
PR   10-APR-2000; 2000DE-1017782.
PR   25-MAY-2000; 2000DE-1025840.
XX
PA   (LABO-) LABOR KOCH MERK GMBH.
XX
PI   Richter W, Rickert M, Rapp I, Dangel W;
XX
DR   WPI; 2001-640702/74.
DR   N-PSDB; AAI68755.
XX
PT   New fusion protein, useful for diagnosis of diabetes type I and other
PT   metabolic diseases, is reactive with autoantibodies against both
PT   glutamate decarboxylase and islet cell antigen -
XX
PS   Disclosure; Page 22-23; 68pp; German.
XX
CC   This invention describes a novel fusion protein (I) that has, at its
CC   N-terminus, one or more epitopes that bind specifically to autoantibodies
CC   (AAb) against the islet cell antigen IA2 and, at its C-terminus, one or
CC   more epitopes that bind specifically to antibodies (Ab) directed against
CC   the glutamate decarboxylase GAD65. (I), also nucleic acid (II) encoding
CC   it, vectors containing (II) and transformed cells, are useful for
CC   diagnosis and prognosis of diabetes mellitus type 1, stiff-man syndrome,
CC   polyglandular autoimmune syndrome or other autoimmune conditions
CC   associated with AAb against GAD65 or IA2. (I) provides a rapid and simple
CC   diagnosis of high specificity and sensitivity, capable of recognizing
CC   antibodies against both IA2 and GAD65, simultaneously. Unlike known
CC   fusions, where the GAD65 component is at the N-terminus, (I) contains
CC   correctly folded conformational epitopes that can react with most MICA
CC   autoantibodies. This sequence represents the human autoantibody MICA-1
CC   variable region heavy chain used in the method of the invention.
```

XX
SQ    Sequence    117 AA;

alignment_scores:
         Quality:    524.00         Length:    116
           Ratio:    4.764            Gaps:      0
Percent Similarity:  94.828   Percent Identity:  84.483

alignment_block:
US-09-019-441-1 x AAG80206    ..

Align seg 1/1   to: AAG80206    from: 1  to: 117

 43 ACAGGATCCTGGGCTCAGTCTGCCCCGACTCAGCCTCCCTCTGTCTCGG  92
    |||||||||||||||||  ::::   |||||||||   ||||||||||||
  2 ThrGlySerTrpAlaGluLeuValValThrGlnProAlaSerValSerGl  18

 93 GTCTCCTGGACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACG 142
    ||||||||||||||::::|||||||||||||||||||:::||||::||||
 18 ySerProGlyGlnSerIleThrIleSerCysThrGlyThrSerSerAspV  35

143 TTGGTGGTTATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAAGCC 192
    ||||||||||||||||||||||||||||:::::|||||||:::||||||
 35 alGlyGlyTyrAsnTyrValSerTrpTyrArgHisHisProAlaLysAla  51

193 CCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGA 242
    |||||||||||||||||||||||:::::|||  ||||||||||||||:::
 52 ProLysLeuMetIleTyrAspValSerAsnArgProSerGlyValSerAs  68

243 TCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTG 292
    :||||||||||||||||||||||||  |||||||||||||||||||||||
 68 nArgPheSerGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerG  85

293 GGCTCCAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACC 342
    ||||||||||||||||||||||||||||  |||||||:::||||::::::
 85 lyLeuGlnAlaGluAspGluAlaAspTyrTyrCysSerTyrThrSer 101

343 AGTAGCACTTTGTTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
    ||||||||||:::|||||  ||||||:::|||||||||||||||||
102 SerSerThrLeuValPheGlyGlyGlyThrArgLeuThrValLeuGly 117

OM of: US-09-019-441-3 to: Pending_Patents_AA_Main:*    out_format : pfs

Date: Sep 23, 2002 10:19 AM

About: Results were produced by the GenCore software, version 4.5,
     Copyright (c) 1993-2000 Compugen Ltd.

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-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
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-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0901941_@CGN1_1_837 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

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Query length: 387
Database: Pending_Patents_AA_Main:*
Database sequences: 3502263
Database length: 351980561
Search time (sec): 811.400000

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| Sequence | Strd | Orig | ZScore | EScore | Len | ! Documentation |
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| /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-760-479-639 | + | 595.00 | 1194.21 | 3.5e-58 | 205 | |
| /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-113-635-8 | + | 594.50 | 1191.82 | 4.1e-58 | 237 | ! |
| /cgn2_6/ptodata/2/paa/US091_COMB.pep:US-09-195-853-1 | + | 590.50 | 1183.70 | 1.2e-57 | 237 | |
| /cgn2_6/ptodata/2/paa/US091_COMB.pep:US-09-195-853-1 | + | 590.50 | 1183.70 | 1.2e-57 | 237 | |
| /cgn2_6/ptodata/2/paa/US100_COMB.pep:US-10-038-591-52 | + | 590.00 | 1182.73 | 1.3e-57 | 236 | |
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| /cgn2_6/ptodata/2/paa/US100_COMB.pep:US-10-038-591-51 | + | 584.00 | 1170.55 | 6.4e-57 | 236 | |
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| /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-18569-2296 | + | 579.00 | 1159.49 | 2.4e-56 | 26 | |
| /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-113-635-11 | + | 578.00 | 1162.90 | 2.7e-56 | 146 | ! |
| /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-197-873-17896 | + | 573.50 | 1149.20 | 9.8e-56 | 237 | ! |
| /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-760-479-852 | + | 568.00 | 1137.57 | 4.1e-55 | 249 | |
| /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-08518-1 | + | 564.50 | 1130.77 | 1.0e-54 | 241 | ! |
| /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-189-417-1 | + | 564.50 | 1130.77 | 1.0e-54 | 241 | |
| /cgn2_6/ptodata/2/paa/US100_COMB.pep:US-10-038-591-47 | + | 562.00 | 1125.90 | 2.0e-54 | 236 | |
| /cgn2_6/ptodata/2/paa/US083_COMB.pep:US-08-341-469-19 | + | 555.50 | 1112.78 | 1.1e-53 | 234 | |
| /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-740-002-24 | + | 551.50 | 1103.65 | 3.4e-53 | 234 | |
| /cgn2_6/ptodata/2/paa/US081_COMB.pep:US-08-157-101-5 | + | 551.00 | 1103.57 | 3.6e-53 | 236 | |
| /cgn2_6/ptodata/2/paa/US096_COMB.pep:US-09-647-468-179 | + | 549.00 | 1105.35 | 5.1e-53 | 127 | |
| /cgn2_6/ptodata/2/paa/US083_COMB.pep:US-08-309-530-5 | + | 548.00 | 1097.56 | 7.5e-53 | 234 | |
| /cgn2_6/ptodata/2/paa/US096_COMB.pep:US-09-647-468-180 | + | 546.00 | 1099.26 | 1.1e-52 | 127 | |
| /cgn2_6/ptodata/2/paa/US098_COMB.pep:US-09-834-366-13317 | + | 544.00 | 1093.64 | 1.9e-52 | 15 | |
| /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-197-873-13317 | + | 544.00 | 1093.64 | 1.9e-52 | 150 | |
| /cgn2_6/ptodata/2/paa/US088_COMB.pep:US-08-815-030-7 | + | 544.00 | 1088.31 | 2.2e-52 | 264 | |
| /cgn2_6/ptodata/2/paa/US088_COMB.pep:US-08-815-030-12 | + | 544.00 | 1081.70 | 2.5e-52 | 532 | |
| /cgn2_6/ptodata/2/paa/US088_COMB.pep:US-08-815-030-9 | + | 544.00 | 1079.91 | 2.6e-52 | 643 | ! |
| /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-177-571-4596 | + | 543.00 | 1092.74 | 2.4e-52 | 133 | |
| /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-14827-14137 | + | 543.00 | 1092.74 | 2.4e-52 | 133 | |
| /cgn2_6/ptodata/2/paa/US098_COMB.pep:US-09-834-366-13330 | + | 543.00 | 1091.18 | 2.5e-52 | 15 | |
| /cgn2_6/ptodata/2/paa/US098_COMB.pep:US-09-834-366-13330 | + | 543.00 | 1091.18 | 2.5e-52 | 157 | ! |
| /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-197-873-13330 | + | 542.50 | 1091.80 | 2.8e-52 | 14 | |
| /cgn2_6/ptodata/2/paa/US098_COMB.pep:US-09-834-366-13329 | + | 542.50 | 1090.72 | 2.8e-52 | 14 | |
| /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-197-873-13329 | + | 542.50 | 1090.72 | 2.8e-52 | 148 | |
| /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-740-002-26 | + | 542.50 | 1086.40 | 3.1e-52 | 234 | |
| /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-60-113-635-7 | + | 542.00 | 1085.30 | 3.6e-52 | 236 | ! |
| /cgn2_6/ptodata/2/paa/US096_COMB.pep:US-09-647-468-181 | + | 540.00 | 1087.09 | 5.3e-52 | 127 | |
| /cgn2_6/ptodata/2/paa/US098_COMB.pep:US-09-834-366-13335 | + | 535.00 | 1075.75 | 2.0e-51 | 14 | |
| /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-197-873-13335 | + | 535.00 | 1075.75 | 2.0e-51 | 144 | |
| /cgn2_6/ptodata/2/paa/US096_COMB.pep:US-09-647-468-182 | + | 534.00 | 1074.91 | 2.5e-51 | 1 |
| /cgn2_6/ptodata/2/paa/US098_COMB.pep:US-09-855-271-26 | + | 534.00 | 1074.83 | 2.5e-51 | 12 |
| /cgn2_6/ptodata/2/paa/US100_COMB.pep:US-10-012-579-26 | + | 534.00 | 1074.83 | 2.5e-51 | 12 |
| /cgn2_6/ptodata/2/paa/US096_COMB.pep:US-09-647-468-183 | + | 532.00 | 1070.85 | 4.2e-51 | 1 |
| /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-760-479-604 | + | 531.00 | 1063.06 | 6.2e-51, | 2 |

seq_name: /cgn2_6/ptodata/2/paa/US092_COMB.pep:US-09-292-053-6

seq_documentation_block:
; Sequence 6, Application US/0929205
; GENERAL INFORMATION:
;  APPLICANT:  REFF, MITCHELL E.
;  APPLICANT:  KLOETZER, WILLIAM S.
;  APPLICANT:  NAKAMURA, TAKEHIKO
;  TITLE OF INVENTION:  GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE
;  TITLE OF INVENTION:  THEREOF AS THERAPEUTICS
;  FILE REFERENCE:  23522.0699
;  CURRENT APPLICATION NUMBER:  US/09/292,053
;  CURRENT FILING DATE:  1999-04-14
;  PRIOR APPLICATION NUMBER:  08/803,085
;  PRIOR FILING DATE:  1997-02-20
;  NUMBER OF SEQ ID NOS:  39
;  SOFTWARE:  PatentIn Ver. 2.1
;
; SEQ ID NO 6
;  LENGTH: 129
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-292-053-6

alignment_scores:
      Quality:     668.00            Length:      129
        Ratio:      5.178              Gaps:        0
Percent Similarity:  100.000     Percent Identity: 100.000

alignment_block:
US-09-019-441-3 x US-09-292-053-6

Align seg 1/1   to: US-09-292-053-6   from: 1   to: 129

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    1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe  17

   51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCTGT  100
      |||||||||||||||||||||||||||||||||||||||||||||||||
   17 uProGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS  34

  101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC  150
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnAsp  50

  151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA  200
      |||||||||||||||||||||||||||||||||||||||||||||||||
   51 IleArgTyrTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy  67

  201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGTCCCATCAAGGT  250
      ||||||||||||||||||||||||||||||||||||||||||||||||
   67 sLeuLeuIleTyrValAlaSerLeuGlnSerGlyValProSerArgP  84

  251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG  300
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   84 heSerGlySerGlySerGlyThrGlnPheThrLeuThrValSerSerLeu  100

  301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC  350
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  101 GlnProGluAspPheAlaThrTyrTyrCysLeuGlnValTyrSerThrPr  117

  351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA  387
      |||||||||||||||||||||||||||||||||||||
  117 oArgThrPheGlyGlnGlyThrLysValGluIleLys  129
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seq_name: /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-760-479-639

seq_documentation_block:
; Sequence 639, Application US/09760479
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT253
; CURRENT APPLICATION NUMBER: US/09/760,479
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 946
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 639
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-479-639

alignment_scores:
                Quality:    595.00                    Length:        129
                Ratio:        4.917                    Gaps:            0
Percent Similarity:    93.798        Percent Identity:    89.922

alignment_block:
US-09-019-441-3 x US-09-760-479-639

Align seg 1/1  to: US-09-760-479-639  from: 1  to: 205        ..

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   51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT  100
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   22 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS  39

  101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCCAGGGCAAGTCAGGAC  150
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   39 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnIle  55

  151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA  200
      |||            ||||||||||||||||||||||||||||||||||
   56 IleSerThrTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy  72

  201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT  250
      |::||||||||      ||||||||||||||||||||||||||||||||
   72 sPheLeuIleTyrArgAlaSerSerLeuGlnSerGlyValProSerArgP  89

  251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACCTCACCGTCAGCAGCCTG  300
      |||||||||||||||||:::::||||||||||||||||||||||||||||
   89 heSerGlySerGlyTyrGlyThrAspPheThrLeuThrIleSerSerLeu  105

  301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC  350
      ||||||||||||||  |||:::||||||    |||::::||||||
  106 GlnProGluAspPheAlaThrTyrTyrCysGlnSerTyrThrThrPr  122

  351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA  387
      |   ||||||||||||||||||||||  |||::||||||
  122 oProThrPheGlyGlnGlyThrLysLeuGluIleLys  134

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-113-635-8

seq_documentation_block:
; Sequence 8, Application US/60113635
; GENERAL INFORMATION:
; APPLICANT: Henry Yue
; APPLICANT: Y. Tom Tang
; APPLICANT: Preeti Lal
; APPLICANT: Jennifer L. Hillman
; APPLICANT: Mariah R. Baughn
; APPLICANT: Aina Lu
; APPLICANT: Leo Shih

alignment_scores:
                Quality:    594.50                    Length:        130
                Ratio:        4.833                    Gaps:            1
Percent Similarity:    94.615        Percent Identity:    90.000

alignment_block:
US-09-019-441-3 x US-60-113-635-8

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      ||||||||||||||||||||||||||||||||||||||||||||||||||
   17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS  34

  101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCCAGGGCAAGTCAGGAC  150
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnInSer  50

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      |||            ||||||||||||||||||||||||||||||||||
   51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy  67

  201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT  250
      |::||||||||      ||||||||||||||||||||||||||||||||
   67 sLeuLeuIleTyrArgAlaAlaSerSerLeuGlnSerGlyValProSerArgP  84

  251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG  300
      |||||||||||||||||:::::||||||||||||||||||||||||||||
   84 heSerGlySerGlyTyrGlyThrAspPheThrLeuThrIleSerSerLeu  100

  301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC  350
      ||||||||||||||  |||:::||||||    |||:::||||||
  101 GlnProGluAspPheAlaThrTyrTyrCysGlnSerTyrSerThrPr  117

  351 TCGG...ACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA  387
      |      ||||||||||||||||||:::::||||||||||
  117 oProIleThrPheGlyGlnGlyThrLeuGluIleLys  130

seq_name: /cgn2_6/ptodata/2/paa/US091_COMB.pep:US-09-195-853-1

seq_documentation_block:
; Sequence 1, Application US/09195853
; GENERAL INFORMATION:
; APPLICANT: Henry Yue
; APPLICANT: Y. Tom Tang
; APPLICANT: Neil C. Corley
; APPLICANT: Karl J. Guegler
; APPLICANT: Gina A. Gorgone
; APPLICANT: Mariah R. Baughn
; APPLICANT: Aina Lu
; TITLE OF INVENTION: HUMAN ANTIGEN RECOGNITION PROTEINS
; FILE REFERNCE: PF-0643 us
; CURRENT APPLICATION NUMBER: US/09/195,853

## Left column

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; CURRENT FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
  SEQ ID NO 1
;   LENGTH: 237
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE: -
;   OTHER INFORMATION: 079785
US-09-195-853-1

alignment_scores:
          Quality:  590.50          Length:     130
          Ratio:    4.801           Gaps:         1
Percent Similarity: 94.615     Percent Identity: 89.231

alignment_block:
US-09-019-441-3 x US-09-195-853-1

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  1 MetAspMetArgValProAlaGlnInLeuLeuGlyLeuLeuLeuLeuTrpLe  17

 51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCCATCTTCCCTGT 100
    ||||||||||||||||||||||||||||||||:::||||||||||
 17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS  34

101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
    |||||||| |||||:::::||||||||||:::::|||:::::::::||
 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaGlyGlnSer  50

151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    |||          |||||||||||||||||||||||||||||||||||
 51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy  67

201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT 250
    ||||||||||||||:::|||||||||||||||||||||||||||||||
 67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgP  84

251 TCAGCCGCAGTGGATCTGGGACAGAGTCCACTCCACCGTCAGCAGCCTG 300
    ||||||||||||:::||||||||:::::|||||||:::||||||||||
 84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
    |||||||||||||:::||||:::|||::||||||||||| |||||||||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrPr 117

351 TCGG...ACGTTCGGCCAAGGGACCCAAGGTGGAAATCAAA 387
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117 oProIleThrPheGlyGlnGlyThrArgLeuGluIleLys 130
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seq_name: /cgn2_6/ptodata/2/paa/US091_COMB.pep:US-09-195-853-1

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seq_documentation_block:
; Sequence 1, Application US/09195853A
; GENERAL INFORMATION:
;   APPLICANT: Henry Yue
;   APPLICANT: Y. Tom Tang
;   APPLICANT: Neil C. Corley
;   APPLICANT: Karl J. Guegler
;   APPLICANT: Gina A. Gorgone
;   APPLICANT: Mariah R. Baughn
;   APPLICANT: Aina Lu
;   TITLE OF INVENTION: HUMAN ANTIGEN RECOGNITION PROTEINS
;   FILE REFERENCE: PF-0643 us
;   CURRENT APPLICATION NUMBER: US/09/195,853A
;   CURRENT FILING DATE: 1998-11-19
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: PERL Program
  SEQ ID NO 1
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## Right column

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;   LENGTH: 237
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE: -
;   OTHER INFORMATION: 079785
US-09-195-853-1

alignment_scores:
          Quality:  590.50          Length:     130
          Ratio:    4.801           Gaps:         1
Percent Similarity: 94.615     Percent Identity: 89.231

alignment_block:
US-09-019-441-3 x US-09-195-853-1

Align seg 1/1  to: US-09-195-853-1  from: 1  to: 237

  1 ATGGACATGAGGGTCCCCGTCCTCAGCTCCTGGGGCTCCTTCTTCTGCTCTGGCT  50
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  1 MetAspMetArgValProAlaGlnInLeuLeuGlyLeuLeuLeuLeuTrpLe  17

 51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCCATCTTCCCTGT 100
    ||||||||||||||||||||||||||||||||:::||||||||||
 17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS  34

101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
    |||||||| |||||:::::||||||||||:::::|||:::::::::||
 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaGlyGlnSer  50

151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    |||          |||||||||||||||||||||||||||||||||||
 51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy  67

201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT 250
    ||||||||||||||:::|||||||||||||||||||||||||||||||
 67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgP  84

251 TCAGCCGCAGTGGATCTGGGACAGAGTCCACTCCACCGTCAGCAGCCTG 300
    ||||||||||||:::||||||||:::::|||||||:::||||||||||
 84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
    |||||||||||||:::||||:::|||::||||||||||| |||||||||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrPr 117

351 TCGG...ACGTTCGGCCAAGGGACCCAAGGTGGAAATCAAA 387
    ||||         |||  |||||||||||||:::::::||||||||
117 oProIleThrPheGlyGlnGlyThrArgLeuGluIleLys 130
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seq_name: /cgn2_6/ptodata/2/paa/US100_COMB.pep:US-10-038-591-52

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seq_documentation_block:
; Sequence 52, Application US/10038591
; GENERAL INFORMATION:
;   APPLICANT: Cohen, Bruce D.
;   APPLICANT: Beebe, Jean
;   APPLICANT: Miller, Penelope E.
;   APPLICANT: Moyer, James D.
;   APPLICANT: Corvalan, Jose R.
;   APPLICANT: Gallo, Michael
;   TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
;   FILE REFERENCE: ABX-PF2
;   CURRENT APPLICATION NUMBER: US/10/038,591
;   CURRENT FILING DATE: 2002-01-04
;   PRIOR APPLICATION NUMBER: 60/259,927
;   PRIOR FILING DATE: 2001-01-05
;   NUMBER OF SEQ ID NOS: 60
;   SOFTWARE: PatentIn Ver. 2.1
  SEQ ID NO 52
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-10-038-591-52

alignment_scores:
    Quality:    590.00        Length:      129
    Ratio:      4.876        Gaps:        0
Percent Similarity: 93.798    Percent Identity: 90.698

alignment_block:
US-09-019-441-3 x US-10-038-591-52

Align seg 1/1 to: US-10-038-591-52  from: 1 to: 236

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  1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpPh  17

 51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
    :|||||||||||||||||||||||||||||||||||||||||||||||||
 17 eProGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS  34

101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
    |||||||||||||||||||||||||||||||||||||||||||||||||
 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly  50

151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    |||||  ||:::||||||||||||||||||||||||||||||||||
 51 IleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLysAlaProLy  67

201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT 250
    |||||||||||||||||||||||||||||||||||||||||||||||||
 67 sArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgP  84

251 TCAGCGGCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
    ||||||||||||||||||||||||||||||||||:::||||||
 84 heSerGlySerGlyThrGluPheThrLeuThrIleSerSerLeu 100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
    ||||||||||||||||||||||||||||||  |||  ||||||||
101 GlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsnSerTyrPr 117

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    |||||||||||||||||||||:::||||||||
117 oTrpThrPheGlyGlnGlyThrLysValGluIleLys 129
```

alignment_scores:
    Quality:    588.00        Length:      129

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US-10-038-591-52

alignment_scores:
    Quality:               Ratio:    4.860    Percent Similarity: 93.798
Percent Similarity: 93.798    Gaps:    0    Percent Identity: 89.922

alignment_block:
US-09-019-441-3 x US-10-038-591-48

Align seg 1/1 to: US-10-038-591-48  from: 1 to: 236

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  1 ATGGACATGAGGGTCCCCGCTCCAGCTCCTGGGCTCCTTCTGCTCTGGCT  50
    |||||||||||||||||||||||||||||||||||||||||||||::|||
  1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpPh  17

 51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
    :|||||||||||||||||||||||||||||||||||||||||||||||||
 17 eProGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS  34

101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
    |||||||||||||||||||||||||||||||||||||||||||||||||
 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly  50

151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    |||||  ||:::||||||||||||||||||||||||||||||||||
 51 IleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLysAlaProLy  67

201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT 250
    |||||||||||||||||||||||||||||||||||||||||||||||||
 67 sArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgP  84

251 TCAGCGGCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
    ||||||||||||||||||||||||||||||||||:::||||||
 84 heSerGlySerGlyThrGluPheThrLeuThrIleSerSerLeu 100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
    ||||||||||||||||||||||||||||||  |||  ||||||||
101 GlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsnSerTyrPr 117

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    |||||||||||||||||||||:::||||||||
117 oTyrThrPheGlyGlnGlyThrLysLeuGluIleLys 129
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seq_name: /cgn2_6/ptodata/2/paa/US100_COMB.pep:US-10-038-591-51

alignment_scores:
    Quality:    584.00        Length:      128
    Ratio:      4.826        Gaps:        0
Percent Similarity: 94.531    Percent Identity: 89.062

alignment_block:
US-09-019-441-3 x US-10-038-591-51

Align seq 1/1 to: US-10-038-591-51 from: 1 to: 236

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      1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCCTGCTCTGGCT 50
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
      1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPh 17

     51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
        :|||||||||||||:|||||||||||||||||||||||||||||||||||:|
     17 eProGlySerArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34

    101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
        :||||||||||||||||||||||||||||||||||||||||||||||||||
     34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnAsp 50

    151 ATTAGTAGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
        |||:|||||||||||||||||:::|||||||||||||||||||||||||||
     51 IleSerArgLeuAlaThrPheThrCysArgAlaSerGlnAsp 67

    201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT 250
        || |||||||:||||||||||||||:|||||||||||||||||||||||||
     67 sArgLeuIleTyrValAlaSerArgLeuGlnSerGlyValProSerArgP 84

    251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
        | ||||||||||||||||||||||||||||:||:::||||||||||||||
     84 heSerGlySerGlyThrGlnSerGlyThrIleSerSerLeu 100

    301 TCAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGGTTTATAGTACCCC 350
        |||||||||||||||||||||||||||:|||:::||||| |||||||||
    101 GlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsnAsnTyrPr 117

    351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATC 384
        ||||||||||||||||||||||||||||||:||||||
    117 oArgThrPheGlyGlnGlyThrGluValGluIle 128
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seq_name: /cgn2_6/ptodata/2/paa/US098_COMB.pep:US-09-859-053-30

seq_documentation_block:
; Sequence 30, Application US/09859053
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, Nobuaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-30

alignment_scores:
        Quality:  582.00          Length:      129
        Ratio:      4.850          Gaps:          0
Percent Similarity:  93.023    Percent Identity:  88.372

alignment_block:
US-09-019-441-3 x US-09-859-053-30   ..

Align seq 1/1 to: US-09-859-053-30 from: 1 to: 236

      1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCCTGCTCTGGCT 50

---

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      1 ||||||||||||||||||||||||||||||||||||||||||||||::||||
      1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPh 17

     51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
        :||||||||||||:|||||||||||||||||||||||||||||||||:::|
     17 eProGlySerArgCysAspIleGlnMetThrGlnSerProSerSerValS 34

    101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 50

    151 ATTAGTAGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
        |||    ||||||    ||||||||||||||||||||||||||||||||
     51 IleSerArgLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLy 67

    201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT 250
        |||||||||||||||||||||||||||||||||||||||||||||||||||
     67 sLeuLeuIleTyrValAlaSerSerLeuGlnSerGlyValProSerArgP 84

    251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
        ||||||||||||||||||||||||||:::|||||||||:::||||||||||
     84 heSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

    301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGGTTTATAGTACCCC 350
        ||||||||||||||||||||||||||||||||||||||| |||:::  ||
    101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnAlaAsnSerPhePr 117

    351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
        |||||||||||||||||||||||||||||||||||
    117 oTrpThrPheGlyGlnGlyThrLysValGluIleLys 129
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seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-18569-2296

seq_documentation_block:
; Sequence 2296, Application PC/TUS0118569
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA133PCT
; CURRENT APPLICATION NUMBER: PCT/US01/18569
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2296
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (99)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (119)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (140)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (146)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-18569-2296

alignment_scores:
        Quality:  579.00          Length:      129
        Ratio:      4.825          Gaps:          0
Percent Similarity:  93.023    Percent Identity:  87.597

us-09-019-441-3.rapm

alignment_block:
US-09-019-441-3 x PCT-US01-18569-2296

Align seg 1/1   to: PCT-US01-18569-2296   from: 1 to: 260

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  1 ATGGACAATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTCTGCTCTGGCT 50
    |||||||||||||||||||||||||||||||||||||||||||||||||
 25 MetAspMetArgValProAlaGlyLeuLeuGlyLeuLeuLeuTrpLe 41

 51 CCCAGGTGCCAGATGCACATCCAGATGACCCAGTCCCATCTTCCCTGT 100
    |  ||||||||||||||||||||||||||||||||||||||||||
 41 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 58

101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
    |||||||||||||||||||||||||||||||||::::||||||||||
 58 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 74

151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    |||           ||||||||||||||||||||||||||||||
 75 IleSerAsnTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 91

201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGT 250
    ||||||||||::::||||||||||||||||||||||||||||
 91 sLeuLeuIleTyrAlaAlaSer***LeuGlnSerGlyValProSerArgP 108

251 TCAGCGGCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
    |||||||||||||::|||||| ||::||||||||
108 heSerGlySerGlyThrAspPheThr***ThrIleSerSerLeu 124

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
    |||||||||||||||||  ||  ||                    :|
125 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrAspAsn***Pr 141

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    ||||||||  |||||||||||||
141 oLeuThrPheGly***GlyThrLysValGluIleLys 153
```

seq_name: /cgn2_6/ptodata/2/paa/US098_COMB.pep:US-09-834-366-17896

seq_documentation_block:
; Sequence 17896, Application US/09834356
; GENERAL INFORMATION:
;   APPLICANT:  Bejanin, Stephane
;   APPLICANT:  Tanaka, Hiroaki
;   APPLICANT:  Dumas Milne Edwards, Jean Baptiste
;   APPLICANT:  Jobert, Severin
;   APPLICANT:  Giordano, Jean-Yves
;   TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;   FILE REFERENCE: 81.US2.REG
;   CURRENT APPLICATION NUMBER: US/09/834,366
;   CURRENT FILING DATE:  2001-04-13
;   PRIOR APPLICATION NUMBER: US 60/197,873
;   PRIOR FILING DATE: 2000-04-18
;   NUMBER OF SEQ ID NOS: 52153
;   SOFTWARE:  Patent.pm
; SEQ ID NO 17896
;   LENGTH: 146
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY:  SIGNAL
;   LOCATION: -22..-1
US-09-834-366-17896

alignment_scores:
             Quality:   578.00                   Length:      129
             Ratio:      4.817                    Gaps:          0
Percent Similarity:  93.023     Percent Identity:  86.822

alignment_block:
US-09-019-441-3 x US-09-834-366-17896

Align seg 1/1   to: US-09-834-366-17896   from: 1 to: 146

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  1 ATGGACAATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTCTGCTCTGGCT 50
    |||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17

 51 CCCAGGTGCCAGATGCACATCCAGATGACCCAGTCCCATCTTCCCTGT 100
    |||||||||||||||||||||||||||||||||||||||||||||
 17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34

101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
    |||||||||||||||||||||||||||||||||||||||||||||||
 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnThr 50

151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    |||           ||||||||||||||||||||||||||||||
 51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67

201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGT 250
    |||||||||||||||::::|||||||||||||||||||||||||
 67 sLeuLeuIleTyrAlaAlaThrAsnLeuGlnSerGlyValProSerArgP 84

251 TCAGCGGCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
    ||||||||||||||||||||||||||||||||||||||:::::||||
 84 heSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
    |||||||||||||||  ||  ||             |||::::|
101 GlnProGluAspPheAlaIleTyrTyrCysGlnGlnSerAspSerSerPr 117

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    ||||||||  |||||||||||||
117 oTyrThrPheGlyGlnGlyThrLysLeuGluIleLys 129
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seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-197-873-17896

seq_documentation_block:
; Sequence 17896, Application US/60197873
; GENERAL INFORMATION:
;   APPLICANT:  Bejanin, Stephane
;   APPLICANT:  Tanaka, Hiroaki
;   APPLICANT:  Dumas Milne Edwards, Jean Baptiste
;   APPLICANT:  Jobert, Severin
;   APPLICANT:  Giordano, Jean-Yves
;   TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;   FILE REFERENCE: 81.US1.PRO
;   CURRENT APPLICATION NUMBER: US/60/197,873
;   CURRENT FILING DATE:  2000-04-18
;   NUMBER OF SEQ ID NOS:  52153
;   SOFTWARE:  Patent.pm
; SEQ ID NO 17896
;   LENGTH: 146
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY:  SIGNAL
;   LOCATION: -22..-1
US-60-197-873-17896

alignment_scores:
             Quality:   578.00                   Length:      129
             Ratio:      4.817                    Gaps:          0
Percent Similarity:  93.023     Percent Identity:  86.822

alignment_block:
US-09-019-441-3 x US-60-197-873-17896

Align seg 1/1   to: US-60-197-873-17896   from: 1 to: 146

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  1 ATGGACAATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTCTGCTCTGGCT 50
    |||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17
```

```
17  uArgGlyAlaAargCysAspIleGlnMetThrGlnSerProSerSerLeuS  34

101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC  150
    |||||||||||||||||||||||||||||||::::||||||||||||:::
34  erAlaSerValGlyAspValThrMetThrCysArgAlaSerGlnSer  50

151 ATTAGGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA  200
    ||| |||||||||||||||||||||||||||||||||||||||||||||
51  IleSerThrTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy  67

201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT  250
    |||||||||||::::||||||||||||||||||||||||||||||||||
67  sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgP  84

251 TCAGCGGCAGTGGATCTGGGACAGAGTCACTCTCACCGTCAGCAGCCTG  300
    |||||||||||||||||||||::::||||||||||::|||||||||||||
84  heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu  100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC  350
    ||||||||||||||||||||||||||||||||||| :||   :::::|||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerPheAsnThrHi  117

351 TCGG...ACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA  387
    ||||||||||||||||||||||:::||
117 sMetTyrThrPheGlyGlnGlyThrArgLeuGluMetLys  130
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seq_name: /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-760-479-852

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alignment_scores:
        Quality:  568.00        Length:    129
        Ratio:      4.773          Gaps:       0
Percent Similarity:  92.248    Percent Identity:  86.047

alignment_block:
US-09-019-441-3 x US-09-760-479-852
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51  CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT  100
    | ||||||||||||||||||||||||||||||||||||||||
17  uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS  34

101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC  150
    |||||||||||||||||||||||||||||||||||||||
34  erAlaSerValGlyAspValThrIleThrCysArgAlaSerGlnSerGlnThr  50

151 ATTAGGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA  200
    ||| ||||||||||||||||||||||||||||||||||||||||
51  IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy  67

201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT  250
    |||||||::::|||||||||||||||||||||||||||||||||
67  sLeuLeuIleTyrAlaAlaThrAsnLeuGlnSerGlyValProSerArgP  84

251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG  300
    |||||||||||||||||::||||||||:||||||||||::|||||||
84  heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu  100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC  350
    |||||||||||||||::||||||||||::||||  ||:::|||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerSerSerPr  117

351 TCGGACGTTCGGCCAAGGGACCAAGGTGAAAATCAAA  387
    | |||||||||||||||||||||:::||
117 oTyrThrPheGlyGlnGlyThrLysLeuGlulleLys  129
```

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-113-635-11

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alignment_scores:
        Quality:  573.50        Length:    130
        Ratio:      4.701          Gaps:       1
Percent Similarity:  93.846    Percent Identity:  86.154

alignment_block:
US-09-019-441-3 x US-60-113-635-11

Align seq 1/1  to: US-60-113-635-11  from:  1  to: 237

1   ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCT  50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1   MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe  17

51  CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT  100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
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Align seg 1/1   to: US-09-760-479-852   from: 1   to: 249

  1 ATGGACATGAGGGTCCCCGCTCCAGCTCCTGGGCTCCTTCTGCTCTGGCT  50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 14 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe  30

 51 CCCAGGTGCCAGATGTGCACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
    | |||||||||||||:::|||||||||||||||||||||||||||||||||
 30 uArgGlyAlaArgCysAspMetGlnMetThrGlnSerProSerSerLeuS  47

101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGCAAGTCAGGAC 150
    |||||||||||||||||||||||||||||||||||||||||:::|||
 47 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer  63

151 ATTAGGTATTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    ||| |||||||||||||||
 64 IleSerAsn***LeuAsnTrpTyrGlnGlnLysProGlyLysAlaPro**  80

201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGT 250
    ||| :::|||||||||||||||||||||||||||||||
 80 *LeuLeuIle***AlaAlaSerThrLeuGlnSerGlyValProSerArgP  97

251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
    ||||||||||||||||||:::||||||||||||||||||||::|||
 97 heSerGlySerGlyThrArgSerGlyThrArgSerGlyThrArgThr***CysLeu 113

301 CAGCCTGAAGATTTGCCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
    ||||||||||||||||||||||| |||     :::|||||
114 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnAsn******ThrPr 130

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    |||||||||||||||||||||||||||||||||||
130 oArgThrPheGlyGlnGlyThrLysValGluIleLys 142
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seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-08518-1

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alignment_scores:
        Quality:    564.50            Length:    134
        Ratio:      4.704             Gaps:      1
Percent Similarity: 89.552   Percent Identity: 83.582

alignment_block:
US-09-019-441-3 x PCT-US01-08518-1

Align seg 1/1   to: PCT-US01-08518-1   from: 1   to: 241

  1 ATGGACATGAGGGTCCCCGCTCCAGCTCCTGGGCTCCTTCTGCTCTGGCT  50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe  17
```

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 51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
    |||||||||||||||||||||||||||||||||||::::|||::::|||
 17 uProGlyAlaLysCysAspIleGlnMetThrGlnSerProSerThrLeuS  34

101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCCAGGCAAGTCAGGAC 150
    ||||||||||||||||||||||||||||||||||||||||||:::|||
 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer  50

151 ATTAGG...........TATTATTAAATTGGTATCAGCAGAAACC 185
    |||               :::||| ||||||||||||||||||
 51 IleSerSerGlnSerIleGlySerTrpLeuAlaTrpTyrGlnGlnLysPr  67

186 AGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTG 235
    |||||||||||||:::||||
 67 oGlyLysAlaProLysLeuLeuIleTyrLysAlaSerSerLeuGluSerG  84

236 GGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTC 285
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 84 lyValProSerArgPheSerGlySerGlyThrGluPheThrLeu 100

286 ACCGTCAGCAGCCTGCAGCCTGAAGATTTGCCGACTTATTACTGTGTCTACA 335
    |||::|||||||||||||:::|||||||||||||||||||||||| |
101 ThrIleSerSerLeuGlnProAspAspPheAlaThrTyrTyrCysGlnGl 117

336 GGTTTATAGTACCCCTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCA 385
    |||| |||||||||||||||||||||||||||||||||||||||
117 nTyrAsnAsnTyrProTrpThrPheGlyGlyGlyThrLysValGluIleL 134

386 AA 387
    ||
134 ys 134
```

```
OM of: US-09-019-441-3 to: A_Geneseq_032802:*    out_format : pfs
Date: Sep 23, 2002 10:06 AM
About: Results were produced by the GenCore software, version 4.5,
        Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame_n2p.model -DEV=xlp
-Q=~/cgn2_1/USPTO_spool/US09019441/runat_23092002_095257_6281/app_query.fasta_1.1860
-DB=A_Geneseq_032802 -QFMT=fastan -SUFFIX=rag -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=1 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09019441_@CGN1_1_175 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-019-441-3
Query length: 387
Database: A_Geneseq_032802:*
Database sequences: 747574
Database length: 111073796
Search time (sec): 193.710000
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score_list:
Sequence                          Strd Orig        ZScore    EScore Len    ! Documentation
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:AAW70379 +  668.00  1280.45  2.8e-63
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:AAY96298 +  594.50  1133.18  2.4e-55
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:AAW22842 +  592.50  1133.89  3.9e-55
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:AAY96289 +  590.50  1125.48  6.5e-55
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:AAB99115 +  580.00  1105.83  7.8e-54
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:AAR57482 +  577.00  1105.22  1.6e-53
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:AAR92085 +  577.00  1105.22  1.6e-53
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:AAY96301 +  573.50  1092.75  4.3e-53
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/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:AAY96300 +  526.00  1001.32  5.3e-48
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/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:AAB15546 +  525.50  1000.32  6.1e-48
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:ABG11908 +  523.00  1001.92  9.7e-48
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:AAY56716 +  523.00  1001.39  9.9e
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:AAY69404 +  520.00  995.61   2.1e
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:AAR64233 +  519.00  993.61   2.6e
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:AAW70379

seq_documentation_block:
ID   AAW70379 standard; Protein; 129 AA.
XX
AC   AAW70379;
XX
DT   18-NOV-1998   (first entry)
XX
DE   Anti-human CD23 5E8 monoclonal antibody light chain variable region.
XX
KW   Anti-human CD23 5E8 monoclonal antibody; light chain variable region;
KW   human CD23; IgE; FceRii/CD23; gamma-1 constant region;
KW   gamma-3 constant region; allergy; inflammation; autoimmune disease;
KW   allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia.
XX
OS   Macaca fascicularis
XX
FH   Key            Location/Qualifiers
FT   Protein        1..22
FT                  /note= "Signal peptide"
FT   Protein        23..129
FT                  /note= "anti-human CD23 5E8 light chain variable
FT                  region"
FT   Binding-site   46..56
FT                  /note= "CDR 1"
FT   Binding-site   72..77
FT                  /note= "CDR 2"
FT   Binding-site   111..119
FT                  /note= "CDR 3"
XX
PN   WO9837099-A1.
XX
PD   27-AUG-1998.
XX
PF   17-FEB-1998;   98WO-US02253.
XX
PR   05-FEB-1998;   98US-0803085.
PR   20-FEB-1997;   97US-0803085.
XX
PA   (IDEC-) IDEC PHARM CORP.
PA   (SEGK ) SEIKAGAKU CORP.
XX
PI   Kloetzer WS, Nakamura T,   Reff ME;
XX
DR   WPI; 1998-467495/40.
DR   N-PSDB; AAV33309.
XX
PT   New anti-human CD23 monoclonal antibody - used for inhibiting IgE
PT   expression to treat or prevent allergic, inflammatory and
PT   auto:immune conditions
XX
PS   Example 1: Pages 106-108; 146pp; English.
XX
CC   The present sequence represents the light chain variable region of
CC   primate monoclonal antibody anti-human CD23 5E8.  The invention
CC   provides primate monoclonal antibodies which specifically bind human
CC   CD23, the low affinity receptor for IgE (FceRii/CD23), and comprise
CC   either of a human gamma-1 or human gamma-3 constant region that binds
CC   to human Fc gamma receptors and inhibits IgE expression.  The monoclonal
CC   antibodies of the invention are claimed to be useful for inhibiting
CC   induced IgE production for treating or preventing allergic, inflammatory
CC   and autoimmune conditions e.g. allergic rhinitis conjunctivitis,
CC   autoimmune haemolytic anaemia, etc.
XX
SQ   Sequence   129 AA;
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alignment_scores:
    Quality:      668.00              Length:      129
    Ratio:        5.178               Gaps:          0
Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-019-441-3 x AAW70379

Align seq 1/1 to: AAW70379  from: 1  to: 129

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  1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuLeuTrpLe 17

 51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 17 uProGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34

101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnAsp 50

151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    |||||||||||||||||||||||||||||||||||||||||||||||||
 51 IleArgTyrTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67

201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT 250
    |||||||||||||||||||||||||||||||||||||||||||||||||
 67 sLeuLeuIleTyrValAlaSerSerLeuGlnSerGlyValProSerArgP 84

251 TCAGCGGCAGTGGATCTGGACAGAGAGTTCACTCTCACCGTCAGCAGCCTG 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 84 heSerGlySerGlyThrGluPheThrLeuThrValSerSerLeu 100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
    ||||||||||||||||||||||||||||||||||||||||||||||||||
101 GlnProGluAspPheAlaThrTyrTyrCysLeuGlnValTyrSerThrPr 117

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    |||||||||||||||||||||||||||||||||||||
117 oArgThrPheGlyGlnGlyThrLysValGluIleLys 129
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:AAY96298

seq_documentation_block:
ID  AAY96298 standard; protein; 237 AA.
XX
AC  AAY96298;
XX
DT  16-AUG-2000  (first entry)
XX
DE  Human IGFAM-10 immunoglobulin.
XX
KW  Human; immunoglobulin; IGFAM-10; IGFAM: immune disorder; cancer;
KW  infection; inflammation; haematopoiesis; AIDS; allergy.
XX
OS  Homo sapiens.
XX
FH  Key            Location/Qualifiers
FT  Peptide        1..22
FT                 /label= signal_peptide
FT  Protein        23..237
FT                 /label= IGFAM-10
FT  Domain         38..112
FT                 /label= Ig_domain
FT  Domain         150..219
FT                 /label= Ig_domain
FT  Domain         193..236
FT                 /label= Ig_domain
XX
PN  WO200029583-A2.
XX

PD  25-MAY-2000.
XX
PF  19-NOV-1999;     99WO-US27566.
XX
PR  19-NOV-1998;     99US-0113635.
PR  22-DEC-1998;     98US-0113635.
PR  07-APR-1999;     99US-0128194.
XX
PA  (INCY-) INCYTE PHARM INC.
XX
PI  Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
PI  Lu DAM, Lal P, Hillman JL, Yang J;
XX
DR  WPI; 2000-387796/33.
DR  N-PSDB; AAA27390.
XX
PT  Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT  protein is useful for preventing and treating disorders associated with
PT  altered levels of the protein such as cancer, immune system disorders
PT  -
XX
PS  Claim 1; Page 85-86; 105pp; English.
XX
CC  The present sequence is the human immunoglobulin superfamily protein
CC  IGFAM-10. Its gene was isolated from a cDNA library of colon
CC  tissue. It is expressed in reproductive, gastrointestinal and
CC  cardiovascular tissue, where cancer and inflammation are common. The
CC  gene, protein, its antibodies, agonists and antagonists are suitable for
CC  diagnosing and treating many diseases, including cancer, immune system
CC  disorders (such as inflammation, AIDS, allergies, anaemia,
CC  arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
CC  disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
CC  multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
CC  systemic lupus erythematosus and ulcerative colitis), complications of
CC  cancer, haemodialysis and extracorporeal circulation, trauma and
CC  haematopoietic cancer (such as leukaemia) and infections caused by
CC  bacteria, viruses, fungi or parasites.
XX
SQ  Sequence  237 AA;

alignment_scores:
    Quality:      594.50              Length:      130
    Ratio:        4.833               Gaps:          1
Percent Similarity: 94.615    Percent Identity: 90.000

alignment_block:
US-09-019-441-3 x AAY96298

Align seq 1/1 to: AAY96298  from: 1  to: 237

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 51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34

101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
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 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50

151 ATTAGGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    |||      |||||||||||||||||||||||||||||||||||||||||
 51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67

201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGT 250
    ||||||||||||||||||||||||| ||||||||||||||||||||||||
 67 sLeuLeuIleTyrValAlaSerSerLeuGlnSerGlyValProSerArgP 84

251 TCAGCGGCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
    ||||||||||||||||||||::::||||||||||||||||||||||||
 67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgP 84
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84 heSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
    |||||||||||||||||||||||||||||||    |||  |||||||||||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrPr 117

351 TCGG...ACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    |||::|||||||||||||||||||::|||||||||||||||
117 oProIleThrPheGlyGlnGlyThrArgLeuGluIleLys 130

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:AAW22842

seq_documentation_block:
ID   AAW22842 standard; Protein; 132 AA.
XX
AC   AAW22842;
XX
DT   12-SEP-1997 (first entry)
XX
DE   Human anti-tumour antigen antibody light chain variable region.
XX
KW   Human; tumour antigen; cancer; monoclonal; antibody; light chain;
KW   variable region; medicine; pharmacology; biochemistry; CDR;
KW   complementarity determining region.
XX
OS   Homo sapiens.
XX
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FT                   /label= sig_peptide
FT   Peptide         23..132
FT                   /label= mat_peptide
FT   Region          46..56
FT                   /label= CDR_1
FT   Region          72..78
FT                   /label= CDR_2
FT   Region          111..119
FT                   /label= CDR_3
XX
PN   JP09100300-A.
XX
PD   15-APR-1997.
XX
PF   03-OCT-1995; 95JP-0278266.
XX
PR   03-OCT-1995; 95JP-0278266.
XX
PA   (HAGI/) HAGIWARA Y.
XX
DR   WPI; 1997-276726/25.
DR   N-PSDB; AAT75423.
XX
PT   Anticancer human monoclonal antibody variable region sequences - and
PT   related DNA and RNA
XX
PS   Claim 9; Page 11; 14pp; Japanese.
XX
CC   The present sequence is a human anti-tumour antigen
CC   monoclonal antibody (MAb) light chain variable region, useful in
CC   medicine, pharmacology and biochemistry. The isotype of a MAb
CC   secreted by the human/human hybridoma HT was determined to be mu
CC   and kappa. Human MAb was purified, and the antigen recognised by
CC   human MAb CLN"-IgM identified by western blotting.
XX
SQ   Sequence  132 AA;

alignment_scores:
      Quality:    592.00    Length:      129
      Ratio:        4.813    Gaps:          0
Percent Similarity: 95.349   Percent Identity: 89.147

alignment_block:

US-09-019-441-3 x AAW22842

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 51 CCCAGTGCCAGATGACATCCAGATGACCCAGTCTCCATCTCCCTGT 100
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 17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerLeuS 34

101 CTGCATCTGTAGGGACCAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
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 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50

151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
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 51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67

201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGTCCCATCAAGGT 250
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 67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgP 84

251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
    |::|||||||||||||||||||||:::||||||||||||||||||||||||
 84 heSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
    ||||||||||||||||||||||||||||   |||  ||||||||||||||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrPr 117

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    |::|||||||||||||||||||||||||||||||||||
117 oGlnThrPheGlyGlnGlyThrLysValGluIleLys 129

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:AAY96289

seq_documentation_block:
ID   AAY96289 standard; protein; 237 AA.
XX
AC   AAY96289;
XX
DT   16-AUG-2000 (first entry)
XX
DE   Human IGFAM-1 immunoglobulin.
XX
KW   Human; immunoglobulin; IGFAM-1; IGFAM; immune disorder; cancer;
KW   infection; inflammation; haematopoiesis; AIDS; allergy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= signal_peptide
FT   Protein         23..237
FT                   /label= IGFAM-1
FT   Domain          38..112
FT                   /label= Ig_domain
FT   Domain          150..219
FT                   /label= Ig_domain
FT   Region          154..176
FT                   /label= Ig_signature
FT   Domain          193..236
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FT   Region          215..232
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PN   WO200029583-A2.
XX
PD   25-MAY-2000.
XX
PF   19-NOV-1999; 99WO-US27566.

```
                                   |||||||||||||||||||||||||    |||||||||||||||
                               101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrPr 117

                               351 TCGG...ACGTTCGGCCAAGGACCAAGGTGGAAATCAAA 387
                                   |||||||||||||||||||||||::::||||||||
                               117 oProIleThrPheGlyGlnGlyThrArgLeuGluIleLys 130

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2001.DAT:AAB99115

seq_documentation_block:
ID   AAB99115 standard; Protein; 146 AA.
XX
AC   AAB99115;
XX
DT   22-AUG-2001 (first entry)
XX
DE   Human protein SEQ ID 12.
XX
KW   Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis;
KW   Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;
KW   signal transduction inhibition; tissue fibrosis; atherosclerosis.
XX
OS   Homo sapiens.
XX
PN   WO200136642-A1.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-JP08129.
XX
PR   18-NOV-1999; 99JP-0328681.
PR   08-NOV-2000; 2000JP-0340216.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
PI   Sakamoto S, Kamada M;
XX
DR   WPI; 2001-343825/36.
DR   N-PSDB; AAH41157.
XX
PT   Human monoclonal antibodies recognizing human TGF-beta II receptor,
PT   useful for treating TGF-beta associated diseases such as tissue
PT   fibrosis -
XX
PS   Claim 11; Page 104-105; 118pp; Japanese.
XX
CC   The present invention relates to novel human monoclonal antibodies. The
CC   antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II
CC   receptor, resulting in the inhibition of the signal transduction of human
CC   TGF-beta into cells. The antibodies can be used for the prevention and
CC   treatment of diseases associated with the production of TGF-beta, such as
CC   tissue fibrosis in the lung, liver, skin, kidney or other tissues,
CC   atherosclerosis, atopy, keloid and arthritis. The present sequence was
CC   used in the present invention.
XX
SQ   Sequence   146 AA;

alignment_scores:
      Quality:   580.00          Length:   129
        Ratio:     4.793           Gaps:     0
Percent Similarity:  93.798  Percent Identity:  89.147

alignment_block:
US-09-019-441-3 x AAB99115

Align seg 1/1 to: AAB99115  from: 1  to: 146

   1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCT 50
     |||||||||||||||||||||||||||||||||||||||||||||::::||
   1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPh 17

  51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
```

```
XX
PR   19-NOV-1998;  99US-0113635.
PR   22-DEC-1998;  98US-0113635.
PR   07-APR-1999;  99US-0128194.
XX
PA   (INCY ) INCYTE PHARM INC.
XX
PI   Yue H,  Tang YT,  Corley NC,  Guegler KJ,  Gorgone GA,  Baughn MR;
PI   Lu DAM,  Lal P,  Hillman JL,  Yang J;
XX
DR   WPI; 2000:387796/33.
DR   N-PSDB; AAA27381.
XX
PT   Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT   protein is useful for preventing and treating disorders associated with
PT   altered levels of the protein such as cancer, immune system disorders
PT   -
XX
PS   Claim 1; Page 77-78; 105pp; English.
XX
CC   The present sequence is the human immunoglobulin superfamily protein
CC   IGFAM-1. Its gene was isolated from a cDNA library of synovial membrane
CC   tissue. It is expressed in reproductive, gastrointestinal and
CC   cardiovascular tissue, where cancer and inflammation are common. The
CC   gene, protein, its antibodies, agonists and antagonists are suitable for
CC   diagnosing and treating many diseases, including cancer, immune system
CC   disorders (such as inflammation, AIDS, allergies, anaemia,
CC   arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
CC   disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
CC   multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
CC   systemic lupus erythematosus and ulcerative colitis), complications of
CC   cancer, haemodialysis and extracorporeal circulation, trauma and
CC   haematopoietic cancer (such as leukaemia) and infections caused by
CC   bacteria, viruses, fungi or parasites.
XX
SQ   Sequence   237 AA;

alignment_scores:
      Quality:   590.50          Length:   130
        Ratio:     4.801           Gaps:     1
Percent Similarity:  94.615  Percent Identity:  89.231

alignment_block:
US-09-019-441-3 x AAY96289

Align seg 1/1 to: AAY96289  from: 1  to: 237

   1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCT 50
     ||||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17

  51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
     |||||||||||||||||::|||||||||||||||||||||||||||||||
  17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34

 101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCGAGGGCAAGTCAGGAC 150
     |||||||||||||||||||||||||||||||||||||||||::||:::||
  34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaGlyGlnSer 50

 151 ATTAGGTATTATTTAAAATGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
     |||       |||||||||||||||||||||||||||||||||||||||
  51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67

 201 GCTCCTGATCTATGTGCATCCAGTTTGCAAAGTGGGGTCCATCAAGGT 250
     |||||::::|||||||||||||||||||||||||||||||||||||||
  67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgP 84

 251 TCAGCGGCCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
     |||||||||||::|||||||||||||||||::::||||||||||||
  84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

 301 CAGCCTGAAGATTTTGCGGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
```

```
   17 eProGlyLeuArgCysAspIleGlnMetThrGlnSerProSerLeuS   34
      :|||||||||||||||||||||||||||||||||||||||||||
  101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC  150
      |||||||||||||||||||||||||||||||||||||||||||||||
   34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly  50
  151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA   200
      ||||| |||::||||||||||||||||||||||||||||||||||||||
   51 IleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLysAlaProLy  67
  201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGT  250
      ||||||||||||||||||||||||||||||||||||||||||||||||
   67 sArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgP  84
  251 TCAGCGGCAGTGATCTGGGACAGAGTTCACCTCCACCGTCAGCAGCCTG   300
      |||||||||||||||||||||||||||||||||||||||||||||||
   84 heSerGlySerAlaSerGlyThrGluPheThrLeuThrIleSerSerLeu  100
  301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC  350
      ||||||||||||||||||||||||||||||||||||||| ||:::||
  101 GlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsnSerAsnPr  117
  351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA  387
      ||||||||| |||||||||||||||||||||||||||
  117 oLeuThrPheGlyGlyGlyThrLysValGluIleLys  129
```

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:AAR57482

seq_documentation_block:
ID  AAR57482 standard; Protein; 129 AA.
XX
AC  AAR57482;
XX
DT  02-OCT-1995 (first entry)
XX
DE  Humanized 1308F VL.
XX
KW  Monoclonal antibody; MAb; respiratory syncytial virus; RSV;
KW  chimeric antibody; humanized antibody; antibody engineering;
KW  light chain; VL; complementarity determining region; CDR.
XX
OS  Synthetic.
XX
FH  Key         Location/Qualifiers
FT  Region      46..54
FT              /label= CDR1
FT  Region      72..78
FT              /label= CDR2
FT  Region      111..119
FT              /label= CDR3
XX
PN  WO9417105-A.
XX
PD  04-AUG-1994.
XX
PF  29-JAN-1993;    93WO-US01168.
XX
PR  29-JAN-1993;    93AU-0036608.
PR  29-JAN-1993;    93WO-US01168.
XX
PA  (MEDI-) MEDIMMUNE INC.
XX
PI  Johnson L;
XX
DR  WPI; 1994-264037/32.
DR  N-PSDB; AAQ67194.
XX
PT  Human-murine chimeric antibodies against respiratory syncytial
PT  virus - comprises at least 1 CDR from each variable heavy and
PT  light chain of at least 1 murine monoclonal antibody
XX
PS  Disclosure; Fig. 4A-4B; 34pp; English.

XX
CC  Synthetic overlapping oligonucleotides and the 5' primer given in
CC  AAQ67197 and 3' primer of AAQ67198 were used to construct a DNA
CC  sequence (AAQ67194) encoding humanized 1308F VL (AAR57482) in which
CC  CDRs of the anti-RSV F antigen murine MAb 1308F VL region were
CC  substituted into the homologous human K102 gene. Similar
CC  procedures were used to obtain humanized 1308F VH for the
CC  construction of anti-RSV F protein humanized antibody.
XX
SQ  Sequence  129 AA;

alignment_scores:
        Quality:    577.00        Length:       129
          Ratio:      4.769        Gaps:           0
Percent Similarity:  93.798    Percent Identity:  85.271

alignment_block:
US-09-019-441-3  x  AAR57482

Align seg 1/1  to: AAR57482   from: 1   to: 129

```
    1 ATGACATGAGGGTCCCCGCTCAGCTCCTGGGCTCCTCTGCTCTGGCT   50
      |||||||||||||||||||||||||||||||||||||||||||||||
    1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe  17
   51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCCCATCTTCCCTGT  100
      |||||||||::|||||||||||||||||||||||||||||||::|||
   17 uProGlyAlaLysCysAspIleGlnMetThrGlnSerProSerThrLeuS  34
  101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC  150
      |||||||||||||||||||||||||||||||||||||||||||||||
   34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnAsp  50
  151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA  200
      |||::::  ||||||||||||||||||||||||||||||||||||||
   51 IleAsnArgTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy  67
  201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGT  250
      |||||||||| |||::: ::|||||||||||||||||||||||||||
   67 sLeuLeuIleTyrArgArgAlaAsnArgLeuValAspGlyValProSerArgP  84
  251 TCAGCGGCAGTGATCTGGGACAGAGTTCACCTCCACCGTCAGCAGCCTG  300
      |||||||||||||||||||||||||||||::|||||||||||||||||
   84 heSerGlySerGlyThrGlyThrGluPheThrLeuThrIleSerSerLeu  100
  301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC  350
      |||||::|||||||||||||||||||||||||  ::::: |
  101 GlnProAspPheAlaThrTyrTyrCysLeuGlnPheHisGluPhePr  117
  351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA  387
      |  ||||||  |||||||||::|||||||||||||||
  117 oTyrThrPheGlyGlyGlyThrLysLeuGluIleLys  129
```

seq_name: /SIDS1/gcgdata/hold-geneseqp-embl/AA1996.DAT:AAR92085

seq_documentation_block:
ID  AAR92085 standard; Protein; 129 AA.
XX
AC  AAR92085;
XX
DT  15-MAY-1996 (first entry)
XX
DE  Humanised antibody 1308 VL.
XX
KW  Humanised antibody; chimeric antibody; antibody engineering;
KW  monoclonal antibody; MAb 1308F; respiratory syncytial virus; RSV;
KW  light chain; complementarity determining region; CDR.
XX
OS  Synthetic.
XX
FH  Key         Location/Qualifiers
FT  Region      46..55

```
FT   Region              /label= CDR1
FT                       72..78
FT   Region              /label= CDR2
FT                       111..119
FT   Region              /label= CDR3
XX
PN   WO9605229-A1.
XX
PD   22-FEB-1996.
XX
PF   09-AUG-1995;   95WO-US10053.
XX
PR   15-AUG-1994;   94US-0290592.
XX
PA   (MEDI-) MEDIMMUNE INC.
XX
PI   Johnson LS;
XX
DR   WPI: 1996-139646/14.
DR   N-PSDB: AAT16181.
XX
PT   New chimeric antibodies against respiratory syncytial virus -
PT   comprise human antibodies with CDR's from the variable heavy and
PT   light chains of a murine antibody
XX
PS   Example 2; Fig 4A-4B; 55pp; English.
XX
CC   A human-mouse chimeric antibody light chain has a human HV3 framework
CC   contg. complementarity determining regions (CDRs) from the variable
CC   light (VL) chain of murine monoclonal antibody (MAb) 1308F active
CC   against respiratory syncytial virus (RSV) glycoprotein F antigenic
CC   site C. DNA (AAT16181) coding for CDR-grafted VL-encoding region,
CC   Hu1308 VL (AAR92085), was synthesized using overlapping
CC   oligonucleotides. The construct was used with Hu1308 VH (see AAR92084)
CC   for prodn. in COS-1 transfectants of humanised antibody useful for
CC   treatment of RSV infection.
XX
SQ   Sequence 129 AA;

alignment_scores:
       Quality:   577.00                   Length:   129
       Ratio:       4.769                   Gaps:       0
Percent Similarity:  93.798      Percent Identity:  85.271

alignment_block:
US-09-019-441-3 x AAR92085

Align seg 1/1  to: AAR92085  from: 1  to: 129

  1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCT 50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17

 51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
    |||||||||||||||::||||||||||||||||||||||||||:::||||
 17 uProGlyAlaLysCysAspIleGlnMetThrGlnSerProSerThrLeuS 34

101 CTGCATCTGTAGGGACACAGAGTCACCATCACTTGCCAGGCAAGTCAGGAC 150
    ||||||||||||||||||||||||||||::||||||||||:::|||||||
 34 erAlaSerValGlyAspArgValThrIleThrCysGlnAlaSerGlnAsp 50

151 ATTAGGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    ||::::  |||||||||||||||||||||||||||||||||||||||||
 51 IleAsnArgTyrTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLeu 67

201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGT 250
    |||||||||||:::||||||||||::::|||||||||||||||||||||||
 67 sLeuLeuIleTyrArgAlaAsnArgLeuvalAspGlyValProSerArgP 84

251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCTCACCAGCCTG 300
    ||||||||||||||||||||||||||||||:::|||||||||||||||||
 84 heSerGlySerGlyThrGlyThrGluPheThrLeuThrIleSerSerLeu 100

301 CAGCCTGAAGATTTGCGACTTATTACTGTCTACAGGTTTTATAGTACCCC 350
    |||||::::|||||||||||||||||||||||||||||||| :::: ||
101 GlnProAspPheAlaThrTyrTyrCysLeuGlnPheHisGluPhePr 117

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    | |||||||  |||||||::|||||||::|||||||
117 oTyrThrPheGlyGlyGlyThrLysLeuGluIleLys 129

seq_name: /SIDS1/gcgdata/hold-geneseqp/geneseqp-embl/AA2000.DAT:AAY96301

seq_documentation_block:
ID   AAY96301 standard; protein; 237 AA.
XX
AC   AAY96301;
XX
DT   16-AUG-2000   (first entry)
XX
DE   Human IGFAM-13 immunoglobulin.
XX
KW   Human; immunoglobulin; IGFAM-13; IGFAM; immune disorder; cancer;
KW   infection; inflammation; haematopoiesis; AIDS; allergy.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   Peptide        1..22
FT                  /label= signal_peptide
FT   Protein        23..237
FT                  /label= IGFAM-13
FT   Domain         38..112
FT                  /label= Ig_domain
FT   Domain         150..219
FT                  /label= Ig_domain
FT   Domain         193..236
FT                  /label= Ig_domain
XX
PN   WO200029583-A2.
XX
PD   25-MAY-2000.
XX
PF   19-NOV-1999;   99WO-US27566.
XX
PR   19-NOV-1998;   99US-0113635.
PR   22-DEC-1998;   98US-0113635.
PR   07-APR-1999;   99US-0128194.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Yue H,  Tang YT,  Corley NC,  Guegler KJ,  Gorgone GA,  Baughn MR;
PI   Lu DAM,  Lal P,  Hillman JL,  Yang J;
XX
DR   WPI: 2000-387796/33.
DR   N-PSDB: AAA27393.
XX
PT   Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT   protein is useful for preventing and treating disorders associated with
PT   altered levels of the protein such as cancer, immune system disorders
PT   -
XX
PS   Claim 1; Page 87-88; 105pp; English.
XX
CC   The present sequence is the human immunoglobulin superfamily protein
CC   IGFAM-13. Its gene was isolated from a cDNA library of lung tumour
CC   tissue. It is expressed in reproductive, gastrointestinal and
CC   cardiovascular tissue, where cancer and inflammation are common. The
CC   gene, protein, its antibodies, agonists and antagonists are suitable for
CC   diagnosing and treating many diseases, including cancer, immune system
CC   disorders (such as inflammation, AIDS, allergies, anaemia,
CC   arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
CC   disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
CC   multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
CC   systemic lupus erythematosus and ulcerative colitis), complications of
```

```
CC   cancer, haemodialysis and extracorporeal circulation, trauma and
CC   haematopoietic cancer (such as leukaemia) and infections caused by
CC   bacteria, viruses, fungi or parasites.
XX
SQ   Sequence   237 AA;

alignment_scores:
     Quality:   573.50          Length:   130
     Ratio:     4.701           Gaps:     1
Percent Similarity: 93.846      Percent Identity: 86.154

alignment_block:
US-09-019-441-3 x AAY96301        ..

Align seg 1/1  to: AAY96301  from: 1  to: 237

   1 ATGGACATGAGGGTCCCCGCTCCAGCTCCTGGGGCTCCTTCTGCTCTGGCT 50
     |||||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetAspMetArgValProAlaGlnLeuLeuLeuLeuLeuLeuLeuTrpLe 17

  51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
     |||||||||||||||||||||||||||||||||||||||||||||||||||
  17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34

 101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
     ||||||||||||||||||||||||::::|||||||||||||:::
  34 erAlaSerValGlyAspArgValThrMetThrCysArgAlaSerGlnSer 50

 151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
     |||     ||||||||||||:::||||||||||||||||||||||
  51 IleSerThrTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67

 201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGT 250
     |||||||||| ||| |||:::|||
  67 sLeuLeuIleTyrValAlaSerLeuGlnSerGlyValProSerArgP 84

 251 TCAGGCGGCAGTCGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
     ||||||||||||||||||:::||||||||||||:::||||||
  84 heSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

 301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
     |||||||||||||||||| ||| :::::|||
 101 GlnProGluAspPheAlaThrTyrTyrCysGlnSerPheAsnThrHi 117

 351 TCGG...ACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
     |||||  |||||||||||||:::||||
 117 sMetTyrThrPheGlyGlnGlyThrArgLeuGluMetLys 130

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:AAY96301

seq_documentation_block:
ID   AAY56724 standard; protein; 129 AA.
XX
AC   AAY56724;
XX
DT   15-FEB-2000 (first entry)
XX
DE   Amino acid sequence of chimpanzee Vkappa cDNA clone 46-14.
XX
KW   Complementarity determining region; antibody; primate; immunogenicity;
KW   Old World ape; Old World monkey; antigen-binding affinity.
XX
OS   Pan troglodytes.
XX
PN   WO995369-A1.
XX
PD   04-NOV-1999.
XX
PF   28-APR-1999;   99WO-US09131.
XX
PR   28-APR-1998;   98US-0083367.
XX
```

```
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Taylor AH;
XX
DR   WPI; 2000-023265/02.
DR   N-PSDB; AAZ39327.
XX
PT   Antibodies containing donor complementarity determining regions and
PT   non-human primate acceptor frameworks, having reduced immunogenicity in
PT   humans -
XX
PS   Example 2; Page 67-68; 123pp; English.
XX
CC   The invention provides an antibody (Ab) comprising donor CDRs
CC   (complementarity determining regions) derived from a non-human antigen-
CC   specific donor antibody, and an acceptor framework from a non-human
CC   primate. The Abs are prepared by grafting CDRs from a non-human antigen-
CC   specific donor antibody onto homologous Old World ape or monkey acceptor
CC   frameworks. The Abs have reduced immunogenicity and are better tolerated
CC   in humans (because of the close similarity between the human and primate
CC   proteins), but retain the full antigen-binding affinity of the donor
CC   antibody.
XX
SQ   Sequence   129 AA.

alignment_scores:
     Quality:   573.00          Length:   129
     Ratio:     4.775           Gaps:     0
Percent Similarity: 93.023      Percent Identity: 86.822

alignment_block:
US-09-019-441-3 x AAY56724        ..

Align seg 1/1  to: AAY56724  from: 1  to: 129

   1 ATGGACATGAGGGTCCCCGCTCCAGCTCCTGGGGCTCCTTCTGCTCTGGCT 50
     |||||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetAspMetArgValProAlaGlnLeuLeuLeuLeuLeuLeuLeuTrpLe 17

  51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
     | |||:||||||||||||||||||||||||||||||||||||||||||||
  17 uSerGlyThrArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34

 101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
     ||||||||||||||||||||||||||||:::
  34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50

 151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
     |||||||||||:::||||||||||||||||||||||||||||||||
  51 IleSerAsnTyrLeuSerTrpTyrGlnGlnLysProGlyLysAlaProLy 67

 201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGT 250
     ||||||||| |||:::|||||||||||||||||||||||||||||||||
  67 sLeuLeuIleTyrValAlaSerThrLeuGlnSerGlyValProSerArgP 84

 251 TCAGGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
     |||||||||||||||||||||::||||||||||||||||||||||||||
  84 heSerGlySerGlyThrGlyThrAspPheThrLeuThrIleSerSerLeu 100

 301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
     |||||||||||||||||||||||||||||||||||:::|||
 101 GlnProGluAspPheAlaThrTyrTyrCysGlnHisGlyTyrGlyThrHi 117

 351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
     |||||||||||||||||||||||||||
 117 sProThrPheGlyGlyGlyThrLysValGlulleLys 129

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:AAB82912

seq_documentation_block:
ID   AAB82912 standard; protein; 241 AA.
XX
```

```
AC   AAB82912;
XX
DT   26-NOV-2001 (first entry)
XX
DE   Human immune response protein HIRP1.
XX
KW   Immune response protein; HIRP1; human; immunological disease;
KW   cell proliferation; cancer; anti-HIV; antiallergic;
KW   antianaemic; antiasthmatic; antiarteriosclerotic; antipsoriatic;
KW   immunosuppressive; dermatological; antidiabetic; antiinflammatory;
KW   neuroprotective; osteopathic; antirheumatic; antiarthritic;
KW   antiulcer; virucide; antibacterial; fungicide; protozoacide;
KW   anthelmintic; vulnerary; hepatotropic; cytostatic; therapy;
KW   diagnosis; vaccine; immunoglobulin.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= Signal_peptide
FT   Protein         22..241
FT                   /label= Mature_protein
FT   Modified-site   36
FT                   /note= "O-phosphorylated"
FT   Modified-site   44
FT                   /note= "O-phosphorylated"
FT   Modified-site   79
FT                   /note= "O-phosphorylated"
FT   Modified-site   80
FT                   /note= "O-phosphorylated"
FT   Modified-site   94
FT                   /note= "O-phosphorylated"
FT   Modified-site   129
FT                   /note= "O-phosphorylated"
FT   Modified-site   189
FT                   /note= "O-phosphorylated"
FT   Modified-site   191
FT                   /note= "O-phosphorylated"
FT   Modified-site   209
FT                   /note= "O-phosphorylated"
FT   Domain          38..117
FT                   /note= "immunoglobulin domain motif"
FT   Region          98..134
FT                   /note= "T-cell glycoprotein CD8 motif"
FT   Region          123..240
FT                   /note= "immunoglobulin kappa complex motif"
FT   Domain          154..223
FT                   /note= "immunoglobulin domain motif"
FT   Region          219..225
FT                   /note= "Ig MHC motif"
FT   Region          197..240
FT                   /note= "immunoglobulin and MHC protein motif"
FT   Region          158..180
FT                   /note= "immunoglobulin and MHC protein motif"
FT   Region          219..236
FT                   /note= "immunoglobulin and MHC protein motif"
XX
PN   WO200168696-A1.
XX
PD   20-SEP-2001.
XX
PF   15-MAR-2001; 2001WO-US08518.
XX
PR   15-MAR-2000; 2000US-189417P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Tang YT, Hillman JL, Baughn MR;
XX
DR   WPI; 2001-590044/66.
DR   N-PSDB; AAH26799.
XX
PT   Novel human immune response proteins, for treating immunological
PT   disorders and cell proliferative disorders, and for assessing the
PT   effects of exogenous compounds on the expression of HIRP molecules -
XX
PS   Claim 1; Page 85; 95pp; English.
XX
CC   The invention is based on the discovery of new human immune
CC   response proteins (HIRP), the polynucleotides encoding them, and
CC   the use of these compositions for the diagnosis, treatment or
CC   prevention of immunological and cell proliferative disorders.
CC   The present sequence is that of human immune response protein 1
CC   (HIRP1, Incyte ID No. 6100311CD1), as determined from a
CC   polynucleotide assembled e.g. from a lung adenocarcinoma cDNA
CC   library clone.  The amino acid sequence shows homology, from
CC   residue W123 to C241, to an HIV-1 antigen binding protein, and
CC   further homologies suggest that it may be an immunoglobulin.  HIRP
CC   polynucleotides and polypeptides are useful for the diagnosis,
CC   treatment and prevention of cell proliferative disorders (e.g.
CC   cancers, arteriosclerosis, actinic keratosis, bursitis, mixed
CC   connective tissue disease (MCTD), myelofibrosis, psoriasis,
CC   leukaemia, hepatitis, cirrhosis and atherosclerosis), and
CC   immunological disorders e.g. AIDS, Addison's disease, adult
CC   respiratory distress syndrome (ARDS), anaemia, asthma, autoimmune
CC   diseases, contact dermatitis, diabetes mellitus, cholecystitis,
CC   Crohn's disease, atrophic gastritis, Goodpasture's syndrome,
CC   multiple sclerosis, irritable bowel syndrome, osteoporosis,
CC   rheumatoid arthritis, ulcerative colitis, trauma, and viral,
CC   bacterial, fungal, parasitic, protozoal and helminthic infections.
CC   The polypeptides are also used to screen for agonist and
CC   antagonist compounds of therapeutic use.
XX
SQ   Sequence   241 AA;

alignment_scores:
          Quality:   564.50                Length:       134
          Ratio:       4.704               Gaps:            1
Percent Similarity:  89.552       Percent Identity:  83.582

alignment_block:
US-09-019-441-3 x AAB82912

Align seg 1/1  to: AAB82912    from: 1  to: 241

  1 ATGGACAATGAGGTCCCCGCTCCCAGCTCCTGGGCTCCTTCTTCTGCTCTGGCT  50
    |||||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuLeuLe  17

 51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT  100
    ||||||||||:::|||||||||||||||||||||||||||||||::|||
 17 uProGlyAlaLysCysAspIleGlnMetThrGlnSerProSerThrLeus  34

101 CTGCATCTGTAGGGACGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC  150
    |||||||||||||||||||||||||||||||||||||||||||:::
 34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer  50

151 ATTAGG..........TATTATTAAATTGGTATCAGCAGAAACC  185
    |||                ::||  |||||||||||||||||||
 51 IleSerGlnSerIleGlySerTrpLeuAlaTrpTyrGlnGlnLysPr  67

186 AGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTGCAAAGTG  235
    ||||||||||||||||||||||||||||||||   ||||||||:::|||
 67 oGlyLysAlaProLysLeuLeuIleTyrLysAlaSerSerLeuGluSerG  84

236 GGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGACAGAGTTCACTCTC  285
    |||||||||||||||||||||||||||||||||||||||||||||||||
 84 lyValProSerArgPheSerGlySerGlyThrGlyThrGluPheThrLeu  100

286 ACCGTCAGCAGCCTGCAGCCTGAAGATTTTGCGACTTATTACTGTCTACA  335
    ||:::|||||||||||||||||||||||||||||||||||||||||| |
101 ThrIleSerSerLeuGlnProAspPheAlaThrTyrTyrCysGlnGlnI  117

336 GGTTTATAGTACCCCTCGGACGTTCGGCCAAGGACCAAGGTGGAAATCA  385
    |||  |||  |||||||||||||||||||||||||||||||||||||||
```

```
117 nTyrAsnTyrProTrpThrPheGlyGlnGlyThrLysValGluIleL 134

386 AA 387
        ||
134 ys 134
```

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:AAY56737

```
seq_documentation_block:
ID  AAY56737 standard; protein; 130 AA.
XX
AC  AAY56737;
XX
DT  15-FEB-2000  (first entry)
XX
DE  Amino acid sequence of Cynomolgus Vkappa cDNA clone 4-10.
XX
KW  Complementarity determining region; antibody; primate; immunogenicity;
KW  Old World ape; Old World monkey; antigen-binding affinity.
XX
OS  Macaca cynomolgus.
XX
PN  WO9955369-A1.
XX
PD  04-NOV-1999.
XX
PF  28-APR-1999;  99WO-US09131.
XX
PR  28-APR-1998;  98US-0083367.
XX
PA  (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI  Taylor AH;
XX
DR  WPI; 2000-023265/02.
DR  N-PSDB; AAZ39340.
XX
PT  Antibodies containing donor complementarity determining regions and
PT  non-human primate acceptor frameworks, having reduced immunogenicity in
PT  humans -
XX
PS  Example 4; Page 96-97; 123pp; English.
XX
CC  The invention provides an antibody (Ab) comprising donor CDRs
CC  (complementarity determining regions) derived from a non-human antigen-
CC  specific donor antibody, and an acceptor framework from a non-human
CC  primate. The Abs are prepared by grafting CDRs from a non-human antigen-
CC  specific donor antibody onto homologous Old World ape or monkey acceptor
CC  frameworks. The Abs have reduced immunogenicity and are better tolerated
CC  in humans (because of the close similarity between the human and primate
CC  proteins), but retain the full antigen-binding affinity of the donor
CC  antibody.
XX
SQ  Sequence  130 AA;
```

```
alignment_scores:
        Quality:  563.00           Length:       129
          Ratio:    4.771            Gaps:         0
Percent Similarity:  91.473    Percent Identity:  86.047
```

```
alignment_block:
US-09-019-441-3 x AAY56737

Align seg 1/1  to: AAY56737  from: 1 to: 130

  1 ATGGACAATGAGGGTCCCCGCTCAGCTCCTGGGCGTCCTTCTGCTCTGGCT 50
    |||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeu 17

 51 CCCAGGTGCCAGAGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
    |||||||||||||||||||||||||||||||||||||||||||||||||
 17 uLeuGlyAlaArgCysAspIleMetThrGlnSerProSerSerLeuS 34
```

```
101 CTGCATCTGTAGGGACAGCAGTCACCATCACTTGCAGGCGCAAGTCAGGAC 150
    |||||||||||||||||||||||||||||||||||::::|||||||
 34 erAlaSerValGlyAspArgValThrIleThrCysGlnAlaSerGlnGly  50

151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    |||   :::|||  |||||||||||||||||||||||||||||||||||
 51 IleSerAsnTrpLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLy 67

201 GCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGT 250
    ||||||||||||::::::||||||||||||||||||||||||||||||
 67 sLeuLeuIleTyrValAlaSerThrPheGlnSerGlyValProSerArgP 84

251 TCAGCGGCAGTGGATCTGGACAGAGTTCACTCACCGTCACCGTCAGCCGCCTG 300
    |||||||||||||||||||||||||||||||::::|||||||
 84 heSerGlySerGlySerGlyThrGlyPheThrLeuThrIleSerSerLeu 100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACACAGTTTATAGTACCCC 350
    |||||||||||||||||||||||||||||||  ||  :::  ||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnThrTyrPr 117

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    |  ||||||||  ||||||||||||||||||||||
117 oLeuThrPheGlyGlyGlyThrLysValGluIleLys 129
```

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:AAR77614

```
seq_documentation_block:
ID  AAR77614 standard; protein; 236 AA.
XX
AC  AAR77614;
XX
DT  15-MAR-1996  (first entry)
XX
DE  Humanised 5G1.1 VL + 012.
XX
KW  Complement C5; haemolysis; kidney; glomerulonephritis;
KW  monoclonal antibody; antiinflammatory; antibody engineering;
KW  humanised antibody; complementarity determining region; CDR;
KW  ds.
XX
OS  Synthetic.
XX
FH  Key            Location/Qualifiers
FT  Peptide        1..23
FT                 /label= sig_peptide
FT  Peptide        23..236
FT                 /label= mat_peptide
FT  Region         47..57
FT                 /label= CDR-L1
FT  Region         73..79
FT                 /label= CDR-L2
FT  Region         112..120
FT                 /label= CDR-L3
XX
PN  WO9529697-A1.
XX
PD  09-NOV-1995.
XX
PF  01-MAY-1995;  95WO-US05688.
XX
PR  02-MAY-1994;  94US-0236208.
XX
PA  (ALEX-) ALEXION PHARM INC.
XX
PI  Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
PI  Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI  Wang Y, Wilkins JA;
XX
DR  WPI; 1995-392923/50.
DR  N-PSDB; AAT08486.
XX
PT  Treating glomerulonephritis with antibody against complement C5
```

PT   component   - to inhibit complement induced cell lysis
XX
PS   Claim 40; Page 132-34; 181pp; English.
XX
CC   A humanised CDR-grafted light chain, designated 5G1.1 VL + 012
CC   (AAR77614), includes CDRs derived from mouse anti-C5 monoclonal
CC   antibody 5G1.1.  DNA (AAT08486) coding for the light chain can be
CC   subcloned together with DNA (AAT08484) coding for a humanised Fd
CC   (AAR77611) into vector APEX-3P (AAT08476) for expression of humanised
CC   antibody in human 293 EBNA cells.  Such recombinant antibodies retain
CC   the ability of MAb 5G1.1 to block human complement C5a generation and
CC   thus to reduce glomerular inflammation and kidney dysfunction
CC   associated with glomerulonephritis.
XX
SQ   Sequence   236 AA;

alignment_scores:
         Quality:   562.00          Length:    129
         Ratio:     4.723           Gaps:      0
Percent Similarity: 92.248   Percent Identity: 85.271

alignment_block:
US-09-019-441-3 x AAR77614    ..

Align seg 1/1  to: AAR77614   from: 1  to: 236

   1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCT 50
     |||||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17

  51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
     | |||||||||||||||||||||||||||||||||||||||||||||||||
  17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34

 101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
     ||||||||||||||||||||||||||||||| |||||::::::|
  34 erAlaSerValGlyAspArgValThrIleThrCysGlyAlaSerGluAsn 50

 151 ATTAGGTATTATTTAAATTGGTATCAGCAGAAAACCAGGAAAAGCTCCTAA 200
     ||| |||||||||||||||||||||||||||||||||||||||||||||||
  51 IleTyrGlyAlaLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67

 201 GCTCCTGACCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGT 250
     ||||||||||||||||  ::|||||||||||||||||||||
  67 sLeuLeuThrTyrGlyAlaThrAsnLeuAlaAspGlyValProSerArgP 84

 251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCCGTCCAGCAGCCTG 300
     ||||||||||||||::|||||||||||||:::||||||||||
  84 heSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

 301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
     ||||||||||||||||||||||||||:::||| :::||||
 101 GlnProGluAspPheAlaThrTyrTyrCysLeuGlnValTyrSerThrPr 117

 351 TCGGACGTTCGGCCAAGGACCAAGGTGGAAATCAAA 387
     | |||||||||||||||||||||||||||||||||
 117 oLeuThrPheGlyGlnGlyThrLysValGlnIleLys 129

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:AAW03725

seq_documentation_block:
ID   AAW03725 standard; Protein; 171 AA.
XX
AC   AAW03725;
XX
DT   02-APR-1997  (first entry)
XX
DE   Humanised MAb 39-1.106 light chain variable region.
XX
KW   light chain; variable region; murine; mouse; anti-human; disease;
KW   glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma;
KW   diagnosis; inhibition; B-cell; activation; treatment; disorder;

---

KW   immune; autoimmune; allergic response; organ rejection; drug;
KW   graft versus host; cell imaging; tumour; targetted; delivery;
KW   targeted; humanised.
XX
OS   Mus musculus.
XX
FH   Key            Location/Qualifiers
FT   Misc-difference 2
FT                  /note= "corresponding codon TAG"
FT   Misc-difference 11
FT                  /note= "corresponding codon TAA"
FT   Misc-difference 157
FT                  /note= "corresponding codon TAA"
FT   Misc-difference 165
FT                  /note= "corresponding codon TAA"
XX
PN   WO9623071-A2.
XX
PD   01-AUG-1996.
XX
PF   26-JAN-1996;  96WO-US01119.
XX
PR   26-JAN-1995;  95US-0379057.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Aruffo AA,  Bajorath J,  Gilliland LK,  Gordon ML;
PI   Harris LJ,  Hollenbaugh D, Siadak AW;
XX
DR   WPI; 1996-362694/36.
DR   N-PSDB: AAT36018.
XX
PT   Monoclonal antibodies specific for different epitope(s) on human
PT   gp39 - used for inhibiting B cell activation and for the diagnosis
PT   of various disorders, e.g. cancer, psoriasis etc..
XX
PS   Example 13; Fig 16; 167pp; English.
XX
CC   The present sequence is the light chain variable region of the
CC   humanised murine anti-human glycoprotein (gp) 39 monoclonal
CC   antibody (MAb) 39-1.106. The MAb may be useful for diagnosing
CC   disease states, inhibiting B-cell activation and for treating
CC   immunological disorders, e.g. autoimmune disorders, allergic
CC   responses, organ rejection and graft versus host disease. It may
CC   also be used for imaging cells which express gp39 on their surface,
CC   e.g. tumour cells, and to target therapeutic agents to such cells.
CC   The MAb inhibits the CD40/gp39 interaction, therefore limiting both
CC   prim. and sec. responses to T-cell dependent antigens and Ab prodn.
CC   specific to these antigens. A typical compsn. for intramuscular
CC   injection pref. contains 50 mg of MAb in 1 ml of sterile buffered
CC   water.
XX
SQ   Sequence   171 AA;

alignment_scores:
         Quality:   557.00          Length:    129
         Ratio:     4.720           Gaps:      0
Percent Similarity: 91.473   Percent Identity: 83.721

alignment_block:
US-09-019-441-3 x AAW03725    ..

Align seg 1/1  to: AAW03725   from: 1  to: 171

   1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCT 50
     :::|||||||||||||||||||||||||||||||||||||||||||||||
  21 IleAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLe 37

  51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
     | ||||||||||||||||||||||||||||||||||||||||||||||||
  37 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 54

```
alignment_scores:
        Quality:  556.00                    Length:      129
          Ratio:    4.712                      Gaps:        0
Percent Similarity:  91.473    Percent Identity: 81.395

alignment_block:
US-09-019-441-3 x AAY56721

Align seg 1/1 to: AAY56721 from: 1 to: 129

  1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTCTGGCT 50
    |||||||||||||||||||||||||||||||||||||||||||::
  1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpPh 17

 51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCTGT 100
    :||||||||||||||||||:::||||||||||||||||||:::|||
 17 eProGlyAlaLysCysAspIleGlnMetThrGlnSerProSerThrLeuS 34

101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGCAAGTCAGGAC 150
    ||||||||:::|||||||||||||||||||||||||||||||
 34 erAlaSerIleGlyAspArgValThrIleThrCysArgAlaSerGlnGly 50

151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    ||| |||||||||||||||||||:::||||||
 51 IleTyrAsnTyrLeuAsnTrpTyrGlnGlnLysProGlyArgAlaProGl 67

201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGTCCCATCAAGGT 250
    ||||||||| || :||||::||||||::||||||||::|||||
 67 yLeuLeuIlePheGlyAlaArgAsnLeuGluThrGlyValProSerThrP 84

251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
    |||||||||||||||||||||:::||||||||||||:||:|||||
 84 heSerGlySerGlyThrGlyThrLeuThrIleSerSerLeu 100

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
    ||||| |||||||||||||||||||  || ||::|||||
101 GlnProGlyAspPheAlaThrTyrTyrCysGlnThrTyrThrThrPr 117

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    |  ||||||||||||||||||||||
117 oTyrThrPheGlyGlnGlyThrLysLeuGluIleLys 129


seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:AAR38162

seq_documentation_block:
ID  AAR38162 standard; protein; 234 AA.
XX
AC  AAR38162;
XX
DT  01-OCT-1993 (first entry)
XX
DE  Sequence of the kappa light chain variable region (VK) of human
DE  immunoglobulin G3 (IgG3) produced by transformed human B-cell line
DE  88BV59, ATCC CRL 10624.
XX
KW  B-cell; immunoglobulin g; cancer; tumour.
XX
OS  Homo sapiens.
XX
FH  Key               Location/Qualifiers
FT  Region            1..214
FT                    /*tag=  a
FT                    /label= 1st AA denoted AA#1
FT  Region            24..49
FT                    /*tag=  b
FT                    /label= CDR 1
FT  Region            50..88
FT                    /*tag=  c
FT                    /label= CDR 2
FT  Region            89..108
FT                    /*tag=  d
FT                    /label= CDR 3
```

```
101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAGGCAAGTCAGGAC 150
    |||||||||||||||||||||||||||||||||||||||||:::
 54 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGluThr 70

151 ATTAGGTAGTATTAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAA 200
    ||| ||||| |||||||||||||||||||:::||||||||||
 71 IleTyrSerTyrLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLy 87

201 GCTCCTGATCTATGTTGCATCCAGTTGCAAAGTGGGGTCCCATCAAGGT 250
    ||||||| ||:::||||  ::||||||||||||||||||
 87 sLeuLeuValTyrAsnAlaLysThrLeuAlaGluGlyValProSerArgP 104

251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
    |||||||||||||||||||:::||||||||||:::||||||||||
104 heSerGlySerGlyThrGlyThrAspPheThrLeuThrIleSerSerLeu 120

301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
    ||||||||||||||||||||||||||  ::: |||||:|||||
121 GlnProGluAspPheAlaThrTyrTyrCysGlnHisHisTyrAsnThrPr 137

351 TCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 387
    |  |||||| ||||||||||||||||||
137 oLeuThrPheGlyGlyGlyThrLysValGluIleLys 149


seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:AAY56721

seq_documentation_block:
ID  AAY56721 standard; protein; 129 AA.
XX
AC  AAY56721;
XX
DT  15-FEB-2000 (first entry)
XX
DE  Amino acid sequence of chimpanzee Vkappa cDNA clone 46-7.
XX
KW  Complementarity determining region; antibody; primate; immunogenicity;
KW  Old World ape; Old World monkey; antigen-binding affinity.
OS  Pan troglodytes.
XX
PN  WO955369-A1.
XX
PD  04-NOV-1999.
XX
PF  28-APR-1999;  99WO-US09131.
PR  28-APR-1998;  98US-0083367.
XX
PA  (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI  Taylor AH;
XX
DR  WPI; 2000-023265/02.
DR  N-PSDB; AA239324.
XX
PT  Antibodies containing donor complementarity determining regions and
PT  non-human primate acceptor frameworks, having reduced immunogenicity in
PT  humans -
XX
PS  Example 2; Page 63-64; 123pp; English.
XX
CC  The invention provides an antibody (Ab) comprising donor CDRs
CC  (complementarity determining regions) derived from a non-human antigen-
CC  specific donor antibody, and an acceptor framework from a non-human
CC  primate. The Abs are prepared by grafting CDRs from a non-human antigen-
CC  specific donor antibody onto homologous Old World ape or monkey acceptor
CC  frameworks. The Abs have reduced immunogenicity and are better tolerated
CC  in humans (because of the close similarity between the human and primate
CC  proteins), but retain the full antigen-binding affinity of the donor
CC  antibody.
XX
SQ  Sequence    129 AA;
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FT   Region          109..214
FT                   /*tag_    e
FT                   /label_ CON
XX
PN   EP546634-A.
XX
PD   16-JUN-1993.
XX
PF   09-DEC-1992;   92EP-0203827.
XX
PR   13-DEC-1991;   91US-0807300.
XX
PA   (ALKU ) AKZO NV.
XX
PI   Crichton V2, Haspel MV, Kobrin BJ;
XX
DR   WPI; 1993-190019/24.
DR   N-PSDB; AAQ43773.
XX
PT   Transformed human B-cell line for monoclonal antibody prodn. for
PT   cancer diagnosis - prepd from peripheral blood B-cells of cancer
PT   patients actively immunised with autologous tumour antigen, for
PT   treating cancers
XX
PS   Claim 9; Fig 3; 18pp; English.
XX
CC   The 88BV59 kappa light chain sequence is indicated by the posns.
CC   of the CDRs and the constant region exon. 88BV59 utilises Vx1 and
CC   Jx5. The first NH2 terminal 22 residues were confirmed by AA
CC   sequencing.
XX
SQ   Sequence     234 AA;
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alignment_scores:
           Quality:   555.50              Length:       127
           Ratio:      4.748              Gaps:           1
Percent Similarity:   92.126   Percent Identity:  86.614

alignment_block:
US-09-019-441-3 x AAR38162

Align seg 1/1  to: AAR38162   from: 1   to: 234

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  10 AGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGC  59
      |||  |||||||||||||||||||||||||||||||||||||||||||||
   1 ArgGlyProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAl  17

  60 CAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTG  109
      ||||||||||||||::||||||||||||||||    ||||||||||||||
  17 aArgCysAspIleGlnLeuThrGlnSerProSerPheLeuSerAlaSerV   34

 110 TAGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTAT  159
      |||||||||||||||||||||||||||||||||||||||   ||
  34 alGlyAspArgvalThrIleThrCysArgAlaSerGlnGlyIleSerSer  50

 160 TATTAAAATTGGTATCAGCAGAAACCAGGAAAAGCTCCTAAGCTCCTGAT  209
      |||||| ||||||||||||||||||||||||||||||||||||||||||
  51 TyrLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuI1  67

 210 CTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCCATCAAGGTTCAGCGGCA  259
      ||||::|||||||||||||||||||||||||||||||||||||||||||||
  67 eTyrAlaAlaSerLeuGlnSerGlyValProSerArgPheSerGlyS    84

 260 GTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAA  309
      ||||||||||||||||||::::||||||||||||||||||||||||||||
  84 erGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnProGlu  100

 310 GATTTTGCCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGG...AC  356
      ||||||||||||||||||||||  ||::::  |||||||||| |  | ||
 101 AspPheAlaThrTyrTyrCysLeuGlnLeuAsnGlyTyrProArgIleTh  117

 357 GTTCGGCCAAGGGACCAAGGTGGAAATCAAA  387
```